

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 15, 2004, 21:05:47 ; Search time 727 Seconds

(without alignments)  
3704.199 Million cell updates/sec

Title: US-10-729-807-10

Perfect score: 2763

Sequence: 1 MKRLLLCLEFFITFSAPPL.....SLSLFIQVHLLKNTSIQ 513

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame\_p2n.model -DEV=xlh  
-Q=/cgn2\_1/USPTO.spool/US10729807/runat\_15112004\_131726\_16835/app\_query.fasta\_1.711  
-DB=N Geneseq 23Sep04 -OFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10729807@cgn\_1\_1\_470 @runat\_15112004\_131726\_16835 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq 23Sep04:\*  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2763	100.0	1627	3 AAA37666	Aaa37666 Human pep
2	2763	100.0	1845	6 AAD23963	Aad23963 Human mac
3	2752	99.6	1542	8 ACB66740	Acdb66740 Secreted
4	2752	99.6	1542	12 ADQ10208	Adq10208 Human pol
5	2752	99.6	1647	4 AAS21339	Aas21339 Human cdn
6	2752	99.6	1647	8 ACA03698	Aca03698 cDNA enco

RESULT 1  
AAA37666  
ID AAA37666 standard; DNA; 1627 BP.  
XX  
AC AAA37666;  
XX  
DT 24-OCT-2000 (first entry)  
XX  
DE Human peptidase, HPEP-10 coding sequence.  
XX

KW Human; peptidase; cell proliferative disorder; arteriosclerosis;  
KW psoriasis; myelofibrosis; cancer; autoimmune disorder; Crohn's disease;  
KW inflammatory disorder; AIDS; anaemia; allergy; asthma; atherosclerosis;  
KW Grave's disease; multiple sclerosis; scleroderma; infection; diabetes;  
KW metabolic disorder; Addison's disease; cystic fibrosis; diagnosis;  
KW glycogen storage disease; obesity; therapy; HPEP-10; ds.  
XX  
OS Homo sapiens.

Key Location/Qualifiers  
CDS 24..1565  
FT /\*tag= a  
FT /product= "HPEP-10"

XX WO2000042201-A2.  
XX  
XX 20-JUL-2000.  
XX  
XX 11-JAN-2000; 2000WO-US000641.  
XX

#### ALIGNMENTS

Abx89236 DNA enco  
Acd41890 Human sec  
Aca04119 Human cdn  
Ada45710 Novel hum  
Ada76141 Human PRO  
Ada18791 Human PRO  
Ada61414 Homo sapi  
Adb19199 Novel hum  
Adb27740 cDNA enco  
Ada86219 Novel hum  
Ada75589 Human PRO  
Ada47569 Human PRO  
Ada67364 Human PRO  
Adb30371 cDNA enco  
Ada85667 Novel hum  
Ada96879 Human PRO  
Ada79183 Human PRO  
Ada87322 Novel hum  
Ada76524 Human PRO  
Ada91616 Novel hum  
Adb14679 Human PRO  
Adb18640 Novel hum  
Ada93855 Human PRO  
Adb19751 Novel hum  
Adb13063 Human PRO  
Acd98519 Novel hum  
Ada74317 Human PRO  
Adb44550 Human PRO  
Ada82074 Human PRO  
Ada75037 Human PRO  
Ada85115 Novel hum  
Ada84563 Novel hum  
Adb29819 cDNA enco  
Ada80347 Human PRO  
Ada75589 Human PRO  
Ada46814 Human PRO  
Adb25110 Human PRO  
Ada93286 Human PRO  
Adb26636 cDNA enco







QY 321 PheTrrProSerLeuProAlaAspLeuGlnAlaalaTyrGluAsnProArgAspLysile 340  
Db 984 TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACAGAGAACCCAGAGATTAAGATT 1043  
QY 341 LeuValPheLysAspGluAsnPheTrrMetIleArgGlyTyrAlaValLeuProAspTyr 360  
Db 1044 CTGGTTTTAAAGATGAAGAACTCTGGATGATCAGAGATATGCTGCTGCCAGATTAT 1103  
QY 361 ProllysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal 380  
Db 1104 CCCAAATCCATCCATACATTAAGTTTCCAGAGCTGTGAAGAAATAGATGACGCCGTC 1163  
QY 381 CysAspLysThrThrArgGlyThrTyrPheValGlyIleTrrCysTrrArgPheAsp 400  
Db 1164 TGTGATAGACCAACAAGAAACCTACTTCTTGTGGCATTTGCTGCTGAGTTTGAT 1223  
QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly 420  
Db 1224 GAAATGACCCAAACCATGGACAAAGGATTCCTCCGACAGAGTGGTAAACACTTTCCTGGA 1283  
QY 421 IleSerIleArgValAspAlaPheGlnTrrLysGlyPhePhePheSerArgGly 440  
Db 1284 ATCAGTATCCGTGTGTGCTGCTTCCAGTACAAAGGATTCCTTTTTCAGCGGTGGA 1343  
QY 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460  
Db 1344 TCAAGCAATTTGAATACACATTAAGACAAAGATATATCCCGATCATGAGACTAAT 1403  
QY 461 ThrTrrPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480  
Db 1404 ACTTGGTTTCAATGCAGAAACCAAGAACTCTCATTTGGTTTGTATATCAACAAGAA 1463  
QY 481 LysAlaHisSerGlyGlyIleLysIleLeuTrrHisLysSerLeuSerLeuPheIlePhe 500  
Db 1464 AAAGCACATTCAGGAGGCATAAAGATATTTGTATCATAGAGTTTAAAGCTTGTATTTT 1523  
QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleTrrGln 513  
Db 1524 GGTATTGTTTCTTCTGTAAGAAACACTTCTATTATCAAA 1562  
RESULT 3  
ACD66740  
ID ACD66740 standard; cDNA; 1542 BP.  
XX AC ACD66740;  
XX DT 17-SEP-2003 (first entry)  
XX DE Secreted polypeptide-related cDNA #31.  
XX Human; gene; ss; TANGO; INTERCEPT; secreted polypeptide; immune disorder;  
KW hormonal disorder; proliferative disorder; cancer; thyroid disorder;  
KW diabetes; multiple sclerosis; lupus; neurological disorder; anaemia;  
KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;  
KW myocardial infarction; congestive heart disease; blood platelet disorder;  
KW thrombocytopenia; blood vessel; atherosclerosis; vasculitis.  
XX  
OS Homo sapiens.  
XX  
PN US2003022279-A1.  
XX  
PD 30-JAN-2003.  
XX  
PF 12-JAN-2001; 2001US-00759130.  
XX  
PR 14-JUN-1999; 99US-00333159.  
PR 29-JUN-1999; 99US-00342364.  
PR 10-SEP-1999; 99US-00393996.  
PR 19-OCT-1999; 99US-00420707.  
PR 07-JAN-2000; 2000US-00479249.  
PR 27-APR-2000; 2000US-00559497.  
PR 24-MAY-2000; 2000US-00578063.  
PR 16-JUN-2000; 2000US-00596194.

23-JUN-2000; 2000US-00602871.  
30-JUN-2000; 2000US-00608452.  
(FRAS)/ FRASER C C.  
(BARN)/ BARNES T M.  
(SHAR)/ SHARP J D.  
(KIRS)/ KIRST S J.  
(MYER)/ MYERS P S.  
(LEIB)/ LEIBY K R.  
(HOLT)/ HOLTZMAN D A.  
(MCCA)/ MCCARTHY S A.  
(WRIG)/ WRIGHTON N.  
(MACK)/ MACKAY C R.  
(GOOD)/ GOODEARL A D J.  
Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;  
Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;  
WPI; 2003-456290/43.  
P-PSDB; ABO32578.  
New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,  
TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or  
treating disorders such as cancer, diabetes or atherosclerosis, and in  
forensic biology.  
Claim 2; Fig 15A-15D; 482pp; English.  
The invention relates to secreted polypeptide-related proteins and  
nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The  
nucleic acids, proteins and antibodies specific to the proteins are  
useful in screening assays, predictive medicine (e.g. diagnostic assays,  
prognostic assays, monitoring clinical trials and pharmacogenetics) and  
prophylactic and therapeutic methods. The sequences are used in  
diagnosing, preventing or treating proliferative disorders (e.g.  
cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune  
disorders (e.g. multiple sclerosis or lupus), neurological disorders  
(e.g. Alzheimer's disease or Parkinson's disease), cardiovascular  
disorders (e.g. myocardial infarction or congestive heart disease), blood  
platelet disorders (e.g. thrombocytopenia or anaemia) and disorders  
involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic  
acids may also be used in chromosome mapping, tissue typing and forensic  
biology, and as surrogate markers. This sequence represents a secreted  
polypeptide-related cDNA of the invention. Note: The sequence data for  
this patent was obtained in electronic format directly from USPTO at  
seqdata.uspto.gov/sequence.html  
XX  
SQ Sequence 1542 BP; 447 A; 322 C; 334 G; 439 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1,49e-294 Length: 1542  
Score: 2752.00 Matches: 512  
Percent Similarity: 99.81% Conservative: 0  
Best Local Similarity: 99.81% Mismatches: 1  
Query Match: 99.60% Indels: 0  
DB: 8 Gaps: 0  
US-10-729-807-10 (1-513) x ACD66740 (1-1542)  
QY 1 MetLysArgLeuLeuLeuLeuLeuCysLeuPhePhePheThrPheSerSerAlaPheProLeu 20  
Db 1 ATGAAGCGCTTCTGCTTCTGTTTGTCTTATACATTTCTCTGCAATTCCTCCCTTA 60  
QY 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTrrLysAsnGlnPhe 40  
Db 61 GTCCGGATGACGGAAATGAAGAAATATGCACTGGCTCAGGCATATCTCAACAGTTC 120  
QY 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60  
Db 121 TACTCTCTGAAATAGAGGGAATCATCTTGTTCAGGCAAGCAATAGGAGTCTCATAGAT 180  
QY 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80

Db 181 GACAAAATTCGGAAATGCAAGCAATTTTGGATTGACAGTGAAGAACTGGAACTCA 240  
 Qy 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
 Db 241 AACACCTTTGAGATCATGAAGACACCCAGGTGGGGTCCCTGATGTGGCCAGATGGC 300  
 Qy 101 TyrThrLeuProGlyTyrPArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120  
 Db 301 TACACCTCCCTGGTGGGAGAAATACACCTCACCTACAGATAATAAATACTACTCG 360  
 Qy 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140  
 Db 361 GATATGGCAGCAGCTGCTGTGATGAGGTATCCAAAGAGGTTTAAAGTGTGAGCAAA 420  
 Qy 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160  
 Db 421 GTCACCTCCACTAAATTCACCAAGATTTCAAGGGGATTCAGACATCATGATTTGCCTTT 480  
 Qy 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180  
 Db 481 AGGACTCGAGTCCATGTCGGTCTCTCGCTATTTTGATGGTCCCTTGGGAGTGTGGC 540  
 Qy 181 HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200  
 Db 541 CATGCCCTTCTCTGCTGGTCCGGTCTGGGTGTGACACTCATTTTCATGAGGATGAAAAC 600  
 Qy 201 TrpThrLysAspGlyValaglyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220  
 Db 601 TGGACCAAGATGGAGCAGATTCACCTGTTTCTGTGGCTCATGAATTTGGTCAAT 660  
 Qy 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240  
 Db 661 GCACCTGGGCTCTCTCACTCCATGATCAACAGCCTTGATGTTCCCAAAATATGTCCTC 720  
 Qy 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260  
 Db 721 CTGGATCCAGAAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 780  
 Qy 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280  
 Db 781 GGAGTCTGCCCTAAGTACTCTAAGCCAAAGAACCCACTATACCCCATGCCCTGTGAC 840  
 Qy 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300  
 Db 841 CCTGACTTGACTTTTGACGCTATCACACTTTCCGACAGAGATGATGTTCTTTAAAGC 900  
 Qy 301 ArgHisLeuThrPArgIleTyrThrAspIleThrAspValGluPheGluLeuIleAlaSer 320  
 Db 901 AGGCACCTATGAGGATCTATTATGATATCAGGATGTTGAGTTTCAATTAATTTGCTTCA 960  
 Qy 321 PheTrpProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnProArgAspLysIle 340  
 Db 961 TTTCTGGCATCTCTGCCAGCTGATCTGCAAGCTGATACGAGAACCCAGAGATAGATTT 1020  
 Qy 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360  
 Db 1021 CTGGTTTTTAAGATGAAACTCTGGATGATCAGAGATGCTGTCTGCCAGATAT 1080  
 Qy 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380  
 Db 1081 CCCAAATCCATCCATACATATAGTGTTCAGGACGTGTGAGAAAATATAGTCAGCCGTC 1140  
 Qy 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400  
 Db 1141 TGTGATAAGACACCAAGAAAACCTACTCTTTTGTGGCATTTGTGCTGGAGGTTTGTAT 1200  
 Qy 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420  
 Db 1201 GAAATGACCCAAACCATGACAAAGGATTCCTCCGACAGAGATGTTAAACACTTTTCTCTGA 1260  
 Qy 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440  
 Db 1261 ATCAGTATCCGTGTTGATGCTGCTTCCAGTACAAAGGATTTCTTTTTCAGCCGTGA 1320

Qy 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460  
 Db 1321 TCAGAAGCAATTTGAATACACATTAAGACAAAGAAATATTACCCGAATCATGAGAACTAAT 1380  
 Qy 461 ThrTrpPheGlnCysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480  
 Db 1381 ACTTGGTTTCAATGCAAGAACCAAGAACTCTCATTTGGTTTTCATATCAACAAGGAA 1440  
 Qy 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500  
 Db 1441 AAAGCACATTCAGGAGGCATTAAGATATTGTATCATATAAGAGTTTAAGCTTGTATTATTTT 1500  
 Qy 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513  
 Db 1501 GGTATTGTTTCATTGCTGAAAACACACTTCTATTATTCAA 1539  
 RESULT 4  
 ADQ10208  
 ID ADQ10208 standard; cDNA; 1542 BP.  
 XX  
 AC ADQ10208;  
 XX  
 DT 09-SEP-2004 (first entry)  
 XX  
 DE Human polynucleotide #31.  
 XX  
 KW Human; gene; ss; cancer; obesity; gastritis; diarrhea; haemorrhoid;  
 KW asthma; anaemia; graft-versus-host reaction; allergic reaction;  
 KW cystic fibrosis; hypogonadism; cardiovascular disorder; arthritis;  
 KW osteoarthritis; arteriosclerosis; hypertension; bacterial infection;  
 KW psoriasis; diabetes mellitus; hepatitis; Alzheimer's disease;  
 KW Huntington's disease; Parkinson's disease; AIDS; tuberculosis;  
 KW viral infection; malaria; goiter; infertility; endometriosis;  
 KW muscular disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2004121396-A1.  
 XX  
 PD 24-JUN-2004.  
 XX  
 PF 19-DEC-2003; 2003US-00741790.  
 XX  
 PR 14-JUN-1999; 99US-00333159.  
 PR 29-JUN-1999; 99US-00342364.  
 PR 10-SEP-1999; 99US-00393996.  
 PR 19-OCT-1999; 99US-00420707.  
 PR 07-JAN-2000; 2000US-00479249.  
 PR 27-APR-2000; 2000US-00559497.  
 PR 24-MAY-2000; 2000US-00578063.  
 PR 16-JUN-2000; 2000US-00596194.  
 PR 23-JUN-2000; 2000US-00602871.  
 PR 30-JUN-2000; 2000US-00608452.  
 PR 12-JAN-2001; 2001US-00759130.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;  
 PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;  
 XX  
 DR WPI; 2004-479675/45.  
 XX  
 PT New TANGO, INTERCEPT, and MANGO, useful in diagnosing, preventing, and  
 PT treating cancer, constipation, hemorrhoids, cystic fibrosis,  
 PT hypogonadism, psoriasis, hepatitis, Alzheimer's disease, AIDS,  
 PT tuberculosis, malaria, goiter, infertility.  
 XX  
 PS Claim 2; SEQ ID NO 172; 483pp; English.  
 XX  
 CC The invention relates to human polynucleotides and the polypeptides they  
 CC encode. The invention also relates to a host cell containing a  
 CC polynucleotide of the invention, an antibody which selectively binds with

Qy	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
Db	661	GCACGGGGCTCTCTCACTCCAAATGATCAACAGCCCTTGATGTTCGCAAAATTATGCTCC	720
Qy	241	LeuAspProArgIysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr	260
Db	721	CTGGATCCCAAGAAAAACCCACATTTCTCAGATGATCAATGGAAATCCAGTCCCATCTAT	780
Qy	261	GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp	280
Db	781	GGAGGTCTGCTAAGGTACCTGCTAAGCCAAAGAAACCCACATATACCCCATGCTGTGAC	840
Qy	281	ProAspLeuThrPheAspAlaIleThrThrPheArgGlnValMetPhePheLysGly	300
Db	841	CCTGACTGTACTTTTGACGCTATCAACAATTTCCGCAGAGAAAGTAATGTTCITTAAGGC	900

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Qy	321	PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle	340
Db	961	TTCTGGCCATCTCTGCAGCTGATCTCGAAGCTGCATACGAGAACCCAGAGATRAAGATT	1020
Qy	341	LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr	360

[illegible]

381	CCCAATCCATCCATCATTAGT	TTTCCAGGACGCTGTGAAGAAATAGATG	CAGCGGTC	1140
Db				
Qy	CysAspLysThrThrArgLysThrTy	PrPhePheValGlyIleTrpCys	TrpArgPheAsp	400
Db	TGTGATAGACCAACAGAAAA	CCTACTCTTTGTGGCATTTGGT	GCTGGAGGTTTGAT	1200
Qy	GluMetThrGlnThrMetAspLys	GlyPheProGlnArgValValLys	HisPheProGly	420
Db	GAATGACCCAAACCATGGACA	AAAGGATTTCCCGCAGAGAGTGT	ATAAACACATTTCTCTGGA	1260
Qy	IleSerIleArgValaspAlaAla	PheGlnTyrLysGlyPhePhePhe	PheSerArgGly	440
Db	ATCAGTATCCGTGTGATGCTGT	CTTCCAGTACAAAGGATCTCT	TTTTTCAGCCCGTGA	1320
Qy	SerLysGlnPheGluTyrAsnIle	LysThrLysAsnIleThrArgIle	MetArgThrAsn	460

D6	L321	TCAAAGCAATTTGGATACATATAGACAAAGGATATATACCCGAAATCATGAGAGACAA	1380
Qy	461	ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu	480
D6	1381	ACTTGGTGTTCATATGTCAAAGAAACCAAGAACTCCTCATTTGGTTTGATATCAACAAGAA	1440
Qy	481	LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe	500
D6	1441	AAAGCACAATTCAGAGGACATAAGATATTGTATCAAGAGAGTTTAAGCTTGTTTATTTT	1500
Qy	501	GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln	513
D6	1501	GGTATTGTTTCATTTGCTGAAAAACACTTCATTATTATCAA	1539
RESULT 5			
AAS21339			
ID	AAS21339 standard; cDNA; 1647 BP.		
XX			

XX  
DT  
XX  
XX  
DE  
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XX

24-OCT-2001 (first entry)

Human cDNA sequence encoding for PRO5992 polypeptide.

XX  
XX  
KW  
KW  
KW

Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;  
prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;

XX DE Human cDNA sequence encoding for PRO5992 polypeptide.

Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor- $\alpha$ ; TNF- $\alpha$ ; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; KW



```
QY 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260
DB 744 CTGGATCCAGAAAAATACCCACTTCTCAGGATGATATCAATGAAATCCAGTCCATCTAT 803
QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
DB 804 GGAGGCTGCTAAGGTACCTGCTAAGCCAAAGAACCCACTATACCCATGCTGTGAC 863
QY 281 ProAspLeuThrPheAspAlaIleThrPheArgArgGluValMetPhePheLysGly 300
DB 864 CCTGACTGACTTTTGACGCTATCACAACTTTCGCGAGAGAAGTAATGTTCTTTAAAGGC 923
QY 301 ArgHisLeuTrpArgIleTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
DB 924 AGGCACCTATGGAGGATCTATTATGATATCACGGATGTTGAGTTGAAATTAATTTGCTCA 983
QY 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340
DB 984 TTCTGGCCATCTCTGCCAGTGTATCTGCAAGCTGCATACGAGAACCCAGAGATAGATT 1043
QY 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
DB 1044 CTGGTTTTTAAAGATGAAAACTTCTGGATGATCAGAGGATGCTGTCTTGCAGATTAT 1103
QY 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380
DB 1104 CCCAAATCCATCCATACATATGAGTTTTCAGGACGCTGTGAAGAAATAGATGAGCGGTC 1163
QY 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTrpAlaGlyPheAsp 400
DB 1164 TGTGTAAGACCAACAAGAAACCTACTTCTTTGTGGGCATTTGGTCTGGAGTTTGAT 1223
QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
DB 1224 GAAATGACCCAAACCATGGACAAAGGATTCGCGCAGAGAGTGGTAAACACTTTCCTGGA 1283
QY 421 IleSerIleArgValAspAlaAlaPheGlnTyrIlyGlyPhePhePheSerArgGly 440
DB 1284 ATCAGTATCCGTGTGATGCTGCTTCCAGTACAAAGGATTTCTTTTTTCAGCCCGGGA 1343
QY 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
DB 1344 TCAAGCAATTTGAATACACATTTAGACAAAGAAATATACCCGAATCATGAGAACTAAT 1403
QY 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
DB 1404 ACTTGGTTTCAATGCAAGAAACCAAGAACTCCTCATTTGGTTTGTATATCAACAGGAA 1463
QY 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
DB 1464 AAAGCAATTCAGAGGCATAAAGATATGTATCATAGAGTTTAAGCTTGTATTATTTT 1523
QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
DB 1524 GGTATTGTTTCATTGCTGAAAAACACTTCTATTATCA 1562

RESULT 6
ACAD3698
ID ACA03698 standard; cDNA; 1647 BP.
XX
AC ACA03698;
XX
DT 23-MAY-2003 (first entry)
XX
DE cDNA encoding human PRO polypeptide #96.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;
KW differentiation; chondrocyte; tumour; genetic disorder; cytosolic; gene;
KW ss.
XX
OS Homo sapiens.
```







```
Db      984  TTCTGCCCTCTCTGCCAGCTGATCTCAAGCTGCATACAGAACCCCGAGATAAGATT 1043
Qy      341  LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
Db      1044  CTGGTTTAAAGATGAAATCTTCTGGATGATCAGAGGATATGCTGCTTGCAGATTAT 1103
Qy      361  ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380
Db      1104  CCCAATCCCATCATACATAGGTGTTTCCAGGACGTGTGAAGAAATAGATGAGCCGTC 1163
Qy      381  CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpA:gpPheAsp 400
Db      1164  TGTGATAAGACCAACAGAAAACCTACTTCTTTGTGGGCATTTGGTCTGGAGGTTTGTAT 1223
Qy      401  GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly 420
Db      1224  GAAATGACCCCAACCATGGAACAAAGGATTCCTCCGACAGAGCTGGTAAACACTTTCCTGGA 1283
Qy      421  IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
Db      1284  ATCAGTATCCGTGTGATGCTGCTTCCAGTACAAAGGATCTCTCTTTTCAGCCGTTGA 1343
Qy      441  SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
Db      1344  TCAAGCAATTTGAATACAACTTAAGACAAAGATATTACCCGAATCATGAGAACTAAT 1403
Qy      461  ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
Db      1404  ACTTGGTTTCAATGCAAAAGAACCAAGAACTCTCTCATTTGGTTTGTATATCAACAAGAA 1463
Qy      481  LysAlaHisSerGlyGlyIleLysIleLysThrLysLysSerLysSerLeuPheIlePhe 500
Db      1464  AAGACCATTCAGGAGGCAATGAAGATATTGTATCAAGATTTTAACTTGTATTATTTT 1523
Qy      501  GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
Db      1524  GGTATTGTTTCTTTGCTGAAACAACTCTTATTATCA 1562

RESULT 7
ABX89236
ID      ABX89236 standard; cDNA; 1647 BP.
XX
AC      ABX89236;
XX
DT      13-MAY-2003 (first entry)
XX
DE      DNA encoding novel secreted and transmembrane protein PRO5992.
XX
KW      Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW      cardiac insufficiency disorder; cancer; tumour; immune response;
KW      adrenal cortical capillary endothelial growth; c-fos induction;
KW      vascular endothelial growth factor inhibition; VEGF inhibition;
KW      endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW      retinal neurons cell survival; rod photoreceptor cell survival;
KW      retinal disorder; retinitis pigmentosa; kidney disorder;
KW      mammalian kidney mesangial cell proliferation; Berger disease;
KW      dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW      chondrocyte redifferentiation; sports injury; arthritis; gene; ss.
XX
OS      Homo sapiens.
XX
PN      US2003017563-A1.
XX
PD      23-JAN-2003.
XX
PF      07-MAY-2002; 2002US-00140808.
XX
PR      31-MAR-1997; 97WO-US005230.
PR      12-JUN-1998; 98WO-US012456.
PR      14-JUL-1998; 98WO-US014552.
PR      28-AUG-1998; 98WO-US017888.
PR      10-SEP-1998; 98WO-US018824.
PR      14-SEP-1998; 98WO-US019093.
PR      98WO-US019094.
PR      98WO-US019177.
PR      98WO-US019330.
PR      98WO-US019437.
PR      98WO-US021141.
PR      98WO-US022991.
PR      98WO-US022992.
PR      98WO-US024855.
PR      98WO-US025108.
PR      99WO-US000106.
PR      99WO-US0005028.
PR      99WO-US0005190.
PR      99WO-US0008615.
PR      99WO-US010733.
PR      99WO-US012252.
PR      99WO-US020111.
PR      99WO-US020594.
PR      99WO-US020944.
PR      99WO-US021547.
PR      99WO-US021090.
PR      99WO-US023089.
PR      99WO-US028214.
PR      99WO-US028313.
PR      99WO-US028409.
PR      99WO-US028301.
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PR      99WO-US028565.
PR      99WO-US030095.
PR      99WO-US030911.
PR      99WO-US030999.
PR      99WO-US030720.
PR      99WO-US031243.
PR      99WO-US031274.
PR      2000WO-US000219.
PR      2000WO-US000277.
PR      2000WO-US000376.
PR      2000WO-US000356.
PR      2000WO-US000341.
PR      2000WO-US000434.
PR      2000WO-US000442.
PR      2000WO-US000491.
PR      2000WO-US005004.
PR      2000WO-US005601.
PR      2000WO-US005746.
PR      2000WO-US005841.
PR      2000WO-US006319.
PR      2000WO-US006884.
PR      2000WO-US007377.
PR      2000WO-US007532.
PR      2000WO-US008439.
PR      2000WO-US013705.
PR      2000WO-US014042.
PR      2000WO-US014941.
PR      2000WO-US015264.
PR      2000WO-US020710.
PR      2000WO-US022031.
PR      2000WO-US023522.
PR      2000WO-US023328.
PR      2000WO-US030952.
PR      2000WO-US030873.
PR      2000WO-US032678.
PR      2000US-00747259.
PR      2000WO-US034956.
PR      2001US-00796498.
PR      2001WO-US006520.
PR      2001WO-US006666.
PR      2001US-00802706.
PR      2001US-00806689.
PR      2001US-00816744.
PR      2001US-00828366.
PR      2001US-00854208.
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10-MAY-2001; 2001US-00854280.  
 PR 18-MAY-2001; 2001US-00860216.  
 PR 25-MAY-2001; 2001US-00866028.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 01-JUN-2001; 2001US-00870992.  
 PR 01-JUN-2001; 2001US-00872035.  
 PR 01-JUN-2001; 2001US-00871800.  
 PR 05-JUN-2001; 2001US-00874503.  
 PR 14-JUN-2001; 2001US-00882636.  
 PR 19-JUN-2001; 2001US-00886342.  
 PR 20-JUN-2001; 2001US-00891992.  
 PR 21-JUN-2001; 2001US-00887879.  
 PR 22-JUN-2001; 2001US-00820116.  
 PR 29-JUN-2001; 2001US-00821066.  
 PR 09-JUL-2001; 2001US-00821735.  
 PR 18-JUL-2001; 2001US-00908827.  
 PR 06-AUG-2001; 2001US-00924419.  
 PR 09-AUG-2001; 2001US-00927796.  
 PR 16-AUG-2001; 2001US-00931836.  
 PR 19-DEC-2001; 2001US-00028072.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI: 2003-148238/14.  
 DR P-PSDB; ABUS9746.  
 XX  
 Two hundred and seventy five nucleic acids encoding PRO polypeptides,  
 PT useful for treating pericyte-associated tumors, diabetes and various bone  
 PT and/or cartilage disorders, e.g. arthritis.  
 XX  
 PS Claim 2; Fig 191; 659pp; English.  
 XX  
 The invention describes an isolated human PRO polypeptide. The PRO  
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
 CC in modulating at least one biological activity of a cell expressing a PRO  
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
 CC stimulate adrenal cortical capillary endothelial growth, and PRO126,  
 CC PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
 CC useful for treating conditions or disorders where angiogenesis would be  
 CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
 CC useful for treating cancerous tumours. PRO812 inhibits vascular  
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
 CC cells and is thus useful for inhibiting endothelial cell growth in  
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
 CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
 CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
 CC rod photoreceptor cells) and therefore are useful for treating retinal  
 CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
 CC and therefore are useful for treating kidney disorders associated with  
 CC decreased mesangial cell function such as Berger disease or other  
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
 CC proliferation and/or re differentiation of chondrocytes in culture and are  
 CC thus useful for treating sports injuries, and arthritis. This sequence  
 CC encodes a novel human PRO protein  
 XX  
 SQ Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;  
 XX

## Alignment Scores:

Pred. No.: 1.64e-294 Length: 1647  
 Score: 2752.00 Matches: 512  
 Percent Similarity: 99.81% Conservative: 0  
 Best Local Similarity: 99.81% Mismatches: 1

Query Match: 99.60% Indels: 0  
 DB: 8 Gaps: 0  
 US-10-729-807-10 (1-513) x ABX89236 (1-1647)  
 QY 1 MetLysArgLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeu 20  
 DB 24 ATGAAGCGCTTCTGCTTCTGTTTCTTTTATAACATTTTCTCTGCAATTCCTTA 83  
 QY 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrIleuAsnGlnPhe 40  
 DB 84 GTCCGGATGACGGAAATGAGAAATATGCAACTGGCTCAGGCATATCTCAACCACTTC 143  
 QY 41 TyrSerLeuGluIleGluGluYasnHisLeuValGlnSerLysAsnArgSerIleuLeasp 60  
 DB 144 TACTCTCTTGAATAGAAGGGAATCATCTGTTCANAGCAAGATAGGAGTCTCATAGAT 203  
 QY 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
 DB 204 GACAAATTCGGAAATGCAAGCATTTTTCGATTGACAGTGTGGAACCTGGACTCA 263  
 QY 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
 DB 264 AACACCTTTGAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGCCAGTATGGC 323  
 QY 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120  
 DB 324 TACACCTCTCCCTGGGTGGAGAAATACACCTCACCTACAGAAATATAAATATATCTCG 383  
 QY 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140  
 DB 384 GATATGGCAGCGCTGCTGTGGATGAGCTATCCAAAGAGGTTTAGAAGTGTGGAGCAA 443  
 QY 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160  
 DB 444 GTCACTCCCAATAATTCACCAAGATTTCAAAGGGGATTCAGACATCATGATTCGCTTT 503  
 QY 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180  
 DB 504 AGGATCCAGTCCATGGTGGTGGTCTCGCTATTTTGATGGTCCCTGGGAGTGTGGC 563  
 QY 181 HisAlaPheProGlyProGlyLeuGlyAspThrHisPheAspGluAspGluAsn 200  
 DB 564 CATGCTTTCTCTCTGGTCCGGTCTGGGTGGTGGTGCATCTATTTGATGAGATGAAAC 623  
 QY 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGlnPheGlyHis 220  
 DB 624 TGGACCAAGGATGGAGCAGGATTCAACTGTTTCTTGTGGTGTCTCATGAATTTGGTCAT 683  
 QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240  
 DB 684 GCATGGGGCTCTCTCACTCAATGATCAACAGCCTTGATGTTCCCAAAATATGTTCTCC 743  
 QY 241 LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr 260  
 DB 744 CTGGATCCAGAAATACCCACTTCTCAGGATGATATCAATGGATCCAGTCCATCTAT 803  
 QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280  
 DB 804 GGAGGTCTGCTTAAGGTACCTGCTAAAGCAAAGGAACCCACTATACCCCATGCTGTGAC 863  
 QY 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300  
 DB 864 CTTGACTTGTCTTTGACGCTATCACAACTTTCCGACAGAGTAATGTTCTTTAAAGGC 923  
 QY 301 ArgHisLeuTyrArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320  
 DB 924 AGGCACCTATGAGGATCTATATGATATCAGGAATGTTGAGTTTGAATTAATTCCTCA 983  
 QY 321 PheTrpProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnProArgAspLysIle 340  
 DB 984 TTCTGGCCATCTCTGCCAGTCTGCTGCAAGCTGCATACGAGAACCCACAGAGATAAGATT 1043

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QY 341 LeuValPheLysAspGluAenPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
Db 1044 CTGGTTTTTAAAGATGAAACTTCTGGATGATCAGAGATATGCTGTCGCCAGATTAT 1103
QY 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal 380
Db 1104 CCCAAATCCATCATCATATTAGGTTTTCCAGGACGTTGAAGAAATAGATGCAGCCGTC 1163
QY 381 CysAspLysThrThrArgLysThrPhePheValGlyIleTrpCysTrpArgPheAsp 400
Db 1164 TGTGATAAGACCAAGAAACCTACTCTTTGTGGGCATTTGGTGCTGGAGTTTGAT 1223
QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly 420
Db 1224 GAATGACCCCAACCATCGACAAAGGATTCGCCAGAGATGTTAAACACTTTCCTGGA 1283
QY 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
Db 1284 ATCAGTATCCGTGTGTGATGCTGCTTTCAGTACAAAGGATCTCTTTTCAGCCGTGA 1343
QY 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
Db 1344 TCAAGCAATTTCAATACAAACATTAAGACAAAGATATTACCCGAATCATGAGAACTAAT 1403
QY 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
Db 1404 ACTGGTTTCATGCAAGAACCAAGAACTCTCATTTGGTTTGTATCAACAGGAA 1463
QY 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
Db 1464 AAAGCATTCCAGAGGCATAAAGATATTGTATCATAAAGATTTAAGCTTTGTTATTTT 1523
QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
Db 1524 GGTATTGTTCAATTGCTGTAAGAAACACTTCTATTATCA 1562

RESULT 8
ACD41890
ID ACD41890 standard; cDNA; 1647 BP.
XX
AC ACD41890;
XX
DT 05-SEP-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) cDNA #96.
XX
KW Human; ss; gene; PRO; secreted protein; transmembrane protein; tumour;
KW cytosolic; gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood;
KW proteoglycan; cartilage; cytokine; peripheral blood mononuclear cell;
KW BMC; glucose uptake; FFA; skeletal muscle cell; adipocyte cell;
KW chondrocyte cell proliferation; chondrocyte cell differentiation;
KW pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell;
KW endothelial cell; A-peptide; factor VIIa.
XX
OS Homo sapiens.
XX
PN US2003036179-A1.
XX
PD 20-FEB-2003.
XX
XX 10-MAY-2002; 2002US-00142431.
XX
PR 31-MAR-1997; 97WO-US0005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
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PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 03-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
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[illegible]



Db	1044	CTGGTTTTTAAAGATGAACCTTCGTGATGATCAGAGGATATGCTGTCTTCCAGATTAT	1103	PR	29-OCT-1998;	98WO-US022991.
				PR	29-OCT-1998;	98WO-US022992.
				PR	20-NOV-1998;	98WO-US024855.
Qy	361	ProlysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal	380	PR	01-DEC-1998;	98WO-US025108.
				PR	05-JAN-1999;	98WO-US000106.
Db	1104	CCCAATCCATCCATACATAGGTTTTCCAGACGCTGTGAAGAAATAGATGCAGCCGTC	1163	PR	08-MAR-1999;	98WO-US005028.
				PR	10-MAR-1999;	98WO-US005190.
Qy	391	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTyrPArgPheAsp	400	PR	20-APR-1999;	98WO-US008615.
				PR	14-MAY-1999;	98WO-US010733.
Db	1164	TGTGATAGACCAACAGAAAACCTACTCTTTGTGGCAATTTGGTGTGGAGGTTTGAT	1223	PR	02-JUN-1999;	98WO-US020111.
				PR	01-SEP-1999;	98WO-US020111.
Qy	401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly	420	PR	08-SEP-1999;	98WO-US020594.
				PR	13-SEP-1999;	98WO-US020944.
Db	1224	GAATGATCCCAAAACCATGCACAAAGCATTCGCGCAGAGAGTGGTAAAAACACTTTTCCTGGA	1283	PR	15-SEP-1999;	98WO-US021090.
				PR	15-SEP-1999;	98WO-US021547.
Qy	421	IleSerIleArgValAspAlaPheGlnTyrLysGlyPhePhePhePheSerArgGly	440	PR	05-OCT-1999;	98WO-US023089.
				PR	29-NOV-1999;	98WO-US028214.
Db	1284	ATCAGTATCCGTTGTGCTCTTCCAGTACAAAGGATCTCTTTTTCAGCCGTGGA	1343	PR	30-NOV-1999;	98WO-US028313.
				PR	30-NOV-1999;	98WO-US028409.
Qy	441	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460	PR	01-DEC-1999;	98WO-US028301.
				PR	01-DEC-1999;	98WO-US028634.
Db	1344	TCAAGCAATTTGAATACACATTAAAGACAAGATATATACCGAATCATGGAACATAAT	1403	PR	02-DEC-1999;	98WO-US028551.
				PR	02-DEC-1999;	98WO-US028564.
Qy	461	ThrTyrPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu	480	PR	02-DEC-1999;	98WO-US028565.
				PR	16-DEC-1999;	98WO-US030095.
Db	1404	ACTTGCTTCAATGATCAAGAACCAAGAACTCCTCATTTGGTTTTGATATCAACAAGGAA	1463	PR	20-DEC-1999;	98WO-US030911.
				PR	20-DEC-1999;	98WO-US030999.
Qy	481	LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerSerLeuSerLeuPheIlePhe	500	PR	22-DEC-1999;	98WO-US030720.
				PR	30-DEC-1999;	98WO-US031243.
Db	1464	AAAGACATCTCAGAGGCATAAAGATATTTGTATCATAGAGTTTAAGCTTGTATTATTTT	1523	PR	30-DEC-1999;	98WO-US031274.
				PR	05-JAN-2000;	2000WO-US000219.
Qy	501	GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln	513	PR	06-JAN-2000;	2000WO-US000277.
				PR	11-FEB-2000;	2000WO-US000376.
Db	1524	GGTATTGTTCAATTCCTGTAAGAACTCTTATTTATCAA	1562	PR	18-FEB-2000;	2000WO-US003565.
				PR	22-FEB-2000;	2000WO-US004341.
RESULT 10				PR	22-FEB-2000;	2000WO-US004342.
ADA45710				PR	24-FEB-2000;	2000WO-US004914.
ID ADA45710 standard; cDNA; 1647 BP.				PR	24-FEB-2000;	2000WO-US005004.
XX	ADA45710;			PR	01-MAR-2000;	2000WO-US005601.
AC	XX			PR	02-MAR-2000;	2000WO-US005746.
XX	XX			PR	02-MAR-2000;	2000WO-US005841.
DT	20-NOV-2003 (first entry)			PR	10-MAR-2000;	2000WO-US006319.
DE	XX			PR	15-MAR-2000;	2000WO-US006884.
XX	Novel human secreted and transmembrane protein PRO5992 cDNA.			PR	20-MAR-2000;	2000WO-US007377.
XX	Human; secreted and transmembrane protein; PRO; gene; ss;			PR	21-MAR-2000;	2000WO-US007532.
KW	Tumour necrosis factor alpha release; TNF-alpha release;			PR	30-MAR-2000;	2000WO-US008439.
KW	glucose uptake modulator; FFA uptake modulator;			PR	17-MAY-2000;	2000WO-US013705.
KW	cell proliferation stimulator; cell differentiation stimulator;			PR	22-MAY-2000;	2000WO-US014042.
KW	cell differentiation inhibitor; cytokine release stimulator; tumour;			PR	30-MAY-2000;	2000WO-US014941.
KW	lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;			PR	02-JUN-2000;	2000WO-US015264.
KW	cervical tumour; liver tumour; chromosome mapping; gene mapping;			PR	28-JUL-2000;	2000WO-US020710.
KW	gene therapy; chromosome identification; chromosome marker.			PR	11-AUG-2000;	2000WO-US022031.
XX	XX			PR	23-AUG-2000;	2000WO-US023522.
OS	Homo sapiens.			PR</		





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Db      1104  CCCAATCCATCCATACATTAGGTTTCCAGGACGGTGTGAAGAAATAGATGCAGCGTC 1163
Qy      381  CysAspLysThrThrArgLysThrTyrPhePheValGlylleTyrCysTrpArgPheAsp 400
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Db      1164  TGTGATAAGACCAACAGAAAACCTACTTCTTGTGGCAATTTGGTCTGGAGGTTTGAT 1223
Qy      401  GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
      |||
Db      1224  GAAATGACCCAAACCAATGGCAAGAGTATCCCGCAGAGATGGTAAACACTTTCCTGGA 1283
Qy      421  IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
      |||
Db      1284  ATCAGTATCCGTGTGTGCTGCTTCCAGTCAAAAGATTCTCTTTTCAGCGGTGGA 1343
Qy      441  SerLysGlnPheGluTyrAsnIleLysThrIleAsnIleThrArgIleMetArgThrAsn 460
      |||
Db      1344  TCAAGCAATTTGAATACAAACATTAACAAAGAAATATACCCGAATCATGAGAACTAAT 1403
Qy      461  ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
      |||
Db      1404  ACTTGGTTTCAATGCAAGAACCAAGAACTCTCAITTTGTTTGTATCAACAAGAA 1463
Qy      481  LysAlaHisSerGlyGlyIleLysIleLysIleLysSerLysSerLeuSerLeuPheIlePhe 500
      |||
Db      1464  AAGCACATTCAGGAGGCATAAAGATATTGTATCAAGAGTTTAAAGCTTGTTTATTTT 1523
Qy      501  GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
      |||
Db      1524  GGTATTGTTGCTGCTGAAACACACTTCTATTATTATCAAA 1562

RESULT 11
ADA76141
ID   ADA76141 standard; cDNA; 1647 BP.
AC   ADA76141;
XX
XX
XX  20-NOV-2003 (first entry)
XX
XX  Human PRO polynucleotide #96.
XX
XX  Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
KW  tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;
KW  cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;
KW  liver; microvascular endothelial cell; glucose; EPA;
KW  skeletal muscle cell; adipocyte cell; pericyte cell;
KW  inner ear utricular supporting cell; T-lymphocyte cell;
KW  endothelial cell tube formation; bone disorder; cartilage disorder;
KW  sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
KW  rheumatoid arthritis; haemoglobin-associated disorder thalassaemia;
KW  immune system cell infiltration.
XX
OS   Homo sapiens.
XX
XX  US2003073212-A1.
XX
XX  17-APR-2003.
XX
XX  16-APR-2002; 2002US-00123903.
XX
XX  31-MAR-1997; 97WO-US005230.
XX  12-JUN-1998; 98WO-US012456.
XX  14-JUL-1998; 98WO-US014552.
XX  28-AUG-1998; 98WO-US017888.
XX  10-SEP-1998; 98WO-US018824.
XX  14-SEP-1998; 98WO-US019093.
XX  14-SEP-1998; 98WO-US019177.
XX  16-SEP-1998; 98WO-US019330.
XX  17-SEP-1998; 98WO-US019437.
XX  07-OCT-1998; 98WO-US021141.
XX  29-OCT-1998; 98WO-US022991.
XX  29-OCT-1998; 98WO-US022992.
XX  20-NOV-1998; 98WO-US024855.
PR      01-DEC-1998; 98WO-US025108.
PR      05-JAN-1999; 98WO-US000106.
PR      08-MAR-1999; 98WO-US005028.
PR      10-MAR-1999; 98WO-US0005190.
PR      20-APR-1999; 98WO-US0008615.
PR      14-MAY-1999; 98WO-US010733.
PR      02-JUN-1999; 98WO-US012252.
PR      01-SEP-1999; 98WO-US020111.
PR      08-SEP-1999; 98WO-US020594.
PR      13-SEP-1999; 98WO-US020944.
PR      15-SEP-1999; 98WO-US021090.
PR      15-SEP-1999; 98WO-US021547.
PR      05-OCT-1999; 98WO-US023089.
PR      29-NOV-1999; 98WO-US028214.
PR      30-NOV-1999; 98WO-US028313.
PR      30-NOV-1999; 98WO-US028409.
PR      01-DEC-1999; 98WO-US028301.
PR      01-DEC-1999; 98WO-US028634.
PR      02-DEC-1999; 98WO-US028551.
PR      02-DEC-1999; 98WO-US028564.
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PR      16-DEC-1999; 98WO-US030095.
PR      20-DEC-1999; 98WO-US030911.
PR      20-DEC-1999; 98WO-US030999.
PR      22-DEC-1999; 98WO-US030720.
PR      30-DEC-1999; 98WO-US031243.
PR      30-DEC-1999; 98WO-US031274.
PR      03-JAN-2000; 2000WO-US000219.
PR      06-JAN-2000; 2000WO-US000277.
PR      11-FEB-2000; 2000WO-US000376.
PR      18-FEB-2000; 2000WO-US0003565.
PR      18-FEB-2000; 2000WO-US000431.
PR      22-FEB-2000; 2000WO-US000432.
PR      22-FEB-2000; 2000WO-US0004414.
PR      24-FEB-2000; 2000WO-US0004914.
PR      24-FEB-2000; 2000WO-US005004.
PR      01-MAR-2000; 2000WO-US005601.
PR      02-MAR-2000; 2000WO-US005746.
PR      02-MAR-2000; 2000WO-US005841.
PR      10-MAR-2000; 2000WO-US006319.
PR      15-MAR-2000; 2000WO-US006884.
PR      20-MAR-2000; 2000WO-US007377.
PR      21-MAR-2000; 2000WO-US007532.
PR      30-MAR-2000; 2000WO-US008439.
PR      17-MAY-2000; 2000WO-US013705.
PR      22-MAY-2000; 2000WO-US014042.
PR      30-MAY-2000; 2000WO-US014941.
PR      02-JUN-2000; 2000WO-US015264.
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PR      11-AUG-2000; 2000WO-US022031.
PR      23-AUG-2000; 2000WO-US023522.
PR      24-AUG-2000; 2000WO-US023328.
PR      08-NOV-2000; 2000WO-US030952.
PR      10-NOV-2000; 2000WO-US030873.
PR      01-DEC-2000; 2000WO-US032678.
PR      20-DEC-2000; 2000US-00747259.
PR      28-DEC-2000; 2000WO-US034956.
PR      28-FEB-2001; 2001US-00796498.
PR      28-FEB-2001; 2001WO-US006520.
PR      01-MAR-2001; 2001US-00066666.
PR      09-MAR-2001; 2001US-00802706.
PR      14-MAR-2001; 2001US-00808689.
PR      22-MAR-2001; 2001US-00816744.
PR      05-APR-2001; 2001US-00828366.
PR      10-MAY-2001; 2001US-00854280.
PR      18-MAY-2001; 2001US-00860216.
PR      25-MAY-2001; 2001US-00866028.
PR      25-MAY-2001; 2001US-00866034.
PR      25-MAY-2001; 2001WO-US017092.
PR      01-JUN-2001; 2001US-00872035.
PR      01-JUN-2001; 2001WO-US017800.
PR      05-JUN-2001; 2001US-00874503.
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QY 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValIleLysIleAspAlaVal 380
Db 1104 CCNAATCCATCATCATAGTGTTCAGGACGTTGTAAGAAATAGATGCGCGC 1163
QY 381 CysAspLysThrThrArgLysThrThrPhePheValGlyIleTrpCysTrpArgPheAsp 400
Db 1164 TGTGATAAGACCAACAGAAAACCTACTTCTTTGTGGCATTGGTGTGGAGTTTGAT 1223
QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValIleHisPheProGly 420
Db 1224 GAATGACCCAAACCATGACAAAGGATTCGCGAGAGAGTGTAAACACTTTCCTGGA 1283
QY 421 IleSerIleArgValAspAlaPheGlnTyrLysGlyPhePhePhePheSerArgGly 440
Db 1284 ATCAGTATCGTGTTGATGCTGCTTCCAGTCAAAAGGATTCCTCTTTTCACCGCTGGA 1343
QY 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
Db 1344 TCAAGCAATTTGAATACACATTAAGACAAAGAAATATTACCCGAATCATGAGAACTAAT 1403
QY 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
Db 1404 ACTTGCTTTCAATGCAAGAACCAAAAGACTCCTCATTTGGTTTGTATATCAACAAGGAA 1463
QY 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
Db 1464 AAGACATTCAGAGGCATTAAGATATTGTATCATTAAGATTAAAGCTTGTATTATTTT 1523
QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
Db 1524 GGTATTGTTTCATTGCTGTAAGAACACTTCTATTATTAACAA 1562

RESULT 12
ADA18791
ID ADA18791 standard; cDNA; 1647 BP.
AC
AC ADA18791;
XX
XX 20-NOV-2003 (first entry)
DT
DE Human PRO polynucleotide #96.
KW Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; lung;
KW colon; breast; prostate; rectum; cervix; liver; tumour; cancer;
KW glucose uptake; FFA; adipocyte cell; pericyte cell; proteoglycan;
KW cartilage; inner ear utricular supporting cell; cytokine; A-peptide;
KW factor VIIA; endothelial cell.
XX
XX Homo sapiens.
XX
XX US2003054517-A1.
XX
XX 20-MAR-2003.
XX
XX 08-MAY-2002; 2002US-00141755.
XX
XX 31-MAR-1997; 97WO-US005230.
XX 12-JUN-1998; 98WO-US012456.
XX 14-JUL-1998; 98WO-US014552.
XX 28-AUG-1998; 98WO-US017888.
XX 10-SEP-1998; 98WO-US018824.
XX 14-SEP-1998; 98WO-US019093.
XX 14-SEP-1998; 98WO-US019094.
XX 14-SEP-1998; 98WO-US019177.
XX 16-SEP-1998; 98WO-US019330.
XX 17-SEP-1998; 98WO-US019437.
XX 07-OCT-1998; 98WO-US021141.
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XX 29-OCT-1998; 98WO-US022392.
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XX 01-DEC-1998; 98WO-US025108.
XX 05-JAN-1999; 99WO-US000106.
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DT 20-NOV-2003 (first entry)  
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KW Tumour necrosis factor alpha release; TNF-alpha release;  
KW Glucose uptake modulator; FFA uptake modulator;  
KW cell proliferation stimulator; cell differentiation stimulator;  
KW cell differentiation inhibitor; cytokine release stimulator; tumour;  
KW lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;  
KW cervical tumour; liver tumour; chromosome mapping; gene mapping;  
KW gene therapy; chromosome identification; chromosome marker.  
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OS human.  
OS secreted.  
OS and.  
OS transmembrane.  
OS protein.  
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OS cDNA.  
XX US2003049816-A1.  
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PR 25-MAY-2001; 2001WO-US017092.  
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PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.



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 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI; 2003-695892/66.  
 DR P-PSDB; ADA61415.  
 XX  
 PT New PRO nucleic acid and encode polypeptides, are useful for  
 PT manufacturing a medicament for diagnosing or treating cancer.  
 XX  
 PS Claim 2; Fig 191; 660pp; English.  
 XX  
 CC The invention describes 305 nucleic acids encoding PRO (secreted and  
 CC transmembrane) polypeptides (I). (I) is useful for stimulating the  
 CC release of TNF-alpha from human blood, for modulating the uptake of  
 CC glucose or FFA by skeletal muscle cells or adipocyte cells, for  
 CC stimulating the proliferation or differentiation of chondrocyte cells,  
 CC for stimulating the proliferation of or gene expression in pericyte  
 CC cells, for stimulating the release of proteoglycans from cartilage, for  
 CC stimulating the proliferation of inner ear utricular supporting cells,  
 CC for stimulating the proliferation of T-lymphocyte cells, for stimulating  
 CC the release of a cytokine from PMBC cells, for inhibiting the binding of  
 CC A-peptide to factor V1RA, for inhibiting the differentiation of adipocyte  
 CC cells, for stimulating proliferation of endothelial cells, for detecting  
 CC the presence of tumour in a mammal. The tumour is lung, colon, breast,  
 CC prostate, rectal, cervical or liver tumour. The oligonucleotide probes  
 CC are useful for isolating genomic and cDNA nucleotide sequences or  
 CC antisense probes. (I) is also useful as therapeutic agent. PRO is useful  
 CC in assays to identify other proteins or molecules involved in binding  
 CC interaction. A polynucleotide (II) encoding (I) is useful in chromosome  
 CC and gene mapping, in generation of antisense RNA and DNA, in the  
 CC preparation of PRO polypeptide, for generating transgenic animals or  
 CC knockout animals which in turn are useful in the development and  
 CC screening of therapeutically useful reagents, in gene therapy, for  
 CC chromosome identification, as chromosome marker, and for generating  
 CC probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.  
 CC detecting its expression in specific cells, tissues or serum, and for  
 CC affinity purification of PRO from recombinant cell culture or natural  
 CC sources. (I) and (II) are useful for tissue typing. This sequence encodes  
 CC a novel human secreted and transmembrane PRO polypeptide.  
 XX  
 SQ Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.64e-294 Length: 1647  
 Score: 2752.00 Matches: 512  
 Percent Similarity: 99.81% Conservative: 0  
 Best Local Similarity: 99.81% Mismatches: 1  
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US-10-729-807-10 (1-513) x ADA61414 (1-1647)

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 Qy 81 AsnThrLeuGluLeuMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
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RESULT 14
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AC ADBI9199;
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DT 20-NOV-2003 (first entry)
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KW Human; secreted and transmembrane protein; PRO; gene; ss;
KW Tumour necrosis factor alpha release; TNF-alpha release;
KW Glucose uptake modulator; FFA uptake modulator;
KW cell proliferation stimulator; cell differentiation stimulator;
KW cell differentiation inhibitor; cytokin.
XX
OS Homo sapiens.
XX
PN US2003068796-A1.
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PD 10-APR-2003.
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PF 15-APR-2002; 2002US-00123261.
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QY      381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTyrArgPheAsp 400
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QY      421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
Db      1284 ATCAGTATCCGTGTGATGCTGCTTCCAGTACAAAGGATTCTTCTTTTCAGCCGTGCA 1343
QY      441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
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QY      461 ThrTyrPheGlnCysLysGluProLysAsnSerPheGlyPheAspIleAsnLysGlu 480
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Db      1524 GGTATTGTTCATTGCTGAAAAACACTTCTATTATCAA 1562
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Search completed: November 15, 2004, 21:23:08  
Job time : 757 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 15, 2004, 21:07:43 ; Search time 6567 Seconds  
(without alignments)  
3694.170 Million cell updates/sec

Title: US-10-729-807-10  
Perfect score: 2763  
Sequence: 1 MKRLLLCLFFITFSAPFL.....SLSLFFGIVHLKNTSIYQ 513

Scoring table: BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delopt 6.0, Delopt 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters: -DEV=xlh

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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
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-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
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Database :

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2: gb.htg.\*  
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4: gb.om.\*  
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6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2763	100.0	1845	6	AX358475 Sequence
2	2752	99.6	1647	6	AX464058 Sequence
3	2752	99.6	1647	9	AX358752 Homo sapi
4	2731	98.8	1655	9	AF195192 Homo sapi

5	2722	98.5	1841	6	AX249969 Sequence
6	2694	97.5	1583	6	AX089610 Sequence
7	2455	88.9	1687	6	AR263900 Sequence
8	2433.5	88.1	1488	6	AX249967 Sequence
9	2347	84.9	1567	4	AF281673 Tupaiia be
10	1520.5	55.0	1587	5	AF062392 Gallus ga
11	1451	52.5	833	6	AX249965 Sequence
12	1286.5	46.6	1479	4	AY183143 Canis fam
13	1272.5	46.1	1795	4	RABSTROM
14	1254	45.4	1434	6	AR380629 Sequence
15	1254	45.4	1434	6	AX402358 Sequence
16	1254	45.4	1434	6	AX481494 Sequence
17	1254	45.4	1434	6	HUMMP3A
18	1254	45.4	1511	9	BC074869 Homo sapi
19	1254	45.4	1649	9	BC069676 Homo sapi
20	1254	45.4	1650	9	BC069716 Homo sapi
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22	1250	45.2	1511	9	BC074815 Homo sapi
23	1250	45.2	1801	6	CQ730209 Sequence
24	1250	45.2	1801	6	AR380829 Sequence
25	1250	45.2	1801	6	AX333235 Sequence
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45	1233	44.6	1783	10	BC006725 Mus muscu

#### ALIGNMENTS

RESULT 1	AX358475	Sequence 1 from Patent WO0190326.	1845 bp	DNA	linear	PAT 13-FEB-2002
LOCUS	AX358475	Sequence 1 from Patent WO0190326.	1845 bp	DNA	linear	PAT 13-FEB-2002
DEFINITION	AX358475	Sequence 1 from Patent WO0190326.	1845 bp	DNA	linear	PAT 13-FEB-2002
ACCESSION	AX358475	Sequence 1 from Patent WO0190326.	1845 bp	DNA	linear	PAT 13-FEB-2002
VERSION	AX358475.1	GI:18675086	1845 bp	DNA	linear	PAT 13-FEB-2002
KEYWORDS	AX358475.1	GI:18675086	1845 bp	DNA	linear	PAT 13-FEB-2002
SOURCE	AX358475.1	GI:18675086	1845 bp	DNA	linear	PAT 13-FEB-2002
ORGANISM	AX358475.1	GI:18675086	1845 bp	DNA	linear	PAT 13-FEB-2002
REFERENCE	AX358475.1	GI:18675086	1845 bp	DNA	linear	PAT 13-FEB-2002
AUTHORS	AX358475.1	GI:18675086	1845 bp	DNA	linear	PAT 13-FEB-2002
TITLE	AX358475.1	GI:18675086	1845 bp	DNA	linear	PAT 13-FEB-2002
JOURNAL	AX358475.1	GI:18675086	1845 bp	DNA	linear	PAT 13-FEB-2002
FEATURES	AX358475.1	GI:18675086	1845 bp	DNA	linear	PAT 13-FEB-2002
source	AX358475.1	GI:18675086	1845 bp	DNA	linear	PAT 13-FEB-2002
location/Qualifiers	AX358475.1	GI:18675086	1845 bp	DNA	linear	PAT 13-FEB-2002
1..1845	AX358475.1	GI:18675086	1845 bp	DNA	linear	PAT 13-FEB-2002
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Percent Similarity:	100.00%	Mismatches:	0
Best Local Similarity:	100.00%		

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	QY	381	CysAspLysThrThrArgLysThrTyrrPhePheValGlyIleTrpCysTrpArgPheAsp	400
	DB	1164	TGTGTAAGAACCAACAAGAAAACCTACTCTTTTGTGGGCATTTGGTCTCTGGAGGTTTGAT	1223
	QY	401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValVallLysHisPheProGly	420
	DB	1224	GAAATCACCCNAACCATTGCACAAAGGATTCGCCAGACAGCTGGTAAACACACTTTTCCTGGA	1283
	QY	421	IleSerIleArgValAspAlaIaPheGlnTyrrLysGlyPhePhePhePheSerArgGly	440
	DB	1284	ATCAGTATCCGTGTGTGATGCTGCTTTCCAGTACAAGGAATCTCTTTTTTCAGCCGTGGA	1343
	QY	441	SerLysGlnPheGluTyrrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
	DB	1344	TCAAAGCAATTTGAATACACCATTAAGACAAAGAATAATTATCCCGAATCATGAGAACTAAT	1403
	QY	461	ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu	480
	DB	1404	ACTTGTGTTTCCAATGCAAGAACAACAAAGAACTCTCATTTGGTTTGTATATCAACAGGAA	1463
	QY	481	LysAlaHisSerGlyGlyIleLysIleLeutyrrHisLysSerLeuSerLeuPheIlePhe	500
	DB	1464	AAGACACATTCAGGAGGCATAAAGATTTGTATCATAAAGATTGTTAAGCTTGTGTTATTTT	1523
	QY	501	GlyIleValHisIleLeuLysAsnThrSerIleTyrrGln	513
	DB	1524	GGTATTGTTTCATTTGCTTGAAAAACACTTCTATTATTATCAA	1562
	RESULT 2			
	AX464058		1647 bp	DNA linear PAT 16-JUL-2000
	LOCUS	AX464058		
	DEFINITION	Sequence 191 from Patent WO0140466.		
	ACCESSION	AX464058		
	VERSION	AX464058.1 GI:21899046		
	KEYWORDS	Homo sapiens (human)		
	SOURCE	Homo sapiens		
	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
	REFERENCE	Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E., Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K., Wood,W.L. and Zhang,Z.,		
	AUTHORS	Secreted and transmembrane polypeptides and nucleic acids encoding same		
	TITLE	Patent: WO 0140466-A 191 07-JUN-2001;		
	JOURNAL	Genentech Inc. (US)		
	FEATURES	Location/Qualifiers		
	SOURCE	1..1647 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"		
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	Score:	2752.00	Matches:	512
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	Best Local Similarity:	99.81%	Mismatches:	1
	Query Match:	99.60%	Indels:	0
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	UTS-10-729-807-10 (1-513) X AX464058 (1-1647)			







JOURNAL REFERENCE	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	5
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## ORIGIN

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Best Local Similarity: 99.78% Mismatches: 0  
Query Match: 88.85% Indels: 1  
DB: 6 Gaps: 0

US-10-729-807-10 (1-513) x AR263900 (1-1687)

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Qy 80 SerAsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyr 99  
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Qy 100 GlyTyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThr 119  
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Qy 160 PheArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeu 179  
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Qy 300 GlyArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAla 319  
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Db 835 ATTCTGGTTTTTAAAGATGAAACTTCTGGATGATCAGAGGATATGCTGTCTTGGCAGAT 776

Qy 360 TyrProLysSerIleHisThrLeuGlyPheProGly-ArgValLysLysIleAspAlaAl 379  
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Qy 499 ePheGlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513  
Db 355 TTTTGGTATTGTTTCATTTGCTGAAAAACACTTCTATTATCAAA 313

## RESULT 8

AX249967 1488 bp DNA linear PAT 28-SEP-2001  
LOCUS Sequence 3 from Patent WO0166766.  
DEFINITION AX249967  
ACCESSION AX249967.1 GI:15864453  
VERSION  
KEYWORDS Homo sapiens (human)  
SOURCE

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Fajardo, M.D., Smith, R. and Moss, P.  
TITLE A matrix metalloproteinase (mmp-25)  
JOURNAL Patent: WO 0166766-A 3 13-SEP-2001;  
DARWIN MOLECULAR CORPORATION (US)

FEATURES  
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Location/Qualifiers  
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/mol\_type="unassigned DNA"  
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Percent Similarity: 90.84% Conservatives: 3  
Best Local Similarity: 90.25% Mismatches: 4  
Query Match: 88.07% Indels: 43  
DB: 6 Gaps: 1

US-10-729-807-10 (1-513) x AX249967 (1-1488)

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Db 113 GTCCGGATGATGGAATAATGAAGAAATGTGCAACTGGCTCAGGCATATCTCAACAGTTC 172



QY 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60  
 Db 173 TACTCTCTGAAATAGAAAGGCAATCACTTCTGTTCBAGACAGATAGAGTCTCATAGAT 232

QY 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
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QY 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
 Db 293 AACACCTTGGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGGCGCATATGGC 352

QY 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120  
 Db 353 TACACCTCCTCGGTGGAGAAATACAACTCCTACCTACAGATATTAATATATATCTCCG 412

QY 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140  
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QY 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaPheIleMetIleAlaPhe 160  
 Db 473 GTCACTCCATTAATTCACAGATTCAGAGGGATTGCAGACATCATGATGCGCTTT 532

QY 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180  
 Db 533 AGGACTCGA----- 541

QY 181 HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200  
 Db 541 ----- 541

QY 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheValAlaAlaHisGluPheGlyHis 220  
 Db 542 -----GGATTCACCTTGTCTTGTGGCTCTCATGAATTTGTGCAT 593

QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240  
 Db 584 GCACTGGGCTCTCTCACTCCATGATCAACAGCCTTGATGTTCCAAATATGCTCC 643

QY 241 LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr 260  
 Db 644 CTGGATCCCAAGAAATACCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCAT 703

QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280  
 Db 704 GGAGTCTGCTTAGGAACCTGCTAAGCCAAAGGAACCCCACTATACCCATGCTGTGAC 763

QY 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300  
 Db 764 CCTGACTTGACTTTTGACGCTATCACTTTCCGACAGAGATGATGTTCTTTAAAGGC 823

QY 301 ArgHisLeuThrArgIleTyrTyrAspIleThrAspValGluPheGluIleAlaSer 320  
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QY 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340  
 Db 884 TTCTGGCCATCTCTGCCAGCTGATCTGAAGCTGCTATGACGATGTTGAGTTTGAATTAATGCTTCA 943

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QY 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500  
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QY 501 GlyIleValHisLeuLysAsnThrSerIleTyrGln 513  
 Db 1424 GGTATTGTTCAATTTGCTGAAACACTTCTATTATCA 1462

RESULT 9  
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 DEFINITION Tupaia belangeri matrix metalloproteinase-27 mRNA, complete cds.  
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 VERSION AF281673.1  
 GI:12006363  
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 SOURCE Tupaia belangeri (northern tree shrew)  
 ORGANISM Tupaia belangeri  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiia.  
 REFERENCE 1 (bases 1 to 1667)  
 AUTHORS Guggenheim, J.A., To, C.H. and Frost, M.R.  
 TITLE Molecular cloning of a novel matrix metalloproteinase (MMP-27) from sclera  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1667)  
 AUTHORS Guggenheim, J.A. and Frost, M.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-JUN-2000) Department of Optometry & Vision Sciences, Cardiff University, King Edward VII Avenue, Cardiff, Wales CF10 3NB, UK

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 Alignment Scores:  
 Pred. No.: 5,03e-222 Length: 1667  
 Score: 2347.00 Matches: 434



Percent Similarity:	90.43%
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Query Match:	84.94%
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US-10-729-807-10 (1-513) x AF281673 (1-1667)

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DB	:	:::	:
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QY	41	TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuLeuLeuAsp	60
DB	214	TACTCTCTTGAATAGAGGGAGGCCATCTCGTTCAAAGCAAAAACGGGAGTCTCTCTAGAC	273
QY	61	AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer	80
DB	274	GGCAAAATTCGGGAAATGCAAGCGTTTTTTTGGATTTGACAGTGACTGGAACGCTGGATTTCA	333
QY	81	AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100
DB	334	AACACTCTTTGAGATCATGAATAACAACCCAGGTGTGGGTGCTCATGTGGGTCAGTATGCG	393
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QY	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180
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QY	181	HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn	200
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QY	201	TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis	220
DB	694	TGGACCAAGGATACAGCAGGATTCAGTTTGTTCCTGTGGCTGCTCATGAATTTGGTFCAC	753
QY	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
DB	754	GGTCTGGGGCTCTCTCATTCCAATGATCAGACAGCCTTGATGTTTCCAACTATGTCCTCC	813
QY	241	LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr	260
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QY	301	ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer	320
DB	994	AGGCACCTGTGGAGGATCTATCATGATATCACCGACGTGGAAATTTGAATTAATTTGCTTCA	1053
QY	321	PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle	340

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Db	1114	CTGGTTTTTAAAGATGAAAACTTCTGCGATGATAGAGCCCTATATATGTGTGTCACCGGTAT	1173
Qy	361	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal	380
Db	1174	CCCAGGTCCATCCCATATCTTGGTTTCTCCAGATATGTGAAGAAAAATTGATGCAGCTGTC	1233
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Db	1234	TGTGACCAAGACACGAGAAAAACCTACTTCTTTCTGGGTATTTGGTCTGTGAGGTATGAT	1293
Qy	401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly	420
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Qy	441	SerLysGlnPheGluTyTrpAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
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Qy	461	ThrTrpPheGlnCysLysGluProLysAsnSerPheGlyPheAspIleAsnLysGlu	480
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DEFINITION			
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VERSION			
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Phasianinae; Gallus.			
1 (bases 1 to 1587)			
Cloning of a novel matrix metalloproteinase (MMP) from chicken			
embryo fibroblasts			
J. Biol. Chem. (1998) In press			
2 (bases 1 to 1587)			
Yang, M. and Kurkinen, M.			
Direct Submission			
Submitted (29-APR-1998) Center for Molecular Medicine and Genetics			
Wayne State University School of Medicine, 5047 Gullen Mall,			
Detroit, MI 48202, USA			
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Query Match: 52.52% Indels: 0
DB: 6 Gaps: 0

US-10-729-807-10 (1-513) x AX249965 (1-833)
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Qy 284 ThrPheAspAlaIleThrPheArgGluValMetPhePheLysGlyArgHisLeu 303
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DEFINITION Canis familiaris Stromelysin 1 (MMP3) mRNA, complete cds.
ACCESSION AY183143
VERSION AY183143.1 GI:34391861
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REFERENCE 1 (bases 1 to 1479)
AUTHORS Sorensen,K.C., Balkin,R.G., Kitchell,B.E., Siegel,A.M. and
Schaeffer,D.
TITLE Isolation, Characterization and Expression of Stromelysin-1 (MMP3)
in Canine Tumors
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1479)
AUTHORS Sorensen,K.C., Balkin,R.G. and Kitchell,B.E.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-2002) Veterinary Clinical Medicine, University of
Illinois at Urbana-Champaign, 1008 W. Hazelwood Dr., Urbana, IL
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Query Match: 46.56% Indels: 17
DB: 4 Gaps: 8

US-10-729-807-10 (1-513) x AY183143 (1-1479)
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Db 85 GACAGAGCTGCAGAGGATGAGAACACACATGGAACACTCCAGCAATACCTAGAAAAC 144
Qy 40 PheTyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIle 59

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DEFINITION
RABSTROM 1795 bp mRNA linear MAM 27-APR-1993
Rabbit metalloproteinase synovial cell activator mRNA, complete cds.
ACCESSION M25664
VERSION M25664.1 GI:165709
KEYWORDS matrix metalloproteinase; stromelysin; transin.
SOURCE Oryctolagus cuniculus (rabbit)
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 1795)
AUTHORS Fini,M.E., Kamilowicz,M.J., Ruby,P.L., Beeman,A.M., Borges,K.A.
and Brinckerhoff,C.E.
TITLE Cloning of a complementary DNA for rabbit proactivator. A
metalloproteinase that activates synovial cell collagenase, shares
homology with stromelysin and transin, and is coordinately
regulated with collagenase
JOURNAL Arthritis Rheum. 30 (11), 1254-1264 (1987)
MEDLINE 88077214
PUBMED 2825726
COMMENT Original source text: Rabbit (strain New Zealand White) synovium,
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Draft entry and computer-readable copy of sequence [1] kindly
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VERSION		AR380629.1	GI:40088263	
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ORGANISM		Unknown.		
REFERENCE		Unclassified.		
AUTHORS		1 (bases 1 to 1434)		
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JOURNAL		Composition for the detection of blood cell and immunological response gene expression		
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ORGANISM Homo sapiens
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AUTHORS Identification of genes and compounds for treatment of cancer
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Job time : 6601 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2004, 20:52:31 ; Search time 27 Seconds  
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Title: US-10-729-807-10

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Searched: 283416 seqs, 96216763 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1271.5	46.0	478	1 KCRBS1	stromelysin 1 (EC
2	1250	45.2	477	1 KCHUS1	stromelysin 1 (EC
3	1243.5	45.0	476	1 JC6505	stromelysin 2 (EC
4	1234	44.7	476	1 KCHUS2	stromelysin 2 (EC
5	1233	44.6	477	1 KMSS1	stromelysin 1 (EC
6	1205	43.6	469	1 KCPGI	interstitial colla
7	1198.5	43.4	476	1 KRTS2	stromelysin 2 (EC
8	1177.5	42.6	469	1 KCRBI	interstitial colla
9	1170.5	42.4	468	1 KCRBI	interstitial colla
10	1169	42.3	475	1 KRTIH	stromelysin 1 (EC
11	1161.5	42.0	469	1 KCHUI	interstitial colla
12	1161	42.0	467	1 KCHUI	interstitial colla
13	1141	41.3	471	2 A53711	stromelysin 1 (EC
14	1133	41.0	470	2 A49499	neutrophil colla
15	1126	40.8	466	2 A23685	collagenase 3 (EC
16	1117	40.4	472	2 S29243	interstitial colla
17	1020.5	36.9	462	2 A42401	interstitial colla
18	1002.5	36.3	484	2 JC5743	macrophage elastase
19	798	28.9	384	2 IS1267	stromelysin 1 (EC
20	797	28.8	660	1 A28153	collagenase 3 (EC
21	790	28.6	662	2 A24386	gelatinase A (EC 3
22	790	28.6	662	2 A24386	gelatinase A (EC 3
23	783	28.3	662	2 S70365	gelatinase A (EC 3
24	769.5	27.9	663	1 S46492	gelatinase A (EC 3
25	715.5	25.9	669	2 I38029	gelatinase A (EC 3
26	713	25.8	582	2 I38028	matrix metallopro
27	698	25.3	582	2 I84471	matrix metallopro
28	667	24.1	582	2 I48673	matrix metallopro
29	626.5	22.7	712	1 I46031	gelatinase B (EC 3

## ALIGNMENTS

### RESULT 1

#### KCRBS1

stromelysin 1 (EC 3.4.24.17) precursor - rabbit

N;Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); pro

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004

C;Accession: A37306; A29157

R;Finl, M.E.; Karmilowicz, M.J.; Ruby, P.L.; Beeman, A.M.; Borges, K.A.; Brinckerhoff, C.

Arthritis Rheum. 30, 1254-1264, 1987

A;Title: Cloning of a complementary DNA for rabbit proactivator. A metalloproteinase tha

ed with collagenase.

A;Reference number: A37306; MUID:88077214; PMID:2825726

A;Accession: A37306

A;Molecule type: mRNA

A;Residues: 1-478 <PIN>

A;Cross-references: UNIPROT:P28863; GB:M25664; NID:G165709; PIDN:AAA31467.1; PID:G165710

R;Whitham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris,

Biochem. J. 240, 913-916, 1986

A;Title: Comparison of human stromelysin and collagenase by cloning and sequence analysis

A;Reference number: A90336; MUID:87156645; PMID:3030290

A;Accession: A29157

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-82,'D',84-127,'K',129-167,'GNS', <MHI>

C;Comment: This enzyme degrades various extracellular matrix proteins, including fibron

C;Comment: Stromelysin 1 hydrolyzes peptide bonds in plasminogen to yield a fragment with

C;Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation

C;Comment: Stromelysin is found in glycosylated and unglycosylated forms, both of whi

C;Function:

A;Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl sid

C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei

C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo

F;1-17/Domain: signal sequence #status predicted <SG>

F;18-478/Product: prostromelysin 1 #status predicted <PRO>

F;18-100/Domain: activation peptide #status predicted <ACT>

F;61-265/Domain: matrix metalloproteinase homology <MMP>

F;91-98/Region: autoinhibitory

F;101-478/Product: stromelysin 1 #status predicted <MAT>

F;285-478/Domain: hemopexin repeat homology <PXN>

F;93,219,223,229/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status

F;121/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;219,223,229/Binding site: zinc, catalytic (His) (active) #status predicted

F;220/Active site: Glu #status predicted

F;291-478/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 46.0%; Score 1271.5; DB 1; Length 478;

Matches 250; Conservative 75; Mismatches 136; Indels 21; Gaps 9;

Qy 1 MKRLLLCLEFFITFSSAFPLVRMTENE--NMQLAQYILNQFYSLTEGHNHLSVSKNRS 58

Db 1 MKTLPTLLLCVALCSAYPLDGASRDATTNMDLLQYLENYNLEKDVQFVKRDKSSP 60

[illegible]

RESULT 2  
(CHUS1

[illegible]

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Db 1 MKSLPIILLLCVAVCSAYPLDGAAGDTSNNLYQKYLENYDLKDKVQFVRKDSGPV 60
QY 60 DDKIREMQAFGLVTGKLDNTLEIMKTRCGVPDVGQGYTLPG---WRKYNLTIRII 116
Db 61 VKKIREMQKFLGLEVTGKLDNTLEIMKTRCGVPDVGQGYTLPG---WRKYNLTIRII 119
QY 117 NYTPDMARAAVDEAIQBLEVSWSKVTLKFTKLSKGTADIMIAFRTRVHGRCPRY-FDGP 175
Db 120 NYTPDLPKDAVSAVEKALKVWEVTLTFRSLYEGEADIMISFAVREHG--DFYPDGP 177
QY 176 LGVLGHAFPPGPGGLGGDTHFEDENWTKGAGNLFVAAHEFGHAGLGHSHNDQTALMF 235
Db 178 GNLAHAYAPGPGINGDAHFDDDEQMTKDTGTGTLNLFVAAHEFGHAGLGHSHNTEALM 237
QY 236 PNVVSL--DPKYPILSODDINGIOSIYG-----GLPKVPK--PKETIPHACDPLTFD 286
Db 238 PLYHSLTLTRFLSODDINGIOSLYGPPDPSPETPLVPTEPVPPEGTPANCDPALSFD 297
QY 287 AITTFREVMFFKGRHLWRIYYDITDVEFELIASFWPSLPADLQAAVE-NPRDKILVFKD 345
Db 298 AVSTLGEILIFKDRHFWKSLRKLPELHLISSFWPSLPDVAAYEVTSKDLVIFKG 357
QY 346 ENFWMIRGVAVLDPDYKPSIHTLGFGRVKKIDAAVCDKTRKTYFFVGVGWCWFDEMTQT 405
Db 358 NOFWAIRGNEVAGYPRGIHTLGFPTVRKIDAAISDKENKTYFFVGVGWCWFDEMTQT 417
QY 406 MDKGFPPQVVKHPPGISIRVDAAFQYKGFPPFSGSKQFQYKNTKNTIRMTNTWFOC 465
Db 418 MBPGPKQIAEDPPGIDSKIDAVFEFPGFYFFTGSSQLEFPNKKVTHTLKNSWLNC 477

RESULT 3
JC6505
stromelysin 2 (EC 3.4.24.22) precursor - mouse
N:Alternate names: matrix metalloproteinase 10
C:Species: Mus musculus (house mouse)
C>Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 09-Jul-2004
C:Accession: JC6505
R:Madlener, M.; Werner, S.
Gene 202, 75-81, 1997
A:Title: cDNA cloning and expression of the gene encoding murine stromelysin-2 (MMP-10).
A:Reference number: JC6505; MUID:98087420; PMID:9427548
A:Accession: JC6505
A:Molecule type: mRNA
A:Residues: 1-476 <MAD>
A:Cross-references: UNIPROT:O55123; GB:Y13185; NID:92791311; PID:927913
C:Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin.
C:Genetics:
A:Gene: MMP-10
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-476/Product: prostromelysin 2 #status predicted <PRO>
F:18-99/Domain: activation peptide #status predicted <ACT>
F:60-264/Domain: matrix metalloproteinase homology <MMP>
F:190-97/Region: autoinhibitory
F:100-476/Product: stromelysin 2 #status predicted <MAT>
F:120-476/Domain: hemopexin repeat homology <PXN>
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted
F:120/Binding site: zinc, catalytic (Asn) (covalent) #status predicted
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F:219/Active site: Glu #status predicted
F:289-476/Disulfide bonds: #status predicted

Query Match 45.0%; Score 1243.5; DB 1; Length 476;
Best Local Similarity 50.8%; Pred. No. 4.3e-93;
Matches 244; Conservative 77; Mismatches 140; Indels 19; Gaps 9;

QY 1 MKRLLLCLLFTTFSSAPPL--VRMTENEENMOLAQVLYNQVSLIEGHNHVLVQSKRSLI 59
Db 1 MEPLAILALLSLPCISAPLHGAVTQGHPSMDLAQQYLEKYNFKKNEKQIFKRDSSPV 60
QY 60 DDKIREMQAFGLVTGKLDNTLEIMKTRCGVPDVGQGYTLPG---WRKYNLTIRII 116

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Db 61 VKKIREMQKFLGLEMTGKLDNTLMELMHKPRCGVPDVGQGYTLPG---TPPGSPKWRKSHITYRII 119
QY 117 NYTPDMARAAVDEAIQBLEVSWSKVTLKFTKLSKGTADIMIAFRTRVHGRCPRY-FDGP 175
Db 120 NYTPDLPKDAVSAVEKALKVWEVTLTFRSLYEGEADIMISFAVREHG--DFYPDGP 177
QY 176 LGVLGHAFPPGPGGLGGDTHFEDENWTKGAGNLFVAAHEFGHAGLGHSHNDQTALMF 235
Db 178 GNLAHAYAPGPGINGDAHFDDDEQMTKDTGTGTLNLFVAAHEFGHAGLGHSHNTEALM 237
QY 236 PNVVSL--DPKYPILSODDINGIOSIYG-----LPKVPKPKETIPHACDPLTFD 286
Db 238 PLYHSLTLTRFLSODDINGIOSLYGPPDPSPETPLVPTEPVPPEGTPANCDPALSFD 297
QY 287 AITTFREVMFFKGRHLWRIYYDITDVEFELIASFWPSLPADLQAAVE-NPRDKILVFKD 345
Db 298 AVSTLGEILIFKDRHFWKSLRKLPELHLISSFWPSLPDVAAYEVTSKDLVIFKG 357
QY 346 ENFWMIRGVAVLDPDYKPSIHTLGFGRVKKIDAAVCDKTRKTYFFVGVGWCWFDEMTQT 405
Db 358 NOFWAIRGNEVAGYPRGIHTLGFPTVRKIDAAISDKENKTYFFVGVGWCWFDEMTQT 417
QY 406 MDKGFPPQVVKHPPGISIRVDAAFQYKGFPPFSGSKQFQYKNTKNTIRMTNTWFOC 465
Db 418 MBPGPKQIAEDPPGIDSKIDAVFEFPGFYFFTGSSQLEFPNKKVTHTLKNSWLNC 476

RESULT 4
KCHUS2
stromelysin 2 (EC 3.4.24.22) precursor [validated] - human
N:Alternate names: matrix metalloproteinase 10 (MMP10); transin-2
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: A28816; A47496
R:Muller, D.; Quantin, B.; Gesnel, M.C.; Millon-Collard, R.; Abecassis, J.; Breathnach, R.;
Biochem. J. 253, 187-192, 1988
A:Title: The collagenase gene family in humans consists of at least four members.
A:Reference number: A90339; MUID:8839885; PMID:2844164
A:Accession: A28816
A:Molecule type: mRNA
A:Residues: 1-476 <MUL>
A:Cross-references: UNIPROT:P09238; EMBL:X07820; NID:936628; PID:CAA30679.1; PID:936629
A:Note: mRNA for this protein was detected in several human tumors
R:Windors, L.J.; Grenett, H.; Birkedal-Hansen, B.; Bodden, M.K.; Engler, J.A.; Birkedal-
J. Biol. Chem. 268, 17341-17347, 1993
A:Title: Cell type-specific regulation of SL-1 and SL-2 genes. Induction of the SL-2 gene
A:Reference number: A47496; MUID:93352520; PMID:8349617
A:Accession: A47496
A:Molecule type: protein
A:Residues: 17-33 <WIN>
C:Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin.
C:Genetics:
A:Gene: GDB:MMP10; STWY2
A:Cross-references: GDB:120392; OMTW:185260
A:Map position: 11q22.3-11q23
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-476/Product: prostromelysin 2 #status experimental <PRO>
F:17-98/Domain: activation peptide #status predicted <ACT>
F:59-263/Domain: matrix metalloproteinase homology <MMP>
F:89-96/Region: autoinhibitory
F:99-476/Product: stromelysin 2 #status predicted <MAT>
F:283-476/Domain: hemopexin repeat homology <PXN>
F:91,217,221,227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted
F:119/Binding site: carboxylate (Asn) (covalent) #status predicted
F:217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted
F:218/Active site: Glu #status predicted
F:289-476/Disulfide bonds: #status predicted

Query Match 44.7%; Score 1234; DB 1; Length 476;
Best Local Similarity 51.4%; Pred. No. 2.5e-92;

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[illegible]

RESULT 6

KCP01

interstitial collagenase (EC 3.4.24.7) precursor [validated] - pig

N:Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue co

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004

C:Accession: S15986; S13597

R:Richards, C.D.; Rafferty, J.A.; Reynolds, J.J.; Saklatvala, J.

Matrix 11, 161-167, 1991

A:Title: Porcine collagenase from synovial fibroblasts: cDNA sequence and modulation of

A:Reference number: S15986; MUID:91333421; PMID:1651440

A:Accession: S15986

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-469 <RIC>

A:Cross-references: UNIPROT:P21692

A:Note: part of the sequence, including the amino end of the proenzyme, was confirmed b

R:Clarke, N.J.; O'Hare, M.C.; Castwton, T.E.; Harper, G.P.

Nucleic Acids Res. 18, 6703, 1990

A:Title: Nucleotide sequence of a cDNA for porcine type I collagenase, obtained by PCR

A:Reference number: S13597; MUID:91067477; PMID:2174547

A:Accession: S13597

C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase; calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase; zinc; zinc, catalytic (Cys, His, His) (inhibited) #status: F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-469/Product: procollagenase #status predicted <PRO>  
F;20-99/Domain: activation peptide #status experimental <ACT>  
F;60-261/Domain: matrix metalloproteinase homology <MMP>  
F;100-469/Product: interstitial collagenase #status predicted <MAT>  
F;272-466/Domain: hemopexin repeat homology <PXN>  
F;92, 218, 222, 228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status: F;120, 143/Binding site: zinc, catalytic (Asn) (covalent) #status predicted  
F;218, 222, 228/Binding site: carbohydrate (Asn) (active) #status experimental  
F;219/Active site: zinc, catalytic (His) (active) #status experimental  
F;278-466/disulfide bonds: #status experimental

C:Genetics: 35/3; 117/2; 167/1; 209/1; 264/1; 311/2; 356/1; 409/2; 444/1  
A:Introns: 35/3; 117/2; 167/1; 209/1; 264/1; 311/2; 356/1; 409/2; 444/1  
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase  
K:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase  
F:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-476/Product: prostromelysin 2 #status predicted <PRO>  
F:18-999/Domain: activation peptide #status predicted <ACT>  
F:60-264/Domain: matrix metalloproteinase homology <MMP>  
F:90-97/Region: autoinhibitory  
F:100-476/Product: stomelysin 2 #status predicted <MAT>  
F:283-476/Domain: hemopexin repeat homology <PXN>  
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted  
F:120/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted  
F:219/Active site: Glu #status predicted  
F:289-476/Disulfide bonds: #status predicted

[illegible]



[illegible]

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QY 5 LLLCLFFITSSAPFLVRMTENEENMQLAQYLNQFYSLEIEGHNHVSQKNSRLDDKIR 64
Db 6 LLLLLMGVSGHGSPAASETQ-EQDVMVQKYLENYNLLKDDWRKXIPKQNGNGLAVEKIK 64
QY 65 EMQAFEGGLTGTGLDNTLIMKTGPRGVDVQGYGT--LPGWRKYNLYRINYTPDM 122
Db 65 QMOEFFGLKVTGKPDATLTKMKQKPRGCGVDVAQFVLTGPNRWEQTHLYRIENYTPDL 124
QY 123 ARAAVDAIOEGLEVWVKVPLTKFKISKGADIMIAFRTRVHGRCRPRYEDGVLGLGHA 182
Db 125 SRADVNAIEKAQQLMSNVTLFTFKVSKGQADIMISF-VRGDHRDNPSPDGGEGQJAH 183
QY 183 FPPGGLGGTHDEDDENMTKDGAGFNLFVAHEFGHGLSHSNDQALMFPNVY-SL 241
Db 184 FQGLGIGGDVHEDDRTWKTFRNLYNLYRVAHELGHSLGSHSTIDIGALMTPNVYFSG 243
QY 242 DPRKYPLSDODDINGISQIYGLPKVPAKXKEPTIPHACDDPLTFDAITTPRRVMPFKGR 301
Db 244 DVQ---LAQDDIDGIAQIYGP-SQNPSPQVPQTPKVCDSKLTFDAITTIRGEIMFFKDR 299
QY 302 HLMRI--YYDITDVEFELIASFWPSLPADLQAAAYE-NPRDKILVFXDENFMIRGVAVLP 358
Db 300 FYMRANPY--SEVELNFIISVFWPHLPNGLOAAAYEVAHREIDILFFKGNKYTWVQGNELP 357
QY 359 DTPKSTH-TLGPGRVKKIDAAVCDKTRTKTYFFVGIWCWREDEMTQTMDKGGPQRVWXH 417
Db 358 GYPKDIHSSFGFPRSNVHIDAAVSEEDTGKTYFFVANKYRWYDEYKRSMDAGYPKMIEYD 417
QY 418 FPGISIRVDAAYQYKGFYFSGSGSKOFEYNKTKNTRIMRTNWTWFOCKE 467
Db 418 FFGIGNKVDVAFKKOGFFYFFHGTGTRQYKDPKTKRILTLQKANSWFCNK 467

RESULT 10
KCRTH
stromelysin 1 (EC 3.4.24.17) precursor - rat
N:Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); p2
C:Species: Rattus norvegicus (Norway rat)
C>Date: 13-Aug-1986 #sequence revision 13-Aug-1986 #text_change 09-Jul-2004
C:Accession: A00997; PS0150; S22767
R:Matrisian, L.M.; Glaichenhaus, N.; Gesnel, M.C.; Breathnach, R.
EMBO J. 4, 1435-1440, 1985
A:Title: Epidermal growth factor and oncogenes induce transcription of the same cellular
A:Reference number: A00997; MUID:85284930; PMID:3875482
A:Accession: A00997
A:Molecule type: mRNA
A:Residues: 1-475 <MAJ>
A:Cross-references: UNIPROT:P03957; GB:X02601; NID:957460; PIDN:CAA26448.1; PID:g57461
R:Umenishi, F.; Yasumitsu, H.; Ashida, Y.; Yamauti, J.; Umeda, M.; Miyazaki, K.
J. Biochem. 108, 537-543, 1990
A:Title: Purification and properties of extracellular matrix-degrading metallo-proteinase
A:Reference number: PS0150; MUID:91154156; PMID:1963430
A:Accession: PS0150
A:Molecule type: protein
A:Residues: 19-20,'X',22-28;110-112,'X',114-115,'X',117,'X',119;309-325 <UMB>
R:Breathnach, R.; Matrisian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P.
Nucleic Acids Res. 15, 1139-1151, 1987
A:Title: Sequences coding for part of oncogene-induced transin are highly conserved in a
A:Reference number: S26403; MUID:87146421; PMID:3547333
A:Contents: annotation; introns
A:Note: intron positions were determined by comparison of the previously reported cDNA s
J. Biol. Chem. 263, 11892-11899, 1988
R:Sanchez-Lopez, R.; Nicholson, R.; Gesnel, M.C.; Matrisian, L.M.; Breathnach, R.
J. Biol. Chem. 263, 11892-11899, 1988
A:Title: Structure-function relationships in the collagenase family member transin.
A:Reference number: S22767; MUID:89298669; PMID:2841336
A:Contents: annotation; active site; activation
A:Note: molecules with mutations in the autoinhibitory region showed a much increased te
A:Note: mutations of His-216, Glu-217, and His-226 inactivate the enzyme
R:Park, A.J.; Matrisian, L.M.; Kelle, A.F.; Pearson, R.; Yuan, Z.; Navre, M.
J. Biol. Chem. 266, 1584-1590, 1991
A:Title: Mutational analysis of the transin (rat stromelysin) autoinhibitor region demon
A:Reference number: A43028; MUID:91107652; PMID:1988438
A:Contents: annotation; autoinhibitory region
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A:Note: Arg-89 and Cys-92 are essential for maintaining latency
C:Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin
C:Comment: Stromelysin 1 hydrolyzes peptide bonds in plasminogen to yield a fragment with
C:Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation
C:Comment: Prostromelysin is found in glycosylated and unglycosylated forms, both of which
C:Genetics:
A:Introns: 33/3; 115/2; 165/1; 207/1; 262/1; 310/2; 355/1; 408/2; 443/1
A:Function:
A:Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl side
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotease
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloprotein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-475/Product: prostromelysin 1 #status predicted <PRO>
F:18-97/Domain: activation peptide #status predicted <ACT>
F:58-262/Domain: matrix metalloproteinase homology <MMP>
F:88-95/Region: autoinhibitory
F:98-475/Product: stromelysin 1 #status predicted <MAT>
F:282-475/Domain: hemopexin repeat homology <PN>
F:90-216,220,226/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:118/Binding site: carbonylhydride (Asn) (covalent) #status predicted
F:216,220,226/Binding site: zinc, catalytic (His) (active) #status predicted
F:217/Active site: Glu #status experimental
F:288-475/Disulfide bonds: #status predicted

Query Match 42.3%; Score 1169; DB 1; Length 475;
Best Local Similarity 49.1%; Pred. No. 4.8e-87;
Matches 235; Conservative 75; Mismatches 151; Indels 18; Gaps 8;

QY 1 MKRLLLCLFFITSSAPFLVRMTENEENMQLAQYLNQFYSLEIEGHNHVSQKNSRLDD 60
Db 1 MKGLPVLWLCTAVCSSYPL-HGSEDAENWVQKYLENYGLEDKVDKQFTKKKSSPV 59

QY 61 DKIREMQAFFGLTGTGLDNTLIMKTGPRGVDVQGYGTLPG---WRKYNLYRINI 117
Db 60 KKIQEMQKFLGKMTGKLDNTMELMHKRCGVDVGGFS-TFPGSPKWKKHISTRI 118

QY 118 YTPDMARAANDPAIOEGLEVWVKVPLTKFKTSKGIADIMIAFRTRVHGRCRPRYED 176
Db 119 YTLDLPRFSDVSAIBRALKWEVEVPLTFPSRSEGEADIMISFAVEEHGDFIP-- 176

QY 177 GVLGHAFPPGGLGDTHTFDEDDENMTKDGAGFNLFVAHEFGHGLSHSNDQALMFP 236
Db 177 MYLAHAYAGPTNGDAHFDDEDDERTDVTGNLFVAHELGHSLGUFHSAEALMYP 236

QY 237 NY-VSLDRPKYPLSDODDINGISQIYGLPKVPAKXKEPTIPHACDDP----- 287
Db 237 VYKSTDLARHLSQDDVDGIQSLYGPPTESDVLVVPKNSLDPEITLPMCSSALS 296

QY 288 ITTFRREVWFFKGRHLRIYVDITDVEFELIASFWPSLPADLQAAAYE-NPRDKIL 346
Db 287 VSTURGEVLFKDRHFWKSLRTPEPGFYLLSSEFWPSLPNNMAYEVNTRDTVILK 356

QY 347 NFWMIRGVAVLPDYPKSIHTLGFGRVKKIDAAVCDKTRTKTYFFVGIWCWREDEMT 406
Db 357 QIMAIRGHEELAGYKPSIHTLGLPETVOKIDAAISLQKKTKTYFFVDEKFRF 416

QY 407 DKGFPQVRVHPGPGISIRVDAAYQYKGFYFSGSGSKOFEYNKTKNTRIMRTNWT 465
Db 417 DPEPRKIAENFPGIGTKVDVAFVFAFGFLYFFSGSSQLPEFDPNACKVTHILKS 475

RESULT 11
KCHUI
interstitial collagenase (EC 3.4.24.7) precursor [validated] - human
N:Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue coll
C:Species: Homo sapiens (man)
C>Date: 13-Aug-1986 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: A37308; S22766; I57620; A00996; D29157; A44518; S06132; B0964; S10595; S53
R:Templeton, N.S.; Brown, P.D.; Levy, A.T.; Margulies, I.M.K.; Liotta, L.A.; Stetler-St
Cancer Res. 50, 5431-5437, 1990
A:Title: Cloning and characterization of human tumor cell interstitial collagenase.
A:Reference number: A37308; MUID:90352587; PMID:2167156
A:Accession: A37308
```



[illegible]

db 421 GIGHKVDAVFMKDGFFYFFHGTROYKFDPKTKRTI.TI.OKANSWENCBY 168

RESULT 12

KCHUN

neutrophil collagenase (EC 3.4.24.34) precursor [validated] - human  
N; Alternate names: matrix metalloproteinase 8  
C; Species: Homo sapiens (man)  
C; Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text change 09-Jul-2004  
C; Accession: A37073; A61175; A36230; S09680; S11026; S19576; S27225; S32527; S6225  
R; Hasty, K.A.; Pourmotabbed, T.F.; Goldberg, G.I.; Thompson, J.P.; Spinella, D.G.; Steved  
J. Biol. Chem. 265, 11421-11424, 1990  
A; Title: Human neutrophil collagenase. A distinct gene product with homology to other ma  
A; Reference number: A37073; MUID:90307647; PMID:2164002  
A; Accession: A37073  
A; Molecule type: mRNA  
A; Residues: 1-467 <HAS>  
A; Cross-references: UNIPROT:P22894; GB:J05556; NID:g180617; PIDN:AAA88021.1; PID:g180618  
R; Devareyan, P.; Mookhtiar, K.; Van Wart, H.; Berliner, N.  
Blood 77, 2731-2736, 1991  
A; Title: Structure and expression of the cDNA encoding human neutrophil collagenase.  
A; Reference number: A61175; MUID:91255696; PMID:1646048  
A; Accession: A61175  
A; Status: not compared with conceptual translation  
A; Molecule type: protein  
A; Residues: 1-31, 'I', '33-86, 'E', '88-467 <DEV>  
A; Accession: B61175  
A; Molecule type: protein  
A; Residues: 263-264, 'X', '266-270, 'X', '272-273, 'X', '275, 'X', '277 <DE2>  
R; Maliya, S.K.; Mookhtiar, K.A.; Gao, Y.; Brew, K.; Dioszegi, M.; Birkedal-Hansen, H.; V  
Biochemistry 29, 10628-10634, 1990  
A; Title: Characterization of 58-kilodalton human neutrophil collagenase: comparison with  
A; Reference number: A36230; MUID:91104978; PMID:2176876  
A; Accession: A36230  
A; Molecule type: protein  
A; Residues: 'X', '86-87, 'X', '89-90, 'X', '92-97, 'X', '99-111, 'X', '113-120 <MAL>  
R; Kraemer, S.; Kraemer, H.; Tschesche, H.  
Eur. J. Biochem. 189, 295-300, 1990  
A; Title: Characterization and activation of procollagenase from human polymorphonuclear  
A; Reference number: S09680; MUID:90249372; PMID:2159879  
A; Accession: S09680  
A; Molecule type: protein  
A; Residues: 21-31, 'I', '33-39, 'I', '41-47, 'V', '49-53, 'I', '55-72, 'G', '74-86, 'E', '88-111, 'X', '113-1  
A; Note: 67-Lys was also found  
R; Kraemer, V.; Kraemer, S.; Reinke, H.; Tschesche, H.  
Biol. Chem. Hoppe-Seyler 371, 733, 1990  
A; Title: Corrigendum. Partial amino-acid sequence of human PMN leukocyte procollagenase.  
A; Reference number: S11026; MUID:91000455; PMID:21659766  
A; Note: original publication was Biol. Chem. Hoppe-Seyler 371 (Suppl.), 295-304, 1990  
A; Accession: S11026  
A; Molecule type: Protein  
A; Residues: 21-31, 'I', '33-53, 'I', '55-72, 'G', '74-111, 'X', '113-140, '183-203, 'X', '205-209; 248-261  
A; Note: 87-Glu was also found  
R; Blaesser, J.; Knaeuper, V.; Osthues, A.; Reinke, H.; Tschesche, H.  
Eur. J. Biochem. 202, 1223-1230, 1991  
A; Title: Mercurial activation of human polymorphonuclear leucocyte procollagenase.  
A; Reference number: S19576; MUID:92111500; PMID:1662606  
A; Accession: S19576  
A; Molecule type: protein  
A; Residues: 69-103 <BL2>  
R; Blaesser, J.; Triebel, S.; Reinke, H.; Tschesche, H.  
FEBS Lett. 313, 59-61, 1992  
A; Title: Formation of a covalent Hg-Cys-bond during mercurial activation of PMNL procoll  
A; Reference number: S27225; MUID:93050220; PMID:1330697  
A; Accession: S27225  
A; Molecule type: protein  
A; Residues: 68-103 <BLA>  
R; Knaeuper, V.; Osthues, A.; DeClerck, Y.A.; Langley, K.E.; Blaesser, J.; Tschesche, H.  
Biochem. J. 291, 847-854, 1993  
A; Title: Fragmentation of human polymorphonuclear-leucocyte collagenase.  
A; Reference number: S32527; MUID:93256897; PMID:8489511  
A; Accession: S32527  
A; Molecule type: Protein

QY 355 AVLPDYPKSIHTLGFPRVKKIDAAVCDKTRTKTYFVGLWCRFDEMOTQMDKGPQV 414  
Db 356 DILQGYPKDISNYGPPSSQVADAAVYRS--KTYFVNDQFVYDNRQRFMEPGPKSI 413  
QY 415 VKHFGISIRVDAAFQYKGFPPSRGSKQFYNKTKNIRIMRTNFWOCK 466  
Db 414 SGAPPGIESKVDAAFOQEHFFVFSGPRYAFDLIAQRVTRVAGNKWLNCR 465

RESULT 13  
A53711  
collagenase 3 (EC 3.4.24.-) - human  
N;Alternate names: matrix metalloproteinase 13 (MMP13)  
C;Species: Homo sapiens (man)  
C;Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 09-Jul-2004  
C;Accession: A53711  
R;Freilje, J.M.P.; Diez-Itza, I.; Balbin, M.; Sanchez, L.M.; Blasco, R.; Toliivia, J.; Lopez  
J. Biol. Chem. 269, 16766-16773, 1994  
A;Title: Molecular cloning and expression of collagenase-3, a novel human matrix metallo  
A;Reference number: A53711; MUID:94266894; PMID:8207000  
A;Accession: A53711  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-471 <PRE>  
A;Cross-references: UNIPROT:P45452; GB:X75308; NID:9516385; PIDN:CA53056.1; PID:9516386  
C;Genetics:  
A;Gene: GDB:MMP13; CLG3  
A;Cross-references: GDB:373966; OMIM:600108  
A;Map position: 11q22.2-11q22.3  
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei  
C;Keywords: hydrolase; metalloproteinase; zinc; zymogen  
F;64-267/Domain: matrix metalloproteinase homology <MMP>  
F;278-471/Domain: hemopexin repeat homology <PXN>  
F;96,222,226,232/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
F;222,226,232/Binding site: zinc, catalytic (His) (active) #status predicted  
F;223/Active site: Glu #status predicted

Query Match 41.3%; Score 1141; DB 2; Length 471;  
Best Local Similarity 49.8%; Pred. No. 9e-85;  
Matches 222; Conservative 62; Mismatches 150; Indels 12; Gaps 8;

QY 26 NEENMOLAQYLNQYF-SLEIEGHLVQSKRSLDDKIREMOAFGLTVTGKLDNSTLE 84  
Db 32 SEEDLQFAERYLYSYHPTNLG--ILKENAASSWTERLREMQSFGLVETGKLDNDTLD 89  
QY 85 IMKTPRCGVPDVGQY--TLPGRKXNLTIRIINYTPDMARAAVDEAIOGLEVWSKV 141  
Db 90 VMKPRCGVPDVGQYVFPRTLK--WSKNLTIRIINYTPDMTHSEVENAKFAKFWGSDV 148  
QY 142 TPLKFTKISGDIADIMAFRTRVHGRCPY--FDGVLGVGHAFPPGPGGLGGDTHFDEDEN 200  
Db 149 TPLNTRLHDGIADIMISFGIKEHG--DFYDFGSGLLAHAFPPGPNYGGDAHFDDDET 206  
QY 201 WTKDAGFNLFLVAAHEFGHGLSHNSDQATLMENYVSLDPRKYPVLSQDDINGIOSIY 260  
Db 207 WTSKSGYNYLFLVAAHEFGHGLSHNSDQATLMENYVSLDPRKYPVLSQDDINGIOSIY 266  
QY 261 GGLPKVPAPKPTIIPACDPOLTDITFRFVNFVFFGRHLWRIYYDITDVEFELIAS 320  
Db 267 GPGDEDP--NPKHPTDKCDPSLSDLAITSRGETIMFKDRFWRHLHPQVDAELFLTKS 325  
QY 321 FWPSLPADIAAYENP--RKILVFKDENTFMIRGYAVLPDYPKSIHTLGFPGVKKIDAA 379  
Db 326 FWPFLPNRIDAAYEHPSHDLIFRGRKFWALNGYDILEGYPKSELGLPKEVKKISAA 385  
QY 380 VCDKTRTKTYFFGIWCRFDEMOTQMDKGPQVVKVHFGISIRVDAAFQYKGFPPSR 439  
Db 386 VHPFEDTGKTLFFSGNQVRIYDDTNHMDKQYPLIEDEFPGIGDKVDVAVKNGIYFFN 445  
QY 440 GSKQFYNKTKNIRIMRTNFWOC 465  
Db 446 GPIQFEYSIWSNIRVWMPANSILWC 471

RESULT 14  
A49499  
metalloelastase HME (EC 3.4.24.-) - human  
C;Species: Homo sapiens (man)  
C;Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A49499  
R;Shapiro, S.D.; Kobayashi, D.K.; Ley, T.J.  
J. Biol. Chem. 268, 23824-23829, 1993  
A;Title: Cloning and characterization of a unique elastolytic metalloproteinase produce  
A;Reference number: A49499; MUID:94043200; PMID:8226919  
A;Accession: A49499  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-470 <SHA>  
A;Cross-references: UNIPROT:P39900; GB:L23808; NID:9435969  
A;Experimental source: alveolar macrophage  
A;Note: sequence extracted from NCBI backbone (NCBIN:139457, NCBI:P139458)  
C;Genetics:  
A;Gene: GDB:MMP12; HME  
A;Cross-references: GDB:266582; OMIM:601046  
A;Map position: 11q22.2-11q22.3  
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei  
C;Keywords: hydrolase; metalloproteinase; zinc; zymogen  
F;60-263/Domain: matrix metalloproteinase homology <MMP>  
F;276-470/Domain: hemopexin repeat homology <PXN>  
F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted  
F;219/Active site: Glu #status predicted

Query Match 41.0%; Score 1133; DB 2; Length 470;  
Best Local Similarity 48.3%; Pred. No. 4e-84;  
Matches 229; Conservative 77; Mismatches 152; Indels 16; Gaps 10;

QY 3 RLLLCLEFFITFSAPFLVMTENEENMQL-AQAYLNQFYSLIEGHLVQSKR--SL 58  
Db 2 KFLTLILQATASGALPLNSSTLEKXNVLFGRYLEKFGLEI--NKLPTKKYKSNL 59  
QY 59 IDDKIREMOAFGLTVTGKLDNSTLEIMKTRCGVPDVGQYTLPG---WRKNLTIRI 115  
Db 60 MKEKIQENQHFLGLKVTGQLDTSILEMHAFCGVPDVHFF-REMPGPGVWRKHVITIRI 118  
QY 116 INYTPDMARAAVDEAIOGLEVWSKVTPKFTKISGDIADIMAFRTRVHGRCPYFDPG 175  
Db 119 NNYTPDMNRDQVDAIRKAFQVSNVTPKFTKISGDIADIMAFRTRVHGRCPYFDPG 177  
QY 176 LGVLGHAFPPGPGGLGGDTHFDEDENWTKDAGFNLFLVAAHEFGHGLSHNSDQATLMF 235  
Db 178 GGIILAHAFPGSGIGGDAHDEDEFTWTHSGGTNLFITAVHIEGHLGSHSDPKAVMF 237  
QY 236 FNVVSLDPRKYPVLSQDDINGIOSIYGGLPKVPAPKPEP--TIPHACDPLDTFDTTFR 293  
Db 238 PTKYKVDINTFLSADDIRGSLYGD-PKENQRLPNPNPNSEPALCDPNLSDFAVTVGN 296  
QY 294 EVMFFKGRHLWRIYYDITDVEFELIASFWPSLPADIAQAYE-NPRDKILVFKDENFWMR 352  
Db 297 KIFFKDFRFLKVSERPKTSVNLISLWPTLFSGIEAAYEIEARNQVFLFKDDKXWLLS 356  
QY 353 GYAVLPDYPKSIHTLGFPGVKKIDAAVCDKTRTKTYFVGLWCRFDEMOTQMDKGPQ 412  
Db 357 NLRFEPNPKSTHSGFNFVKKIDAAVFNFRFYTYFFVDNQWYEDRQWMDPGYFK 416  
QY 413 RVVKGIPPGISIRVDAAFQYKGFPPSRGSKQFYNKTKNIRIMRTNFWOC 465  
Db 417 LITKNFQIGPKIDAVFYKKNKYVFFGSGNQFVEYDFLLQRIITKILKSNWFGC 470

RESULT 15  
A23685  
interstitial collagenase (EC 3.4.24.7) precursor - rat (fragment)  
N;Alternate names: matrix metalloproteinase 1 (MMP1); vertebrate collagenase  
C;Species: Rattus norvegicus (Norway rat)

C>Date: 04-Oct-1991 #sequence\_revision 04-Oct-1991 #text\_change 09-Jul-2004  
C/Accession: A23685  
R/Quinn, C.O.; Scott, D.K.; Brinckerhoff, C.E.; Matrisian, L.M.; Jeffrey, J.J.; Partridge  
J. Biol. Chem. 265, 22342-22347, 1990  
A/Title: Rat collagenase. Cloning, amino acid sequence comparison, and parathyroid hormone  
A/Reference number: A23685; MUID:91093077; PMID:2176215  
A/Accession: A23685  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-466 <QUI>  
A/Cross-references: UNIPROT:P23097; GB:M60616; GB:M36452; NID:G203498; PIDN:AAA72124.1;  
C/Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotease  
C/Keywords: hydrolase; metalloprotease; zinc; zymogen  
F/53-262/Domain: matrix metalloprotease homology <MMP>  
F/273-466/Domain: hemopexin repeat homology <PXX>  
F/91,217,221,227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
F/217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted  
F/218/Active site: Glu #status predicted

Query Match 40.8%; Score 1126; DB 2; Length 466;  
Best Local Similarity 49.2%; Pred. No. 1.5e-83;  
Matches 219; Conservative 67; Mismatches 149; Indels 10; Gaps 7;

QY	26	NEEMOLAAQAYLNQFYSLEIEGHHVQSKNRSLLDDKIREMQAPFGLTGTGKLDSTLEI	85
Db	27	SEEDLEFAEHLKSYHVPVTLGILKXSTVTSTV-DLREMQSFGLDVTGKLDDEPTDI	85
QY	86	MKTPRCGVPDVGQGYG---TLPGWKYNLTIRIINTEDMARAAVDEAIOEGLEWVKVT	142
Db	86	MRKPRCGVPDVGYYVFPRTLK-WSQTNLTIRIINTPDISHSEVEKAFKAFKWSVDVT	144
QY	143	PLKFTWISGDIADIMIAFTRVHRCPRY-FDGLGLVGHAFPPGPGGLGGDTHFDEENW	201
Db	145	PLNFTRIHDGTADIMISFGTKHG--DFYFDPGSGLLAHAFPPGNLGGDAHFDDDET	202
QY	202	TKDGGFNFLVAAHEFGHGLSHSDQTALMFPNYSLDPRKYPPLSQDDINGIQSIYG	261
Db	203	TSSSGYNLFIVAAHELGHSLGHDHSGKOPGALMFPITYTYTGKSHFMLPDDDDVQGIQSLYG	262
QY	262	GLPKVPAPKPEPTIPHACDPLDFTDAITFRREVMEFKGHLWRIYYDITDVEFELIASF	321
Db	263	PGDEDP-NPKHPKTEKCDPALSLDAITSLRGETMIFKDRFFWRLHPQOQVEPELTKSF	321
QY	322	WPSLPADLOAAENP-RDKILVFDENFMWIRGYAVLPDYKPSIHTLPGPGRVKKIDAAV	380
Db	322	WPELENHVDAAVEHPSRDLMFIFGRKFWALNGYDIMEGYPKISDLGFPKEVKLSAAV	381
QY	381	CDKTRTKTYFFVGIWCRFDEMTQMDKGFPOVVVKHFPFGISIRVDAAPQYKGFPPFSRG	440
Db	382	HFEDTGKTLFFSGNHVSYDDANQTMKDYPRLIEEFEGIGDKVDVAVYKNGYIYFFNG	441
QY	441	SKQFEYNIKTKNITRIMRTNTWFOC	465
Db	442	PIQFEYSIWSNRIVRVMTNSLLWC	466

Search completed: November 15, 2004, 21:01:48  
Job time : 28 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2004, 20:51:16 ; Search time 110 Seconds  
(without alignments)  
2683.338 Million cell updates/sec

Title: US-10-729-807-10

Perfect score: 2763

Sequence: 1 MKRLLLCLEFFITFSSAFPL.....SLSLFIFGIVHLKNTSIQ 513

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_02:\*

1: uniprot\_spport:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	2752	99.6	513	2	Q6UWK6		Q6UWK6 homo sapien
2	2752	99.6	513	2	AAQ89112		AAQ89112 homo sapi
3	2731	98.8	513	2	Q9H306		Q9H306 homo sapien
4	2347	84.9	512	2	Q9GKE1		Q9GKE1 tupiaia gilis
5	1520.5	55.0	472	2	Q9J342		Q9J342 gallus gall
6	1286.5	46.6	478	2	Q6Y4Q5		Q6Y4Q5 canis famil
7	1286.5	46.6	478	2	AAO63580		AAO63580 canis fam
8	1271.5	46.0	478	1	MM03_RABIT		MM03_RABIT
9	1254	45.4	477	2	AAH69716		AAH69716 homo sapi
10	1254	45.4	477	2	AAH69716		AAH69716 homo sapi
11	1250	45.2	477	1	MM03_HUMAN		MM03_HUMAN
12	1247	45.1	483	2	Q98857		Q98857 cynops pyrr
13	1244	45.0	477	1	MM03_HORSE		MM03_HORSE
14	1243.5	45.0	476	1	MM10_MOUSE		MM10_MOUSE
15	1234	44.7	476	1	MM10_MOUSE		MM10_MOUSE
16	1234	44.7	476	2	AAH69716		AAH69716 homo sapi
17	1233	44.6	477	1	MM03_MOUSE		MM03_MOUSE
18	1233	44.6	479	2	Q922W6		Q922W6 mus musculu
19	1218	44.1	472	2	Q10833		Q10833 xenopus lae
20	1212.5	43.9	469	1	MM13_XENLA		MM13_XENLA
21	1205	43.6	469	1	MM01_PIG		MM01_PIG
22	1200.5	43.4	464	1	MM12_RABIT		MM12_RABIT
23	1200.5	43.4	464	2	Q9TV75		Q9TV75
24	1198.5	43.4	476	1	MM10_RAT		MM10_RAT
25	1196	43.3	469	1	MM01_HORSE		MM01_HORSE
26	1195	43.3	469	2	Q98858		Q98858 cynops pyrr
27	1190.5	43.1	466	2	Q7SYX1		Q7SYX1 cynops pyrr
28	1183.5	42.8	471	2	Q98859		Q98859 cynops pyrr
29	1177.5	42.6	469	1	MM01_BOVIN		MM01_BOVIN
30	1170.5	42.4	468	1	MM01_RABIT		MM01_RABIT
31	1169	42.3	475	1	MM03_RAT		MM03_RAT

32	1167	42.2	467	1	MM18_XENLA		MM18_XENLA
33	1161.5	42.0	469	1	MM01_HUMAN		MM01_HUMAN
34	1161.5	42.0	469	2	AAH35520		AAH35520 homo sapi
35	1161	42.0	467	1	MM08_HUMAN		MM08_HUMAN
36	1159	41.9	465	2	AAH42742		AAH42742 mus muscu
37	1159	41.9	465	2	BAC40805		BAC40805 mus muscu
38	1158.5	41.9	471	1	MM13_RABIT		MM13_RABIT
39	1155	41.8	472	1	MM13_HORSE		MM13_HORSE
40	1154	41.8	465	2	Q8C209		Q8C209 mus musculu
41	1154	41.8	465	2	Q8C230		Q8C230 mus musculu
42	1150	41.6	465	1	MM08_MOUSE		MM08_MOUSE
43	1143.5	41.4	466	1	MM08_RAT		MM08_RAT
44	1141	41.3	471	1	MM13_HUMAN		MM13_HUMAN
45	1141	41.3	471	2	AAH67522		AAH67522 homo sapi

## ALIGNMENTS

### RESULT 1

Q6UWK6	PRELIMINARY;	PRT;	513	AA.
AC	Q6UWK6;			
DT	05-JUL-2004 (Tremblrel. 27, Created)			
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)			
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)			
DE	MMP27.			
GN	ORFNames=UNQ2503;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=22887296; PubMed=12975309;			
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,			
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,			
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,			
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,			
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,			
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,			
RA	Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,			
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,			
RA	Godowski P.;			
RT	"The secreted protein discovery initiative (SPDI), a large-scale			
RT	effort to identify novel human secreted and transmembrane proteins: a			
RT	bioinformatics assessment."			
RL	Genome Res. 13:2265-2270(2003).			
DR	EMBL; AY358752; AAQ89112.1; -.			
DR	InterPro; IPR000585; Hemopexin.			
DR	InterPro; IPR006026; Peptidase M.			
DR	InterPro; IPR001818; Pept M10A_M12B.			
DR	InterPro; IPR006025; Pept_M_Zn_BS.			
DR	Pfam; PF00045; Hemopexin; 4.			
DR	Pfam; PF00413; Peptidase_M10; 1.			
DR	Pfam; PF03933; Peptidase_M10_N; 1.			
DR	PRINTS; PR00138; MATRXIN.			
DR	SMART; SM00120; HX; 4.			
DR	SMART; SM00235; ZnMc; 1.			
DR	PROSITE; PS00546; CYSTEINE_SWITCH; 1.			
DR	PROSITE; PS00024; HEMOPEXIN; 1.			
DR	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.			
SQ	SEQUENCE 513 AA; 58994 MW; 1B1D55695553DCD CRC64;			

Query Match 99.6%; Score 2752; DB 2; Length 513;

Best Local Similarity 99.8%; Pred. No. 8.7e-216;

Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKRLLLCLEFFITFSSAFPLVRMTENENMQLAQYLNQFVLSIEGNHLVQSKNSRID 60

Db 1 MKRLLLCLEFFITFSSAFPLVRMTENENMQLAQYLNQFVLSIEGNHLVQSKNSRID 60

Qy 61 DKIREMQAFTLVTKGLDSNTLEIMKTPRCGVDPVQGYGTYLFGWRKYNLYRIINYP 120

Tue Nov 16 16:10:24 2004

Db 121 DKIREMAFFGLTVTGKLSNTLEIMKTPRCGVPDVGQYGYTLPGWRKYNLTIRIINYTP 120  
QY 121 DWAAVDAEAIQEGLEWWSKVPLKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180  
Db 121 DWAAVDAEAIQEGLEWWSKVPLKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180  
QY 181 HAPFPGLGGDTHFDEDENTWKDAGFNLFLVAAHEFGHALGSLHSDQATLMFFNYVS 240  
Db 181 HAPFPGLGGDTHFDEDENTWKDAGFNLFLVAAHEFGHALGSLHSDQATLMFFNYVS 240  
QY 241 LDPKPYLSODDINGIQSIYGGPLPKPAKPKETIIPHACDPDLTDAITTFREVVFFKG 300  
Db 241 LDPKPYLSODDINGIQSIYGGPLPKPAKPKETIIPHACDPDLTDAITTFREVVFFKG 300  
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGAVLDPY 360  
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGAVLDPY 360  
QY 361 PKSHTLGFPRGVKKIDAAVCDKTRKTYFFVGIWCRFDEMTQMDKGPQVVKHPPG 420  
Db 361 PKSHTLGFPRGVKKIDAAVCDKTRKTYFFVGIWCRFDEMTQMDKGPQVVKHPPG 420  
QY 421 ISIRVDAAPQYKGFPPFSRSGSKQFEYNIKTNITRIMRTNTWFOCKEPKSSFGDINKE 480  
Db 421 ISIRVDAAPQYKGFPPFSRSGSKQFEYNIKTNITRIMRTNTWFOCKEPKSSFGDINKE 480  
QY 481 KAHSGGKILYHKSLSLFIQVHLLKNTSIYQ 513  
Db 481 KAHSGGKILYHKSLSLFIQVHLLKNTSIYQ 513

RESULT 2  
AAQ89112 ID AAQ89112 PRELIMINARY; PRT; 513 AA.  
AC AAQ89112; Q9H306;  
DT 02-MAR-2004 (TREMBlrel. 27, Created)  
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)  
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)  
DE MMP27  
GN UNQ2503.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
EN [1]\_SEQUENCE FROM N.A.  
RP SEQUENCE FROM N.A.  
RX PubMed=12975309;  
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,  
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,  
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hase P.E., Heldens S.,  
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,  
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,  
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,  
RA Vandlen R., Watanabe C., Wicand D., Woods K., Xie M.H., Yansura D.,  
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,  
RA Godowski P.;  
RT "The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
RT Effort to Identify Novel Human Secreted and Transmembrane Proteins: A  
RT Bioinformatics Assessment.";  
RL Genome Res. 13:2265-2270(2003).  
DR EMBL; AY358752; AAQ89112.1; -.  
SQ SEQUENCE 513 AA; 58994 MW; 1BD556995553DCD CRC64;  
Query Match 99.6%; Score 2752; DB 2; Length 513;  
Best Local Similarity 99.8%; Pred. No. 8.7e-216;  
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MKRLLLLCLFFITFSSAPPLVRMTENEENQIAQAYLNQFYSLEIGNHLVQSKNSLID 60  
Db 1 MKRLLLLCLFFITFSSAPPLVRMTENEENQIAQAYLNQFYSLEIGNHLVQSKNSLID 60  
QY 61 DKIREMAFFGLTVTGKLSNTLEIMKTPRCGVPDVGQYGYTLPGWRKYNLTIRIINYTP 120

Db 61 DKIREMAFFGLTVTGKLSNTLEIMKTPRCGVPDVGQYGYTLPGWRKYNLTIRIINYTP 120  
QY 121 DWAAVDAEAIQEGLEWWSKVPLKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180  
Db 121 DWAAVDAEAIQEGLEWWSKVPLKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180  
QY 181 HAPFPGLGGDTHFDEDENTWKDAGFNLFLVAAHEFGHALGSLHSDQATLMFFNYVS 240  
Db 181 HAPFPGLGGDTHFDEDENTWKDAGFNLFLVAAHEFGHALGSLHSDQATLMFFNYVS 240  
QY 241 LDPKPYLSODDINGIQSIYGGPLPKPAKPKETIIPHACDPDLTDAITTFREVVFFKG 300  
Db 241 LDPKPYLSODDINGIQSIYGGPLPKPAKPKETIIPHACDPDLTDAITTFREVVFFKG 300  
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGAVLDPY 360  
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGAVLDPY 360  
QY 361 PKSHTLGFPRGVKKIDAAVCDKTRKTYFFVGIWCRFDEMTQMDKGPQVVKHPPG 420  
Db 361 PKSHTLGFPRGVKKIDAAVCDKTRKTYFFVGIWCRFDEMTQMDKGPQVVKHPPG 420  
QY 421 ISIRVDAAPQYKGFPPFSRSGSKQFEYNIKTNITRIMRTNTWFOCKEPKSSFGDINKE 480  
Db 421 ISIRVDAAPQYKGFPPFSRSGSKQFEYNIKTNITRIMRTNTWFOCKEPKSSFGDINKE 480  
QY 481 KAHSGGKILYHKSLSLFIQVHLLKNTSIYQ 513  
Db 481 KAHSGGKILYHKSLSLFIQVHLLKNTSIYQ 513

RESULT 3  
Q9H306 ID Q9H306 PRELIMINARY; PRT; 513 AA.  
AC Q9H306;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 26, Last annotation update)  
DE Matrix metalloprotease MMP-27.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
EN [1]\_SEQUENCE FROM N.A.  
RP SEQUENCE FROM N.A.  
RA Benoit de Coignac A., Elson G., Magistrelli G., Jeannin P.,  
RA Delneste Y., Aubry J.P., Berthier O., Bonnefoy J.Y., Gauchat J.F.;  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF195192; AAG28453.1; -.  
DR HSSP; P08254; 1HV7.  
DR MEROPS; M10.027; -.  
DR Genew; HGNC:14250; MMP27.  
DR GO; GO:0005578; C:extracellular matrix; IEA.  
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR000585; Hemopexin.  
DR InterPro; IPR006026; Peptidase M.  
DR InterPro; IPR001818; Pept\_M10A\_M12B.  
DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
DR InterPro; IPR009070; PGHD\_like.  
DR Pfam; PF00045; Hemopexin; 4.  
DR Pfam; PF00413; Peptidase M10; 1.  
DR Pfam; PF03933; Peptidase\_M10\_N; 1.  
DR PRINTS; PR00138; MATRXIN.  
DR SMART; SM00120; HX; 4.  
DR SMART; SM00235; ZnMC; 1.  
DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
DR PROSITE; PS00024; HEMOPEXIN; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
KW Metalloprotease; Protease.  
SQ SEQUENCE 513 AA; 59023 MW; ED3C9B175C014683 CRC64;



Query Match 98.8%; Score 2731; DB 2; Length 513;  
 Best Local Similarity 99.0%; Pred. No. 4.5e-214;  
 Matches 508; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKELLLLCFFITFSSAFPLVRMTENENMOLAQAYLNQFYSLEIEGNHVLVQSKNSLID 60  
 DB 1 MKELLLLCFFITFSSAFPLVRMTENENMOLAQAYLNQFYSLEIEGNHVLVQSKNSLID 60

QY 61 DKIREMQAFGLTVTKGLDNTLEIMKTPRCGVDPDVGQYTLPGWRKYNLTTRIINYTP 120  
 DB 61 DKIREMQAFGLTVTKGLDNTLEIMKTPRCGVDPDVGQYTLPGWRKYNLTTRIINYTP 120

QY 121 DNARAADVAIQBLEVWSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180  
 DB 121 DNARAADVAIQBLEVWSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180

QY 181 HAPPPGGLGGDTHFDEDENTWKDAGFNLFLVAAHEFGHALGLSHSDQTALMFPNYS 240  
 DB 181 HAPPPGGLGGDTHFDEDENTWKDAGFNLFLVAAHEFGHALGLSHSDQTALMFPNYS 240

QY 241 LDPKPYLSQDDINGIQSYGGLPKVPAPKPEPTIPHACDPDLTDAITTRFREVMPFKG 300  
 DB 241 LDPKPYLSQDDINGIQSYGGLPKVPAPKPEPTIPHACDPDLTDAITTRFREVMPFKG 300

QY 361 PKSIHTLGPGRVKKIDAAVCKTKTKTYFFVGIWCRWDEMTQTMKGFPPQVVKHFFG 420  
 DB 361 PKSIHTLGPGRVKKIDAAVCKTKTKTYFFVGIWCRWDEMTQTMKGFPPQVVKHFFG 420

QY 421 ISIRVDAAFQYKGFPPFSGSKQFBNYIKNTKTRITMRTNTWFOCKEPKNSSGFDINKE 480  
 DB 421 ISIRVDAAFQYKGFPPFSGSKQFBNYIKNTKTRITMRTNTWFOCKEPKNSSGFDINKE 480

QY 481 KAHSGGKILYHKSLSLFIQVHLLKNTSIY 513  
 DB 481 KAHSGGKILYHKSLSLFIQVHLLKNTSIY 513

RESULT 4  
 Q9GKE1 PRELIMINARY; PRT; 512 AA.

ID Q9GKE1  
 AC Q9GKE1  
 DT 01-MAR-2001 (TremBLrel. 16, Created)  
 DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)  
 DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)  
 DE Matrix metalloproteinase-27.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiidae; Tupaiidae;  
 OC NCBI\_TaxID=37347;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Sclera;  
 RA Guggenheim J.A., To C.H., Frost M.R.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF281673; AAG44844.1; -  
 DR HSSP; P03956; 1CGL.  
 DR MEROPS; M10.027; -  
 DR GO; GO:0005578; C:extracellular matrix; IEA.  
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000585; Hemopexin.  
 DR InterPro; IPR006026; Peptidase M.  
 DR InterPro; IPR001818; Pept M10A M12B.  
 DR InterPro; IPR006025; Pept M Zn\_BS.  
 DR InterPro; IPR009070; PGSD\_Like.  
 DR Pfam; PF00045; Hemopexin; 4.  
 DR Pfam; PF00413; Peptidase M10; 1.  
 DR Pfam; PF03933; Peptidase M10\_N; 1.  
 DR PRINTS; PR00138; MATRINXIN.

DR SMART; SM00120; HX; 4.  
 DR SMART; SM00235; ZMC; 1.  
 DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
 DR PROSITE; PS00024; HEMOPEXIN; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN 1.  
 SQ SEQUENCE 512 AA; 58816 MW; 9CB089C4F807CEFF5 CRC64;

Query Match 84.9%; Score 2347; DB 2; Length 512;  
 Best Local Similarity 84.8%; Pred. No. 9.8e-183;  
 Matches 434; Conservative 29; Mismatches 49; Indels 0; Gaps 0;

QY 1 MKELLLLCFFITFSSAFPLVRMTENENMOLAQAYLNQFYSLEIEGNHVLVQSKNSLID 60  
 DB 1 MKELLLLCFFITFSSAFPLVRMTENENMOLAQAYLNQFYSLEIEGNHVLVQSKNSLID 60

QY 61 DKIREMQAFGLTVTKGLDNTLEIMKTPRCGVDPDVGQYTLPGWRKYNLTTRIINYTP 120  
 DB 61 DKIREMQAFGLTVTKGLDNTLEIMKTPRCGVDPDVGQYTLPGWRKYNLTTRIINYTP 120

QY 121 DNARAADVAIQBLEVWSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180  
 DB 121 DNARAADVAIQBLEVWSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180

QY 181 HAPPPGGLGGDTHFDEDENTWKDAGFNLFLVAAHEFGHALGLSHSDQTALMFPNYS 240  
 DB 181 HAPPPGGLGGDTHFDEDENTWKDAGFNLFLVAAHEFGHALGLSHSDQTALMFPNYS 240

QY 241 LDPKPYLSQDDINGIQSYGGLPKVPAPKPEPTIPHACDPDLTDAITTRFREVMPFKG 300  
 DB 241 LDPKPYLSQDDINGIQSYGGLPKVPAPKPEPTIPHACDPDLTDAITTRFREVMPFKG 300

QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360  
 DB 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360

QY 361 PKSIHTLGPGRVKKIDAAVCKTKTKTYFFVGIWCRWDEMTQTMKGFPPQVVKHFFG 420  
 DB 361 PKSIHTLGPGRVKKIDAAVCKTKTKTYFFVGIWCRWDEMTQTMKGFPPQVVKHFFG 420

QY 421 ISIRVDAAFQYKGFPPFSGSKQFBNYIKNTKTRITMRTNTWFOCKEPKNSSGFDINKE 480  
 DB 421 ISIRVDAAFQYKGFPPFSGSKQFBNYIKNTKTRITMRTNTWFOCKEPKNSSGFDINKE 480

QY 481 KAHSGGKILYHKSLSLFIQVHLLKNTSIY 512  
 DB 481 KAYSGEVETLHQSLSLFIQVHLLKNTSIY 512

RESULT 5  
 O93342 PRELIMINARY; PRT; 472 AA.

ID O93342  
 AC O93342  
 DT 01-NOV-1998 (TremBLrel. 08, Created)  
 DT 01-NOV-1998 (TremBLrel. 08, Last sequence update)  
 DT 01-MAR-2004 (TremBLrel. 26, Last annotation update)  
 DE Matrix metalloproteinase.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Yang M., Kurkinen M.;  
 RT "Cloning of a novel matrix metalloproteinase (CMMP) from chicken embryo fibroblasts";  
 RL J. Biol. Chem. 0:0-0(1998).  
 DR EMBL; AF062392; AAC33733.1; -  
 DR HSSP; P45452; 830C.  
 DR MEROPS; M10.027; -  
 DR GO; GO:0005578; C:extracellular matrix; IEA.  
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR



FT DISULFID 291 478 By similarity  
 FT CONFLICT 83 N -> D (in Ref. 2).  
 FT CONFLICT 128 R -> K (in Ref. 2).  
 SQ SEQUENCE 478 AA; 53942 MW; CA742E31A4549D40 CRC64;

Query Match 46.0%; Score 1271.5; DB 1; Length 478;  
 Best Local Similarity 51.9%; Pred. No. 5.4e-95;  
 Matches 250; Conservative 75; Mismatches 136; Indels 21; Gaps 9;

QY 1 MKRLLLCLFFITFSSAFPLVRMTENE--NMOLAQAYLNQFYSLEBIEGHLVOSKNSRL 58  
 DB 1 MKTLPILLLCVACSAYPLDGASROADTTNMDLLQQLYENYINLEKDVQKQFVRKDDSP 60

QY 59 IDKIREMQAFGLTGTGKLDNTLEIMKTPTGCGVDVQGYGTLPG---WRKXNLTTRI 115  
 DB 61 VKKIOEMQKFLGLEVTGKLDNTLEIRKPCGVPDVGHFS--TFPGTPKWTHTLTYRI 119

QY 116 INYTPDMARAADVEAIOEGLVMSKVTPLKFTKISKGIADIAMIATFRTRVHGR--CPRYFDG 174  
 DB 120 VNTYTPDLPRDAVDAAIEKALKVWEVTPLTFSRKYEGEADIMISFGVREHGDRI--FDG 177

QY 175 PLGVGLHAFPPGGLGGDTHFDEENWTKDAGNLFVLAHBEFGHALGSHNDQTALM 234  
 DB 178 PGNVLAHAYAPGPGINGDAHFDDEQWTKDTGTNLFVAAHEHGLHSLGLFHSANPEALM 237

QY 235 FPNVSL--DPRKPYLSQDDINGIQSIY-----GLPKVPKPKPTIPHACDPLT 284  
 DB 238 YPVYNAFTDLARFLSQDDVDGIGLSYGPAPASPNDSGVMEPVPPGSGT--FVWCDPLDS 296

QY 285 FDAITTFRRVMPFKGHLRIYDIITDVEFLIASFWPSLPADLOAAYE--NPRDKILVF 343  
 DB 297 FDLSTLURGEILLFKDRIYFRKRSRLLEPEHLISSFWPSLPSAVDAAYEIVISRTVFI 356

QY 344 KDNFWMIRGAVLPDYPKSIHTLGFGRVKKIDAAVCDKTKTKTYTFVGLVWCRPDM 403  
 DB 357 KGTQFWAIRGNVQAGYPRSIHTLGFSTIRKIDAAISDKERKTKTYFVEDKYRFDK 416

QY 404 QTMKGFQPVVKKHFFGISIRVDAAFQYKGFPPFSRGSKOFENYKNTKNTIRMTWTF 463  
 DB 417 QSLPFGPRHTAEDFPFGINPKIDAVFAEFGFFYFSGSSQSEFDPENAKKVTHVLKNSWF 476

QY 464 QC 465  
 DB 477 QC 478

RESULT 9  
 AAH69716 PRELIMINARY; PRT; 477 AA.  
 ID AAH69716  
 AC AAH69716  
 DT 20-MAY-2004 (TRENBLrel. 27, Created)  
 DT 20-MAY-2004 (TRENBLrel. 27, Last sequence update)  
 DT 20-MAY-2004 (TRENBLrel. 27, Last annotation update)  
 DE Matrix metalloproteinase 3, preproprotein.  
 GN MMP3.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PCR rescued clones;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusan K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PCR rescued clones;  
 RA Strausberg R.;  
 RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.  
 DR ENBL; BC069676; AAH69676.1; -;  
 SQ SEQUENCE 477 AA; 53978 MW; 7497490A861DEEA9 CRC64;

Query Match 45.4%; Score 1254; DB 2; Length 477;  
 Best Local Similarity 51.5%; Pred. No. 1.4e-93;  
 Matches 247; Conservative 70; Mismatches 145; Indels 18; Gaps 9;

QY 1 MKRLLLCLFFITFSSAFPLVRMTENE--NMOLAQAYLNQFYSLEBIEGHLVOSKNSRL 59  
 DB 1 MKSLPILLLCVACSAYPLDGASROADTTNMDLLQQLYENYINLEKDVQKQFVRKDDSP 60

QY 60 DDKIREMQAFGLTGTGKLDNTLEIMKTPTGCGVDVQGYGTLPG---WRKXNLTTRI 116  
 DB 61 VKKIREMQKFLGLEVTGKLDNTLEIMKTPTGCGVDVQGHF--RTFPGIPKWKTKHTLTYRI 119

QY 117 NYTPDMARAADVEAIOEGLVMSKVTPLKFTKISKGIADIAMIATFRTRVHGRCPY--PDGP 175  
 DB 120 NYTPDLPKDAVDSAVEKALKVWEVTPLTFSRKYEGEADIMISFAVREHG--DFYPPDGP 177

QY 176 LGVLGHAFPPGGLGGDTHFDEENWTKDAGNLFVLAHBEFGHALGSHNDQTALM 235  
 DB 178 GNVLAHAYAPGPGINGDAHFDDEQWTKDTGTNLFVAAHEHGLHSLGLFHSANPEALM 237

QY 236 FPNVSL--DPRKPYLSQDDINGIQSIY-----GLPKVPKPK--PKEPTIPHACDPLT 286  
 DB 238 PLVHSLTDLTFRLSQDDINGIQSIYGPDPSPETPLVPTPEVPPEPGTPANCDPALSFD 297

QY 287 AITTFRRVMPFKGHLRIYDIITDVEFLIASFWPSLPADLOAAYE--NPRDKILVFD 345  
 DB 298 AVSTLRGEILLFKDRIYFRKRSRLLEPEHLISSFWPSLPSGVDAAYEIVISRTVFI 357

QY 346 ENFWMIRGAVLPDYPKSIHTLGFGRVKKIDAAVCDKTKTKTYTFVGLVWCRPDM 405  
 DB 358 NQFWAIRGNVQAGYPRSIHTLGFSTIRKIDAAISDKERKTKTYFVEDKYRFDK 417

QY 406 MDKGFQPVVKKHFFGISIRVDAAFQYKGFPPFSRGSKOFENYKNTKNTIRMTWTF 465  
 DB 418 MERGPKQIAEDFPFGIDSKIDAVFAEFGFFYFSGSSQSEFDPENAKKVTHVLKNSW 477

RESULT 10  
 AAH69716 PRELIMINARY; PRT; 477 AA.  
 ID AAH69716  
 AC AAH69716  
 DT 20-MAY-2004 (TRENBLrel. 27, Created)  
 DT 20-MAY-2004 (TRENBLrel. 27, Last sequence update)  
 DT 20-MAY-2004 (TRENBLrel. 27, Last annotation update)  
 DE Matrix metalloproteinase 3, preproprotein.  
 GN MMP3.  
 OS Homo sapiens (Human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PCR rescued clones;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusan K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,



RN X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 18-272.  
 RP MEDLINE=96117647; PubMed=8535233;  
 RA Becker J.W., Marcy A.I., Rokosz L.L., Axel M.G., Burbaum J.J.,  
 RA Fitzgerald P.M.D., Cameron P.M., Esser C.K., Hagmann W.K.,  
 RA Hermes J.D., Springer J.P.,  
 RA "Stromelysin-1: three-dimensional structure of the inhibited catalytic  
 RT domain and of the C-truncated proenzyme.";  
 RL Protein Sci. 4:1966-1976(1995).  
 [10]  
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-266.  
 RP MEDLINE=96311273; PubMed=8740360;  
 RA Dhanraj V., Ye Q.-Z., Johnson L.L., Hupe D.J., Ortwein D.F.,  
 RA Dunbar J.B., Rubin J.R., Pavlovsky A., Humblet C., Blundell T.L.,  
 RA "X-ray structure of a hydroxamate inhibitor complex of the stromelysin  
 RT catalytic domain and its comparison with members of the zinc  
 RT metalloproteinase superfamily.";  
 RL Structure 4:375-386(1996).  
 [11]  
 RN X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 105-264.  
 RP MEDLINE=97236965; PubMed=9083493;  
 RA Esser C.K., Buglianesi R.L., Caldwell C.G., Chapman K.T., Durette P.L.,  
 RA Girotta N.N., Kopka I.E., Lanza T.J., LeVorse D.A., Maccoss M.,  
 RA Owens K.A., Pompiom M.M., Simeone J.P., Harrison R.K.,  
 RA Niedzwiecki L., Becker J.W., Marcy A.I., Axel M.G., Christen A.J.,  
 RA McDonnell J., Moore V.I., Olaszewski J.M., Saphos C., Visco D.M.,  
 RA Shen F., Colletti A., Krieter P.A., Hagmann W.K.,  
 RA "Inhibition of stromelysin-1 (MMP-3) by P1'-biphenyllethyl  
 RT carboxyalkyl dipeptides.";  
 RL J. Med. Chem. 40:1026-1040(1997).  
 [12]  
 RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 100-267 IN COMPLEX WITH  
 RP TIMP1.  
 RP MEDLINE=97433330; PubMed=9288970;  
 RA Gomis-Ruth F.-X., Maskos K., Betz M., Berger A., Huber R.,  
 RA Suzuki K., Yoshida N., Nagase H., Brew K., Bourenkov G.P.,  
 RA Bartunik H., Bode W.,  
 RA "Mechanism of inhibition of the human matrix metalloproteinase  
 RT stromelysin-1 by TIMP-1.";  
 RL Nature 389:77-81(1997).  
 [13]  
 RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 100-264.  
 RP MEDLINE=99006562; PubMed=9792098;  
 RA Finzel B.C., Baldwin E.T., Bryant G.L. Jr., Hess G.F., Wilks J.W.,  
 RA Trepoed C.M., Mott J.E., Marshall V.P., Petzold G.D., Poorman R.A.,  
 RA O'Sullivan T.J., Schostarez H.J., Mitchell M.A.,  
 RA "Structural characterizations of nonpeptidic thiazole inhibitors of  
 RT matrix metalloproteinases reveal the basis for stromelysin  
 RT selectivity.";  
 RL Protein Sci. 7:2118-2126(1998).  
 [14]  
 RN X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-272.  
 RP MEDLINE=20013067; PubMed=10543949;  
 RA Chen L., Rydel T.J., Gu F., Dunaway C.M., Pikul S., Dunham K.M.,  
 RA Barnett B.L.,  
 RA "Crystal structure of the stromelysin catalytic domain at 2.0-A  
 RT resolution: inhibitor-induced conformational changes.";  
 RL J. Mol. Biol. 293:545-557(1999).  
 [15]  
 RN X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 100-267.  
 RP MEDLINE=99349695; PubMed=10422833;  
 RA Pavlovsky A.G., Williams M.G., Ye Q.-Z., Ortwein D.F.,  
 RA Purchase C.F. II, White A.D., Dhanraj V., Roth B.D., Johnson L.L.,  
 RA Hupe D., Humblet C., Blundell T.L.,  
 RA "X-ray structure of human stromelysin catalytic domain complexed with  
 RT nonpeptide inhibitors: implications for inhibitor selectivity.";  
 RL Protein Sci. 8:1455-1462(1999).  
 [16]  
 RN STRUCTURE BY NMR OF 100-272.  
 RP MEDLINE=98434377; PubMed=9760240;  
 RA Li Y.C., Zhang X., Melton R., Ganu V., Gonnella N.C.,  
 RA "Solution structure of the catalytic domain of human stromelysin-1  
 RT complexed to a potent, nonpeptidic inhibitor."

RL Biochemistry 37:14048-14056(1998).  
 CC -!- FUNCTION: Can degrade fibronectin, laminin, gelatins of type I,  
 CC III, IV, and V; collagens III, IV, X, and IX, and cartilage  
 CC proteoglycans. Activates procollagenase.  
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage where P1', P2' and P3'  
 CC are hydrophobic residues.  
 CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.  
 CC -!- SIMILARITY: Belongs to peptidase family M10A.  
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
 CC -----  
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 CC -----  
 DR EMBL; X05232; CAA38859.1; -;  
 DR EMBL; J03209; AAA36321.1; -;  
 DR EMBL; U78045; AAB36942.1; -;  
 DR EMBL; AF405705; AAK95247.1; -;  
 DR PIR; A28156; KCHUS1.  
 DR PDB; 1B3D; X-ray; A/B=100-272.  
 DR PDB; 1B8Y; X-ray; A=100-266.  
 DR PDB; 1BIW; X-ray; A/B=100-272.  
 DR PDB; 1BME; NMR; @=100-272.  
 DR PDB; 1BQO; X-ray; A/B=100-272.  
 DR PDB; 1C31; X-ray; A/B=100-272.  
 DR PDB; 1C8T; X-ray; A/B=103-269.  
 DR PDB; 1CAQ; X-ray; A=100-267.  
 DR PDB; 1CI2; X-ray; A=100-267.  
 DR PDB; 1CQR; X-ray; A/B=100-272.  
 DR PDB; 1DSJ; X-ray; A/B=100-272.  
 DR PDB; 1D7X; X-ray; A/B=100-272.  
 DR PDB; 1D8F; X-ray; A/B=100-272.  
 DR PDB; 1D8N; X-ray; A/B=100-272.  
 DR PDB; 1G05; X-ray; A/B=100-272.  
 DR PDB; 1G49; X-ray; A/B=100-272.  
 DR PDB; 1G4K; X-ray; A/B/C=100-267.  
 DR PDB; 1HFS; X-ray; @=105-264.  
 DR PDB; 1HY7; X-ray; A/B=100-272.  
 DR PDB; 1M1W; Model; A=100-268.  
 DR PDB; 1M1W; Model; A=100-268.  
 DR PDB; 1O09; NMR; A=100-267.  
 DR PDB; 1Q1A; X-ray; A/B/C/D=106-267.  
 DR PDB; 1Q1C; X-ray; A/B/C/D=106-266.  
 DR PDB; 1SLM; X-ray; @=18-272.  
 Query Match 45.2%; Score 1250; DB 1; Length 477;  
 Best Local Similarity 51.2%; Pred. No. 3e-93;  
 Matches 246; Conservative 71; Mismatches 145; Indels 18; Gaps 9;  
 Qy 1 MKRLLLCLEFFITSSAPFLVRMTENESE-NMQLAAQVLYNQFYSLEIGHNLVQSKNRLI 59  
 Db 1 MKSLPILLLLCVAVCSAYPLDGAARGEDTSNNLVQKYLENYIDLUKKVQVRRKDSGPV 60  
 Qy 60 DDKIREMQAFGLVTGKLSNTLEIMKTPRCGVDVGQGYTLFG---WRKYNLYTYRII 116  
 Db 61 VKKIREMQKFLGLEVTGKLSNTLEIMKTPRCGVDVGQGYTLFG---WRKYNLYTYRII 119  
 Qy 117 NYTPDMARAAVDEAIQOEGLEVSWKVTPFKTKISKGDIADIMAFRTVHGRCPRY-FDGP 175  
 Db 120 NYTPDLPKDAVDSAVKALKVWEVETPLTFSRLEGEADIMISFAVREHG--DFYPPDPG 177  
 Qy 176 LGVIGHAFPPGGLGGTHDEDEENWKDAGENFLVAHEFGHALGLSHNDQALMF 235  
 Db 178 GNVLAHAYAPGPGINGDAHFDDEQWTKDTTGNLFLVAHEIHSGLGFLFSANTEALMY 237  
 Qy 236 PNYVSL-DPRKYPLSQDDINGIQSIYG-----GLPKVPKAK--PKEPTIPHACDPLDTPD 286  
 Db 238 PLYHSLTDLTFRFLSQDDINGIQSLYGPDPSPETFLVTPETVPEPGTPANCDDPALSFD 297  
 Qy 287 AITFRREVMPFKGRLWRIIYYDITDVEFELIASFWPSLPADLQAAEY-NPRDKILVFKD 345



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Db 298 AVSTLRGEILLFKDRHFWKSLRKLPELHLISFWSLPSGVDAAEVTSKDLVFPKG 357
Qy 346 ENFWIRGYAVLPDYPKSIHTLPGFGRVKKIDAAVCDKTRTKTYFFVGVGWCWREDEMTQT 405
Db 358 NQFWAIRNEVRAGYPRGIHTLGPFTVRKIDAAISDKENKNTYFFVEDKYWREDEKRS 417
Qy 406 MDKGFQVRVHFGPISIRVDAAYQYKGFPSRSGSKQFENYKNTKNTIRMTNTPQC 465
Db 418 MEFGPKQIAEDFGIDSKDAVFEFGFFFTGSSQLFEDPNAKKVTHTLKNSMLNC 477

RESULT 12
Q98857 PRELIMINARY; PRT; 483 AA.
AC Q98857;
DT 01-FEB-1997 (TREMELrel. 02, Created)
DT 01-FEB-1997 (TREMELrel. 02, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Stromelysin-1/2-a.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Limb;
RX MEDLINE=96270627; PubMed=8629202;
RA Miyazaki K., Uchiyama K., Imokawa Y., Yoshizato K.;
RA "Cloning and characterization of cDNAs for matrix metalloproteinases
RT of regenerating newt limbs.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:6819-6824 (1996).
RN EMBL; D82053; BA011524.1; -.
DR HSSP; P33435; ICKV.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
SQ SEQUENCE 483 AA; 54171 MW; 4ABDF98A36E90EAF CRC64;

Query Match 45.1%; Score 1247; DB 2; Length 483;
Best Local Similarity 51.0%; Pred. No. 5.4e-93;
Matches 247; Conservative 72; Mismatches 137; Indels 28; Gaps 9;

Qy 4 LLLCLFFITSSAPPLVRYMTENE-ENMQLAQYALNQYSLEIEGNHLVQSKRSLIDDK 62
Db 6 LLLLC---VHTYAPFAVPATEDRGNEQLAEYLKFFYNLNEODGTPITRKKH-SPFSEK 61
Qy 63 IREMQAFGLVTGKLDNTLEIMKTPRCGPDVGQYGV--TLPGWRKYNLTIRIINTP 120
Db 62 LQEMQAFGLEVTGKLDNTLEIMHKPRCGVADVAEYSHFGFRPTWRTSLTYRILGTP 121
Qy 121 DMARAANDVATIRRAFKWSDVTPLTFSRIYECTAQISFGAGVHG--DFYPFDGPHGTL 179
Db 122 DMAEADVDTAIRRAFKWSDVTPLTFSRIYECTAQISFGAGVHG--DFYPFDGPHGTL 179
Qy 180 GHAPFPGLGSDTHFDEDEWTKDAGFNELVAHAEFGHGLSHSDQALMFPNIV 239
Db 180 AHAFAPGNSIGDAHDFDEDTWTAGSAGYNFLVAHAEFGHGLSHSGDRSALMYPTYS 239
Qy 240 SLDRPKYPLSQDDINGIOSIYGLPK-VPAPKP-----EPTIPHACDPD 282

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Db 240 YIDPARFLPQDDVDGIALYGASFPVPTTPQATTTTSTSSPINSDCPT 299
Qy 283 LTFDAITTFREVMFPKGRHLWRIYYDITDVEFLIASFWLSLADLOAAAYENPR-DKIL 341
Db 300 LVFDAITTLRGEIILFFKDSSEFWRRVPTIKYVNYPISTSWESLPSGIAAYENPETDQIF 359
Qy 342 VFKDENVIRGIRGYAVLPDYPKSIHTLPGFGRVKKIDAAVCDKTRTKTYFFVGVGWCWREDE 401
Db 360 LFGSKTALQGFILLNYPKNIKDLGFRVRKHNAAVYLSQTKTYFFAGEQYWSYDE 419
Qy 402 MTQTMKGFQVRVHFGPISIRVDAAYQYKGFPSRSGSKQFENYKNTKNTIRMTNTPQC 461
Db 420 ARKTMKESPRIEDDFPGIGKGVHAFVFDNGLLYFFSGHKGQFENMKSKKVTRTLKNTS 479
Qy 462 WFQC 465
Db 480 WLCG 483

RESULT 13
MM03 HORSE
ID MM03 HORSE STANDARD; PRT; 477 AA.
AC Q28397;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Stromelysin-1 precursor (EC 3.4.24.17) (Matrix metalloproteinase-3)
DE (MMP-3).
GN Name=MMP3;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=99074117; PubMed=9858406;
RA Richardson D.W., Dodge G.R.;
RT "Molecular characteristics of equine Stromelysin and the tissue
RT inhibitor of metalloproteinase 1.";
RL Am. J. Vet. Res. 59:1557-1562 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=98104320; PubMed=9442239;
RA Balkman C.E., Nixon A.J.;
RT "Molecular cloning and cartilage gene expression of equine Stromelysin
RT 1 (matrix metalloproteinase 3).";
RL Am. J. Vet. Res. 59:30-36 (1998).
RN [3]
RP 3D-STRUCTURE MODELING.
RA Mallena S.C., Sharma J.A.R.P.;
RT "Theoretical model of horse Stromelysin.";
RT Submitted (MAR-2002) to the PDB data bank.
CC -!- FUNCTION: Can degrade fibronectin, laminin, gelatins of type I,
CC III, IV, and V; Collagens III, IV, X, and IX, and cartilage
CC proteoglycans. Activates procollagenase.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage where P1', P2' and P3'
CC are hydrophobic residues.
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
CC similarity).
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC
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CC EMBL; U62529; AAB05774.1; -.

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DR PDB: 1L9L; Model; A=100-267.
DR MEROPS; M10.005; -.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept M10A.M12B.
DR InterPro; IPR006025; Pept M Zn BS.
DR InterPro; IPR009070; PGSD_like.
DR Pfam; PF00045; Hemopexin_4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRILIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR 3D-structure; Calcium-binding; Collagen degradation;
KW Extracellular matrix; Glycoprotein; Hydrolase; Metal-binding;
KW Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 17 Potential.
FT PROPEP 18 99 Activation peptide.
FT CHAIN 100 477 Hemopexin-1.
FT DOMAIN 287 477 Hemopexin-like.
FT SITE 92 92 Cysteine switch (Potential).
FT METAL 124 124 Calcium 1 (By similarity).
FT METAL 158 158 Calcium 2 (By similarity).
FT METAL 168 168 Zinc 1 (By similarity).
FT METAL 170 170 Zinc 1 (By similarity).
FT METAL 175 175 Calcium 3 (By similarity).
FT METAL 176 176 Calcium 3 (via carbonyl oxygen) (By
FT METAL 178 178 Calcium 3 (via carbonyl oxygen) (By
FT METAL 180 180 Calcium 3 (via carbonyl oxygen) (By
FT METAL 183 183 Zinc 1 (By similarity).
FT METAL 190 190 Calcium 2 (via carbonyl oxygen) (By
FT METAL 192 192 Calcium 2 (via carbonyl oxygen) (By
FT METAL 194 194 Calcium 2 (By similarity).
FT METAL 196 196 Zinc 1 (By similarity).
FT METAL 198 198 Calcium 3 (By similarity).
FT METAL 199 199 Calcium 1 (By similarity).
FT METAL 201 201 Calcium 1 and 3 (By similarity).
FT METAL 218 218 Zinc 2 (catalytic) (By similarity).
FT ACT_SITE 219 219 By similarity.
FT METAL 222 222 Zinc 2 (catalytic) (By similarity).
FT METAL 228 228 Zinc 2 (catalytic) (By similarity).
FT METAL 297 297 Calcium 4 (via carbonyl oxygen) (By
FT METAL 389 389 Calcium 4 (via carbonyl oxygen) (By
FT METAL 438 438 Calcium 4 (via carbonyl oxygen) (By
FT CARBOHYD 120 120 N-linked (GlcNAc... ) (Potential).
FT DISULFID 290 477 By similarity.
FT CONFLICT 346 346 V -> E (in Ref. 2).
FT TURN 104 105
FT STRAND 113 118
FT TURN 123 124
FT HELIX 127 144
FT STRAND 148 151
FT STRAND 159 164
FT STRAND 182 184
FT TURN 180 193
FT STRAND 195 198
FT TURN 199 200
FT STRAND 203 204
FT STRAND 210 211
FT HELIX 212 224
FT TURN 225 225
FT TURN 232 233

FT TURN 235 236
FT HELIX 253 263
SQ SEQUENCE 477 AA; 54190 MW; 361CE1427E09A272 CRC64;

Query Match 45.0%; Score 1244; DB 1; Length 477;
Best Local Similarity 50.8%; Pred. No. 9.4e-93;
Matches 244; Conservative 73; Mismatches 145; Indels 18; Gaps 8;

QY 1 MKGLLLCLFFITFSAPFLVMTENEE-NMQLAQAYLNQFYSLIEGHNHLVSKNRSLI 59
Db 1 MKNLPITILLILCVAAACSAYPLDRSARDESDNMDLLQYLEKYDYGKEMROYVRKDSGPI 60
QY 60 DDKIREMOAQFGLTVTKGLSDNTLEMTKPRCGVPDVGQVGYTLPG---WRKNLTVRII 116
Db 61 VKKIEMQKPLGLKVKTKGLSDSIVEMHKSRCCGVPDVGHF-TTFPGMPKWSKTHLYRIIV 119
QY 117 NYTPDMARAADDEAIQEGLEVMSKVTPKFTKISKIADIIMIAFRTRVHGR-CPRYFDGP 175
Db 120 NYTQDLPRDAVSDSDEKALKIWEVTPLTFSRIYEGEADIMITFAVREHGDFP--FDGP 177
QY 176 LGVIGHAFPPGCGLGDTDFDEDEWTKGAGNLFVAAHEFGHALGSHSNDQTALMF 235
Db 178 GKVLAHAYPPGPGMGMDAHFDDEHWTKDASGINFLLVAAHELGHSLGLYHSTNTALMY 237
QY 236 PNVVSL-DRPKYPLSODDINGQSIYGLPKVPKPKPTIPH-----ACDPDLTFD 286
Db 238 PLYNTLKGPARVLSQDDVTGQSLGPPSPASPDSPVEPPEPPAPGTLAMCDPALSPD 297
QY 287 AITFERREVMFPKGRHLRIYYDITDVEFELIASFWPSLPADLQAAAYE-NPRDKILVFKD 345
Db 298 AISTLGRGELFFKDRYFWRKTRTLVDFEHPHPISSFWPSLPSGIDAAAEVTSRDSVRFKG 357
QY 346 ENFMWIRGVAVLPDYPKSIHTLGFGRVKIDAAVCDCKTRKTYFFVGVIGWCFDEMTQT 405
Db 358 NKFMAIRGNEBQAGYPRGIHTLGFPTVRKIDAAIEFKQKTYFFVEDKYWRDFEKQRS 417
QY 406 MDKGFQRVVKVPPPGISIRVDAAFQYKGFPPFSRGSQKFEYNLTKNITRIMTNTWFOC 465
Db 418 MEGYPKQIAEDFPGLDSDKLDAAEFSGFYFFSGSSQFEFDDNAKVTHLVKSNWFNC 477

RESULT 14
MM10_MOUSE STANDARD; PRT; 476 AA.
AC Q55123;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Stromelysin-2 precursor (EC 3.4.24.22) (Matrix metalloproteinase-10)
DE (MMP-10) (Transin-2) (SL-2).
GN Name=Mmp10;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=98087420; PubMed=9427548;
RA Madlener M., Werner S.;
RT "cDNA cloning and expression of the gene encoding murine Stromelysin-2
(RMMP-10).";
RL Gene 202:75-81(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: November 15, 2004, 20:20:25 ; Search time 218.5 Seconds  
(without alignments)  
5269.233 Million cell updates/sec

Title: US-10-729-807-28

Perfect score: 2930

Sequence: 1 gcttcagctgaagaagaga.....aattcgtctcaaatagaa 1627

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Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 3137398

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications AA\_QMFT-fastcan -SUFFIX=rapb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100  
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-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-XGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA:

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20:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result \* Query

No.	Score	Match	Length	DB	ID	Description
1	2763	94.3	513	10	US-09-862-631-4	Sequence 4, Appli
2	2763	94.3	513	16	US-10-729-807-10	Sequence 10, Appl
3	2752	93.9	513	10	US-09-759-130B-173	Sequence 173, App
4	2752	93.9	513	14	US-10-028-072-192	Sequence 192, App
5	2752	93.9	513	14	US-10-140-808-192	Sequence 192, App
6	2752	93.9	513	14	US-10-121-049-192	Sequence 192, App
7	2752	93.9	513	14	US-10-123-904-192	Sequence 192, App
8	2752	93.9	513	14	US-10-140-470-192	Sequence 192, App
9	2752	93.9	513	14	US-10-175-746-192	Sequence 192, App
10	2752	93.9	513	14	US-10-176-918-192	Sequence 192, App
11	2752	93.9	513	14	US-10-176-921-192	Sequence 192, App
12	2752	93.9	513	14	US-10-137-865-192	Sequence 192, App
13	2752	93.9	513	14	US-10-140-474-192	Sequence 192, App
14	2752	93.9	513	14	US-10-142-431-192	Sequence 192, App
15	2752	93.9	513	14	US-10-143-114-192	Sequence 192, App
16	2752	93.9	513	14	US-10-140-002-192	Sequence 192, App
17	2752	93.9	513	14	US-10-142-419-192	Sequence 192, App
18	2752	93.9	513	14	US-10-123-262-192	Sequence 192, App
19	2752	93.9	513	14	US-10-142-423-192	Sequence 192, App
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41	2752	93.9	513	14	US-10-128-693A-192	Sequence 192, App
42	2752	93.9	513	14	US-10-131-813A-192	Sequence 192, App
43	2752	93.9	513	14	US-10-131-818A-192	Sequence 192, App
44	2752	93.9	513	14	US-10-131-823A-192	Sequence 192, App
45	2752	93.9	513	14	US-10-131-824A-192	Sequence 192, App

## ALIGNMENTS

RESULT 1  
US-09-862-631-4  
; Sequence 4, Application US/09862631  
; Publication No. US20030032164A1  
; GENERAL INFORMATION:  
; APPLICANT: Holmgren, Erik  
; APPLICANT: Kihlen, Mats  
; APPLICANT: Wood, Tim  
; APPLICANT: Ekblom, Jonas  
; TITLE OF INVENTION: Novel Matrix Metalloproteinases  
; FILE REFERENCE: 00014regus  
; CURRENT APPLICATION NUMBER: US/09/862,631  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: 206119  
; PRIOR FILING DATE: 2000-05-22  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 513  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-862-631-4

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Best Local Similarity:	100.00%	Mismatches:	0		
Query Match:	94.30%	Indels:	0		
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QY	144	TACTCTCTGAAATAGAGGGAATCATCTTGTTCAAAGCAAGATAGAGTCTCATAGAT	203		
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QY	864	CCTGACTTGACTTTTTCAGCGTATCACAACTTTCGCGAGAGAATATGTTCTTTAAAGC	923		
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QY	924	AGGCACCTATGGAGATCTATTATGATATCACGGATGTTGAGTTTGAATTAATTTGCTTCA	983		





PRIOR APPLICATION NUMBER:	US 09/333,159
PRIOR FILING DATE:	1999-06-14
PRIOR APPLICATION NUMBER:	US 09/596,194
PRIOR FILING DATE:	2000-07-14
PRIOR APPLICATION NUMBER:	US 09/342,364
PRIOR FILING DATE:	1999-06-29
PRIOR APPLICATION NUMBER:	US 09/608,452
PRIOR FILING DATE:	2000-06-30
PRIOR APPLICATION NUMBER:	US 09/393,996
PRIOR FILING DATE:	1999-09-10
PRIOR APPLICATION NUMBER:	US 09/602,871
PRIOR FILING DATE:	2000-06-23
PRIOR APPLICATION NUMBER:	US 09/420,707
PRIOR FILING DATE:	1999-10-19
NUMBER OF SEQ ID NOS:	460
SOFTWARE:	FastSeq for Windows Version 4.0
SEQ ID NO 173	
LENGTH:	513
TYPE:	PRF
ORGANISM:	Homo sapiens
US-09-759-130B-173	

  

Alignment Scores:	
Pred. No.:	1-98e-273
Score:	2752.00
Percent Similarity:	99.81%
Best Local Similarity:	99.81%
Query Match:	93.92%
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APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang  
TITLE OF INVENTION:  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/028,072  
CURRENT FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
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7	PRIOR FILING DATE: 1998-06-26
7	PRIOR APPLICATION NUMBER: 60/091360
7	PRIOR FILING DATE: 1998-07-01
7	PRIOR APPLICATION NUMBER: 60/091519
7	PRIOR FILING DATE: 1998-07-02
7	PRIOR APPLICATION NUMBER: 60/091982
7	PRIOR FILING DATE: 1998-07-07

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 QY 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCCTCATTTGGTTTGTATATCAACAAGGAA 1463  
 Db 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480  
 QY 1464 AAAGCACATTCAGGAGGATAAAGATATGTATCATAGAGTTTAAGCTTGTATTTT 1523  
 Db 481 LysAlaHisSerGlyGlyIleLysIleLeuTyHisLysSerLeuSerLeuPheIlePhe 500  
 QY 1524 GGTATTGTTCATTCTGCAAAACACTTCTATTATCAAA 1562  
 Db 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyGln 513

## RESULT 5

US-10-140-808-192  
 ; Sequence 192, Application US/10140808  
 ; Publication No. US20030017563A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeForge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3330R1C182  
 ; CURRENT APPLICATION NUMBER: US/10/140,808  
 ; CURRENT FILING DATE: 2002-05-07  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 192  
 ; LENGTH: 513  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-140-808-192

Alignment Scores:  
 Pred. No.: 1,98e-273 Length: 513  
 Score: 2752.00 Matches: 512  
 Percent Similarity: 99.81% Conservative: 0  
 Best Local Similarity: 99.81% Mismatches: 1  
 Query Match: 93.92% Indels: 0  
 DB: 14 Gaps: 0

US-10-729-807-28 (1-1627) x US-10-140-808-192 (1-513)

QY 24 ATGAAGGCGCTTCTGCTTCTGTGTTGTTCTTTATACATTTTCTTCTGCATTTCCCTTA 83  
 Db 1 MetLysArgLeuLeuLeuPheLeuPheIleThrPheSerAlaPheProLeu 20  
 QY 84 GTCGGATGACGGAATGAAGAAATATCAACTGGCTCAGGCATATCTCAACCCAGTTC 143  
 Db 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyLeuAsnGlnPhe 40  
 QY 144 TACTCTCTGAATAGAGGGAATCATCTTGTTCAGAGCAAGAAATAGGAGTCTCATAGAT 203  
 Db 41 TySerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60  
 QY 204 GACAAATTCGGGAATGCAAGCATTTTGGATTGACAGTACTGGAAACTGGACTCA 263

Db 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
 QY 264 AACACCCCTTGATGATCAAGACACCCAGGTGTGGGTGCTGATGTGGCCAGTATGCG 323  
 Db 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyGly 100  
 QY 324 TACACCCCTCCCTGGGTGAGAAAATACAACTCACCTACAGATAATAAATATACTACTCG 383  
 Db 101 TyrThrLeuProGlyTyProArgLysTyAsnLeuThrTyArgIleIleAsnTyThrPro 120  
 QY 384 CATATGGCAGCAGCTGCTGTGGATGAGCTATCCAAAGAGGTTTAAAGTGTGGAGCAAA 443  
 Db 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140  
 QY 444 GTCACCTCCACTAAATTCACCAAGATTTCAAAGGGATTGCAGACATCATGATTCCTTT 503  
 Db 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160  
 QY 504 AGGACTCGAGTCCATGTCGGTGTCTCTGCTATTTTGTATGTCCTTGGAGTGTCTGCG 563  
 Db 161 ArgThrArgValHisGlyArgCysProArgTyPheAspGlyProLeuGlyValLeuGly 180  
 QY 564 CATGCTTTCTCTCTGGTCCGGTCTGGGTGTGCTGACACTCATTTTGTAGAGATGAAAC 623  
 Db 181 HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200  
 QY 624 TGGACCAAGGATGGAGCAGGATTCAACTTGTCTTCTGCTGCTCATGAATTCGTTCAT 683  
 Db 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGlnPheGlyHis 220  
 QY 684 GCACCTGGGGCTCTCTCACTCCAAATGATCAAAAGAGCTTGTATGTCCTCCAAATATGTC 743  
 Db 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyValSer 240  
 QY 744 CTGGATCCCGAGAAATACCCACTTTTCTCAGGATGATATCAATGGAATCCAGTCCATCAT 803  
 Db 241 LeuAspProArgLysTyProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTy 260  
 QY 804 GGAGTGTGCTTAAGTACTCTGCTAAGCAAGGACCCACTATACCCCATCCCTGTGAC 863  
 Db 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280  
 QY 864 CTGACTTGACTTTTGAGCTATCACACTTCCGAGAGAGATGATGTTCTTTAAAGGC 923  
 Db 281 ProAspLeuThrPheAspAlaIleThrPheArgArgGluValMetPhePheLysGly 300  
 QY 924 AGGCACCTATGAGGATCTATTATGATATCACGGATGTTGAGTTTGAATTAATTTGTTCA 983  
 Db 301 ArgHisLeuTrpArgIleTyTyAspIleThrAspValGluPheGluLeuIleAlaSer 320  
 QY 984 TTCTGGCGATCTCTCCAGCTGATCTGGAAGCTGCATACGAGAACCCAGAGATAGATT 1043  
 Db 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyGluAsnProArgAspLysIle 340  
 QY 1044 CTGGTTTTTAAAGATGAAAACCTTCTGGATGATCAGAGGATATGCTGCTTGCAGATTAT 1103  
 Db 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyAlaValLeuProAspTy 360  
 QY 1104 CCCAAATCCATCATACATTAGTGTTCAGGACGCTGTGAAGAAATAGATGACGCGCTC 1163  
 Db 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380  
 QY 1164 TGTGATAAGACCAAGAAAACCTTCTTCTTGTGGGCTTGTGGTGTGGAGTTTGTAT 1223  
 Db 381 CysAspLysThrThrArgLysThrTyPhePheValGlyIleTyProCysTrpArgPheAsp 400  
 QY 1224 GAAATCACCAACCACTGACAAAGATTCGCGCAGAGAGTGGTAAACACATTTCTCTGA 1283  
 Db 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly 420  
 QY 1284 ATCAGTATCCGTGTGTGATGCTGCTTCCAGTACAAAGGATTCCTTTTTCAGCCGTGA 1343

Db 421 IleSerIleArgValAlaAlaPheGlnTyrIysGlyPhePhePheSerArgGly 440  
QY 1344 TCRAAGCAATTTGATACAAATTAAGCAAGATATATTACCGAATCATGAGAACTAAT 1403  
Db 441 SerIysGlnPheGluTyrAsnIleIysThrLysAsnIleThrArgIleMetArgThrAsn 460  
QY 1404 ACTTGGTTTCAATGCACAAAGAACCAAGAACTCTCATTTGTTTGTATATCAACAAAGAA 1463  
Db 461 ThrTrpPheGlnCysLysGluProLysAsnSerPheGlyPheAspIleAsnLysGlu 480  
QY 1464 AAAGCAATTCAGAGGCAATAAGATATGTATCATAGAGTTTAAGCTTGTATTTT 1523  
Db 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500  
QY 1524 GGTATTGTTCAATTCCTGAAACACATCTCTATTTATCAA 1562  
Db 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513

## RESULT 6

US-10-121-049-192  
; Sequence 192, Application US/10121049  
; Publication No. US20030022239A1

## ; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3330R1C17

; CURRENT APPLICATION NUMBER: US/10/121,049

; CURRENT FILING DATE: 2002-04-12

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 192

; LENGTH: 513

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-121-049-192

## Alignment Scores:

Pred. No.: 1.98e-273 Length: 513  
Score: 2752.00 Matches: 512  
Percent Similarity: 99.81% Conservative: 0  
Best Local Similarity: 99.81% Mismatches: 1  
Query Match: 93.92% Indels: 0  
DB: 14 Gaps: 0

US-10-729-807-28 (1-1627) x US-10-121-049-192 (1-513)

QY 24 ATGAAGCGCTTCTGCTTCTGTGTTCTTTTATACATTTTCTTCTGATTTCCCTTA 83  
Db 1 McLysArgLeuLeuLeuPheLeuPhePheIleThrPheSerAlaPheProLeu 20  
QY 84 GTCGGATGACGAAATGAGAAATATGCAACTGGCTCAGGCATATCTCAACCACTTC 143  
Db 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40  
QY 144 TACTCTTCAATAGAGGATCATCTTGTTCAAAGCAAGATAGGAGTCTCATAGAT 203

Db 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60  
QY 204 GACAAAATTCGGGAAATGCAAGCAATTTTTCGATTTGACAGTCACTGGAATACTGACATCA 263  
Db 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
QY 264 AACACCTTTCGATGATGAGACACACCCAGGTGTGGGTGCTGATGCGGCAGTATGCG 323  
Db 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
QY 324 TACACCTTCCTCGGTGAGAAAATACAACTCACCTACACATAAATAAATACTACTCCG 383  
Db 101 TyrThrLeuProGlyTyrPargLysTyrAsnLeuThrTyrArgLleIleAsnTyrThrPro 120  
QY 384 GATATGCGACAGCTGCTGTGGATGAGGCTATCAAGAAGGTTTAGAAGTGTGGAGCAAA 443  
Db 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140  
QY 444 GTCACTCCACTTAAATTCACCAAGATTTCAAAGGGATTCGACACATCATGATTCCTTT 503  
Db 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160  
QY 504 AGGACTCGAGTCCATGCTCGGTGCTCGCTATTTTGTATGTCCTTGGAGTGTGCTGCG 563  
Db 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180  
QY 564 CATGCCCTTCTCCTGCTCGGTGCTGGGTGTCGACACTCATTTTGTAGAGGATGAAAC 623  
Db 181 HisAlaPheProGlyProGlyLeuGlyAspThrHisPheAspGluAspGluAsn 200  
QY 624 TGGACCAAGATGAGGACAGGATCAACTGTTCTTCTGCTGCTGCTCATGATTTGGTCAT 683  
Db 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220  
QY 684 GCACGTGGGCTCTCTCACTCCAATGATCAAAACAGCCTTGATGTTCCCAAAATATGTCCTC 743  
Db 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240  
QY 744 CTGATCCCGAGAAATACCCACTTTCTCAGATGATATCAATGGAATCCAGTCCATCTAT 803  
Db 241 LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr 260  
QY 804 GAGAGTCTGCTTAAGTACCTGCTAGCCAAAGAACCCACTATACCCCATGCTGTCAC 863  
Db 261 GlyGlyLeuProLysValProAlaLysProLysGlnProThrIleProHisAlaCysAsp 280  
QY 864 CCGACTTGACTTTTGACGCTATCACAACTTTCCGACAGAGAAGTAATGTTCTTTAAAGGC 923  
Db 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300  
QY 924 AGGCACCTATGGAGGATCTATTATGATATCACGGATGTTGAGTTGAAATTAATGCTTCA 983  
Db 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320  
QY 984 TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCTATACAGAACCCAGAGATAAGATT 1043  
Db 321 PheTrpProSerLeuProAlaAspLeuGlnAlaTyrGluAsnProArgAspLysIle 340  
QY 1044 CTGGTTTTTAAGATGAAAACCTTCTGGATGATCAGAGGATATGCTGTCTGCCAGATTAT 1103  
Db 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360  
QY 1104 CCCAAATCCATACATACATAGGTTTCCAGGACGTTGAGAGAAATAGATGACGGCTC 1163  
Db 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380  
QY 1164 TGTGATAAGACCAACAAAGAAAACCTACTCTTTTGTGGGCAATTTGGTCTCGAGTTTGTAT 1223  
Db 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400  
QY 1224 GAAATGACCCAAACCATGACAAAGGATTTCCCGACAGAGTGTGTAAACACTTTCCTGGA 1283  
Db 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420

QY 1284 ATCAGTATCCGTGTGTGATGCTTTTCAGTACAAAGAAATCTCTTTTTCAGCGGTGGA 1343  
 Db 421 IISerileArgValAspAlaAlaPheGlnTyrIysGlyPhePhePheSerArgGly 440  
 QY 1344 TCAAGCAATTTGATCAACATTAAGACAAAGAAATATCCCGAATCATGAGAACTAAT 1403  
 Db 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460  
 QY 1404 ACTTGGTTTCAATGCAGAAAGAACCAAGAACTCTCATTTGGTTTTGTATATCAACAGGAA 1463  
 Db 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480  
 QY 1464 AAAGCACATTCAGGAGGATTAAGATATGTATCATAGAGTTTAAGCTTCTTTATTTTT 1523  
 Db 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500  
 QY 1524 GGTATGTCTTCTGCTGAAAACACTCTCTATTTATCAA 1562  
 Db 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513

## RESULT 7

US-10-123-904-192  
 ; Sequence 192, Application US/10123904  
 ; Publication No. US20030022328A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeForge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3330R1C54  
 ; CURRENT APPLICATION NUMBER: US/10/123,904  
 ; CURRENT FILING DATE: 2002-04-16  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 192  
 ; LENGTH: 513  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-123-904-192

Alignment Scores:  
 Pred. No.: 1.98e-273 Length: 513  
 Score: 2752.00 Matches: 512  
 Percent Similarity: 99.81% Conservative: 0  
 Best Local Similarity: 99.81% Mismatches: 1  
 Query Match: 93.92% Indels: 0  
 DB: 14 Gaps: 0

US-10-729-807-28 (1-1627) x US-10-123-904-192 (1-513)

QY 24 ATGAAGCGCTTCTGCTTCTGTGCTTTTGTCTTTTATACATTTTCTCTGCAATTTCCCTTA 83  
 Db 1 MetLysArgLeuLeuLeuLeuPhePhePheIleThrPheSerSerAlaPheProLeu 20  
 QY 84 GTCCGATGACGGAATTAAGAAATATCAACTGGCTCAGGCATATCTCAACCAAGTTC 143  
 Db 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40

QY 144 TACTCTCTTGAATAGAGGAATCATCTCTTCCAAAGCAAGAATAGGAGTCTCATAGAT 203  
 Db 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60  
 QY 204 GACAAAATTCGGGAAATGCAAGCAATTTTTCGATTTGACAGTGCAGTGGAAAACTGACTCA 263  
 Db 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
 QY 264 AACACCTTGTAGATCATGACACACCCAGCGTGTGGGTGCTGATGCGGCAGCATATCGC 323  
 Db 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
 QY 324 TACACCTCTCCCTGGTGGAGAAAATACAACTCCACTACAGAAATAATAAACTATACTCCG 383  
 Db 101 TyrThrLeuProGlyTyrPargLysTyrAsnLeuThrTyrArllelleAsnTyrThrPro 120  
 QY 384 CATATGGCAGCAGCTGCTGTGTGATGAGCTATCCAAAGAGTTTAGAAGTGTGGAGCAAA 443  
 Db 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140  
 QY 444 GTCACCTCCACTAAAATTCCCAAGATTTCAAGGGGATTGCAGACATCATGATTCCTTT 503  
 Db 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160  
 QY 504 AGGACTCGAGTCCATGCTCGGTCTCTCGCTATTTTGTATGGTCCCTTGGGAGTGTTCG 563  
 Db 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180  
 QY 564 CATGCTTTCTCTGCTGGTCCGGTCTGGGTGTGACACTCATTTTGTAGAGATGAAAC 623  
 Db 181 HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200  
 QY 624 TGGACCAAGATGAGCAGGATTCACACTGTTTCTGTGGCTGCATCAATTCGTTCAT 683  
 Db 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGlnPheGlyHis 220  
 QY 684 GCACCTGGGCTCTCTCACTCCCAATCATCAACAGCGCTTGATGTTCCCAAAATATGTC 743  
 Db 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240  
 QY 744 CTGGATCCCAAGAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803  
 Db 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260  
 QY 804 GGAGTCTGCTTAAGTACTCTTAAGCCAAAGGACCCACTATACCCCTGCTGTGAC 863  
 Db 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280  
 QY 864 CTGACTTTCACCTTTTGACGCTATCAACTTTCCGACAGAGAAAGTATGTTCTTTAAAGGC 923  
 Db 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300  
 QY 924 AGGCACCTATGAGGATCTATTATGATATCAGGATGTTGAGTTTGAATTAATTCCTTCA 983  
 Db 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320  
 QY 984 TTCTGSCCATCTGCGCAGCTGATCTGCAAGCTGCATACGAGAACCCAGAGATAAGATT 1043  
 Db 321 PheTrpProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnProArgAspLysIle 340  
 QY 1044 CTGGTTTTTAAAGATGAAAACCTTCTGGATGATGATCAGAGGATATGCTGCTTTCAGAGATTAT 1103  
 Db 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360  
 QY 1104 CCCAAATCCATCATACATTAGGTTTTCCAGACGCTGTGAAGAAATAGATGACGCGCTC 1163  
 Db 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380  
 QY 1164 TGTGATAACCAACAGAAAACCTTCTTGTGGCATTTGCTGCTGGAGTTTGTAT 1223  
 Db 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400

QY 1224 GAATAGCCCAACCAATGACCAAGGATTCGCCAGAGAGTGTAACACATTTCTCTGGA 1283  
Db GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420  
QY 1284 ATCAGTATCCGTGTGTGCTGTTTCCAGTACAAAGGATTTCTTTTTCAGCCGTGGA 1343  
Db IleSerIleArgValAspAlaPheGlnIleLysGlyPhePhePheSerArgGly 440  
QY 1344 TCAAGCAATTTGAATCAACATTAAGCAAGGATATTCACCGATCATCAGAACTAAT 1403  
Db SerLysGlnPheGluIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460  
QY 1404 ACTTGGTTTCAATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1463  
Db ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480  
QY 1464 AAGCACATTCAGGAGGCAATGATATTTGATATCATGAGTTTAAAGTTCTTTATTTT 1523  
Db LysAlaHisSerGlyGlyIleLysIleLeuIleLysSerLysSerLeuPheIlePhe 500  
QY 1524 GGTATTGTTTCAATTCGTAACCAACATCTCTATTTATCAA 1562  
Db GlyIleValHisLeuLeuLysAsnThrSerIleIleGln 513

## RESULT 8

US-10-140-470-192  
; Sequence 192, Application US/10140470  
; Publication No. US20030022331A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Fillardoff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: F3330R1C160  
; CURRENT APPLICATION NUMBER: US/10/140,470  
; CURRENT FILING DATE: 2002-05-06  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 192  
; LENGTH: 513  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-140-470-192

## Alignment Scores:

Pred. No.:	1,98e-273	Length:	513
Score:	2752.00	Matches:	512
Percent Similarity:	99.81%	Conservative:	0
Best Local Similarity:	99.81%	Mismatches:	1
Query Match:	93.92%	Indels:	0
DB:	14	Gaps:	0

US-10-729-807-28 (1-1627) x US-10-140-470-192 (1-513)

QY 24 ATGAGCGCTTCTGCTGCTGTTGTTGTTTATTAACATTTCTTCTGCAATTCCTCTTA 83  
Db 1 MetLysArgLeuLeuLeuPhePheIleThrPheSerSerAlaPheProLeu 20

QY 84 GTCGGATGACGGAATTAAGAAATATGCAACTGGCTCAGGCATATCTCAACAGTTC 143  
Db ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaIleLysLeuAsnGlnPhe 40  
QY 144 TACTCTCTTGAATAGAGGGAATCATCTCTTCAAGCAAGGATAGAGTCTCATAGAT 203  
Db TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60  
QY 204 GACAAAATTCGGGAAATTCAGCAAGCAATTTTTCAGATTTGACAGTCTGAGAAATCTGACTCA 263  
Db AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
QY 264 AACACCTTCAGATCATGAGACACACAGGTGTGGGTGCTGTGTGTGGCCAGTATGGC 323  
Db AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnIleTyrGly 100  
QY 324 TACACCTTCCTCGGTGGAGAAAATACAACTCTACCTACAGAAATATAAATACTATCTCCG 383  
Db TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120  
QY 384 GATATGCGACAGCTGCTGTGGATGAGGCTATCCAGAAAGTTTAGAAGTGTGAGCAAA 443  
Db AspMetAlaArgAlaAlaValAspGluAlaIleGlnGlyLeuGluValTrpSerLys 140  
QY 444 GTCACTCCACTAAATTCACCAAGATTTCAAGGGGATTCAGACATCATCATGTCCTT 503  
Db ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160  
QY 504 AGGACTCGAGTCCATGCTCGTCTCTCGCTATTTTGTGCTCCTTGGGAGTCTTGGC 563  
Db ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180  
QY 564 CATGCCCTTCTCTCGTCTCGGTCTGGGTGTGGTGCACATCATTTTGTAGAGGATGAAAC 623  
Db HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200  
QY 624 TGGACCAAGGATGAGCAGGATTCACCTGCTTCTTGTGGCTCTCATGATTTGGTCAT 683  
Db TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220  
QY 684 GCATCGGGCTCTCTCACTCCAAATGATCAACAGCCTTGATGTTCCTCAAAATTTATGTCCTC 743  
Db AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240  
QY 744 CTGGATCCCAAGAAATACCCACTTCTCAGATGATATCAATGGAATCCAGTCCATCAT 803  
Db LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260  
QY 804 GGAGGTCTGCTAAGGTACTCTGCTAAGCCAAAGAAACCCACTATACCCCATGCTGTGAC 863  
Db GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280  
QY 864 CTGACTTTCATTTTCAGCTATCACAACCTTTCGCCAGAGAAAGTAATGTTCTTTAAAGGC 923  
Db ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300  
QY 924 AGGCACCTATGAGGATCTATATGATATCACGGATTTGAGTTTGAATTAATGCTTCA 983  
Db ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320  
QY 984 TTCTGGCCATCTCTGCCAGCTCATCTGCAAGCTGTCATACAGAAACCCAGAGATAAGATT 1043  
Db PheTrpProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnProArgAspLysIle 340  
QY 1044 CTGGTTTTTAAAGATGAAAACCTTCTGGATGATCAGAGGATATGCTGTCTTTCAGATTAT 1103  
Db LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360  
QY 1104 CCCAAATCATCATCATATAGTTTTCAGAGCGGTGTCAAGAAATATAGATGAGCGGTC 1163  
Db ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaIleVal 380  
QY 1164 TGTGATAGCACCAAGAAAAACCTACTTCTTTTGTGGCATTTGGTCTGGAGGTTTGTAT 1223



Db 381 CysAspLeuThrThrArgLysThrTyPhePheValGlyIleTyrCysTyrPargPheAsp 400  
QY 1224 GAAATGACCCAAACACCATGACAAAGATCCCGCAGAGAGTGGTAAACATTTCTCTGGA 1283  
Db 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420  
QY 1284 ATCAGTATCCGTTGATGCTGCTTCCAGTACAAAGGATTTCTTTTCAGCCGTGGA 1343  
Db 421 IleSerIleArgValAspAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440  
QY 1344 TCAAAGCAATTTGAATACACATTAAGACAAAGAAATATTACCGAATCATGAGAACTAAT 1403  
Db 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460  
QY 1404 ACTGGTTTCAATGAAAGACAAAGAACTCTCTCATTTGGTTTGGATATCAACAAAGGAA 1463  
Db 461 ThrTyrPheGlnCysLysGluProLysAsnSerPheGlyPheAspIleAsnLysGlu 480  
QY 1464 AAGACACATTCAGGAGGCATTAAGATATTGTATCATTAAGAGTTTAAGCTGTGTTATT 1523  
Db 481 LysAlaHisSerGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500  
QY 1524 GGTATTGTTTCATTTGCTGAAAAACATTTCTATTATCAA 1562  
Db 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513

## RESULT 9

US-10-175-746-192  
; Sequence 192, Application US/10175746  
; Publication No. US20030027270A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin J.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330RIC353  
; CURRENT APPLICATION NUMBER: US/10/175,746  
; CURRENT FILING DATE: 2002-06-19  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 192  
; LENGTH: 513  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-175-746-192

Alignment Scores:  
Pred. No.: 1,98e-273 Length: 513  
Score: 2752.00 Matches: 512  
Percent Similarity: 99.81% Conservative: 0  
Best Local Similarity: 99.81% Mismatches: 1  
Query Match: 93.92% Indels: 0  
DB: 14 Gaps: 0

US-10-729-807-28 (1-1627) x US-10-175-746-192 (1-513)

QY 24 ATGAAGCGCCTTCGTCTCTGCTTCTGTTGTTCTTTTATAACATTTTCTTCGTGATTTCCCTTA 83

Db 1 MetLysArgLeuLeuLeuLeuPheLeuPhePheIleThrPheSerSerAlaPheProLeu 20  
QY 84 GTCCGAGTACCGAAAAATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACACGATTC 143  
Db 21 ValArgMetThrGluAsnGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40  
QY 144 TACTCTCTTGAATAGNAGGGAATCATCTTGTCTTAAAGCAAGAAATAGGAGTCTCATAGAT 203  
Db 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60  
QY 204 GACAAAATTCGGGAAATGCAAGCATTTTGGATTGACAGTGCACCTGACGAAAACTGGACTCA 263  
Db 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
QY 264 AACACCTTGAAGATCATGAAGACACCCAGGTGTGGGGTCCCTGATGTGGCCAGTATGCG 323  
Db 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
QY 324 TACACCTCCCTGGGTGGGAAATACACCTCACCTACAGAATATAAATATACTACTCCG 383  
Db 101 TyrThrLeuProGlyTyrPargLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120  
QY 384 GATATGGCACGAGCTGCTGTGGATGAGGCTATCCAAAGAGGTTTAGAAGTGGAGCAAA 443  
Db 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140  
QY 444 GTCACCTCCATAAAATTCACCAAGATTTCAAAGGGGATTCGACGACATCATGATGCTTT 503  
Db 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160  
QY 504 AGGACTCGAGTCCAGTCCGCTGCTGCTCTATTTTGTGCTCCCTGGAGTGGCTGGC 563  
Db 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180  
QY 564 CATGCTTTTCTCTCGTCCGGTCTGGGTGTGTCGACACTCATTTTGTGATGAGGATGAAAAC 623  
Db 181 HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200  
QY 624 TGGACCAAGATGGAGCAGGATTCAACTGTTTCTTGTGGCTGCTCATGAATTTGGTCAT 683  
Db 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220  
QY 684 GCACCTGGGGCTCTCTCACCTCAATGATCAACAGAGCTGATGTCCTCCCAATATGCTCC 743  
Db 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240  
QY 744 CTGGATCCCGAAAAATACCCACTTTCTCAGGATGATATCAATCGAATCCAGTCCATCTAT 803  
Db 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260  
QY 804 GGAGTCTGCTTAAGTACTCTGTAAGCCAAAGGAACCCACTATATCCCATGCTGTGTGAC 863  
Db 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280  
QY 864 CTGACTTGCATTTTGACGCTATCAACTTTCCGACAGAGAAGTAAATGTTCTTTAAAGGC 923  
Db 281 ProAspLeuThrPheAspAlaIleThrThrPheArgGlyValMetPheLysGly 300  
QY 924 AGGCACCTATGAGGATCTATTATGATATCAGGATTTGAGTTTGAATTAATTTGCTTCA 983  
Db 301 ArgHisLeuTyrArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320  
QY 984 TTCTGGCCATCTCTGCGAGCTGATCTGCAAGCTGCATACGAGAACCCGACAGATTAAGATT 1043  
Db 321 PheTyrProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340  
QY 1044 CTGGTTTTAAAGATCAAACTTCTGGATGATCAGAGGATATGCTCTTGGCCAGATTAT 1103  
Db 341 LeuValPheLysAspGluAsnPheThrPheMetIleArgGlyTyrAlaValLeuProAspTyr 360  
QY 1104 CCCAAATCCATCATACATTTAGTGTTCAGGACCTGTGAGAAATAGATGACGCGCTC 1163



Db 361 ProlyserIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal 380  
QY 1164 TGTGATAGACCACCAAGAAACCTACTTTTGTGGCATTGGTGTGGAGTTTGAT 1223  
Db 381 CysAspLysThrThrArgLysThrTyPhePheValGlyIleTrpCysTrpArgPheAsp 400  
QY 1224 GAAATGACCCAAACCAAGGATCCCGCAGAGAGTGGTAACACTTTCCTGGA 1283  
Db 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420  
QY 1284 ATCAGTATCCGTGTGTGCTGCTTTCCAGTACCAAGGATTTCTTTTTCAGCCGTGGA 1343  
Db 421 IleSerIleArgValAspAlaPheGlnTyrlsGlyPhePhePheSerArgGly 440  
QY 1344 TCAAGCAATTGAAATCAACATTAAAGCAAGAAATATTACCCGAATCATGAGAACTAAT 1403  
Db 441 SerLysGlnPheGluTyrlsAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460  
QY 1404 ACTTGGTTTCAATCAAGAAACCAAGAACTCCCTCATTTGGTTTTTGATATCAACAAAGAA 1463  
Db 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480  
QY 1464 AAAGCAATTGAGGAGCATAAAGATATTGTATCAAGAGTTTAAAGCTTGTATTATTTT 1523  
Db 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrlsSerLysSerLeuSerLeuPheIlePhe 500  
QY 1524 GGTATTGTTCAATTGCTGAAAAACACTTCTATTATCA 1562  
Db 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrlsGln 513

## RESULT 10

US-10-176-918-192  
; Sequence 192, Application US/10176918  
; Publication No. US20030027275A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Deanoyers, Luc  
; APPLICANT: Flivaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C382  
; CURRENT APPLICATION NUMBER: US/10/176,918  
; CURRENT FILING DATE: 2002-06-20  
; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 192  
; LENGTH: 513  
; TYPE: PRT  
; ORGANISM: Homo Sapien

## US-10-176-918-192

Alignment Scores:  
Pred. No.: 1.98e-273 Length: 513  
Score: 2752.00 Matches: 512  
Percent Similarity: 99.81% Conservative: 0  
Best Local Similarity: 99.81% Mismatches: 1  
Query Match: 93.92% Indels: 0  
DB: 14 Gaps: 0

US-10-729-807-28 (1-1627) x US-10-176-918-192 (1-513)  
QY 24 ATGAGCGCCTTCTGCTTCTGTGTTCTTTTATAACATTTCTTCTGCAATTTCCCTTA 83  
Db 1 MetLysArgLeuLeuLeuPhePheIleThrPheSerSerAlaPheProLeu 20  
QY 84 GTCGGATGACGGAATATGAGAAATATCACTGCTCAGGCATATCTCAACAGTTC 143  
Db 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrlsLeuAsnGlnPhe 40  
QY 144 TACTCTCTTGAATAGAGGAATCATCTTGTTCAAAGCAAGAAATAGAGTCTCATAGAT 203  
Db 41 TyrlsSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60  
QY 204 GACAAATTCGGGAATATGCAAGCATTTTGGATTTGAGTGTAGTGTGAGAACTGGACTCA 263  
Db 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
QY 264 AACACCTCTCAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGGCACGTATGGC 323  
Db 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProaspValGlyGlnTyrlsGly 100  
QY 324 TACACCTCTCCTGGTGGAGAAATACACCTCACCTACAGAAATAATAAATACTACTCCG 383  
Db 101 TyrlsLeuProGlyTrpArgLysTyrlsAsnLeuThrTyrlsArgIleIleAsnTyrlsPro 120  
QY 384 GATATGGCAGAGCTGCTGTGGATGAGGCTATCCAGAAAGTTTAGAAGTGTGGAGCAA 443  
Db 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140  
QY 444 GTCACCTCACTAAATTCACCAAGATTTCAAAGGGATTCAGACATCATGATTCCTTT 503  
Db 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaIleMetIleAlaPhe 160  
QY 504 AGGACTCGAGTCCATGCTCGGTGCTCTGCTATTTTGTATGCTGCTTGGAGTGTGGC 563  
Db 161 ArgThrArgValHisGlyArgCysProArgTyrlsPheAspGlyProLeuGlyValLeuGly 180  
QY 564 CATGCTTTCTCTGCTCGGTCTGGGTGTGGTGTGACATCATTTTGTAGTGGAGTGAAC 623  
Db 181 HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200  
QY 624 TGCACCAAGGATGGAGCAGGATTCACCTGCTTCTGCTGCTGCTCATGAATTTGGTGCAT 683  
Db 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220  
QY 684 GCACTGGGCTCTCTCACTCAATGATCAAAAGCCTGTGATGTTCCCAATATTATGCTCC 743  
Db 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrlsValSer 240  
QY 744 CTGGATCCCAAGAAATACCACTTCTCAGGATCATCAATGAATCCAGTCCATCTAT 803  
Db 241 LeuAspProArgLysTyrlsProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyrls 260  
QY 804 GAGAGTCTGCTAAGGTACCTGCTTAAGCCAAAGAACCCACTATACCCCATGCTGTGAC 863  
Db 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280  
QY 864 CTTGACTTGATCTTTGACGTATCAAACTTTCCGAGAGAGTAATGTTCTTTAAAGGC 923  
Db 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300  
QY 924 AGGCACCTATGGAGGATCTATATGATATCACGGATGTTGAGTTGATTAATGCTTCA 983  
Db 301 ArgHisLeuTrpArgIleTyrlsAspIleThrAspValGluPheGluLeuIleAlaSer 320  
QY 984 TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGTGCAAGTGTGCAAGAACCCAGAGATAAGATT 1043  
Db 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrlsGluAsnProArgAspLysIle 340  
QY 1044 CTGTTTTTAAAGATGAAACTTCTGAGTATCAGAGATATGCTGTGCTGCCAGATAT 1103  
Db 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrlsAlaValLeuProAspTyrls 360

QY 1104 CCCAAATCCATCATACATTAGCTTTCCAGGACGCTGAGCAAAATAGATGACAGCCGTC 1163  
DB 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380  
QY 1164 TGTGATAAGACACCAAGAAAAACCTACTTCTTTGTGGGCACTTGGTGGAGGTTTGAT 1223  
DB 381 CysAspLysThrThrArgLysThrTyrrPhePheValGlyIleTrpCysTrpArgPheAsp 400  
QY 1224 GAAATGACCAACATGACAAAGATTCGCGCAGAGAGTGTTGATAAAACATTTCTCGGA 1283  
DB 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420  
QY 1284 ATCAGTATCCGCTGTCATCGCTTTCCAGTACAAGGATTCCTTTTTCAGCCGTGGA 1343  
DB 421 IleSerIleArgValAspAlaIlePheGlnTyrrLysGlyPhePhePheSerArgGly 440  
QY 1344 TCAAGCAATTTGAATACAACTTAAGACAAAGAAATATTACCCGAAATCATGAGAACTAAT 1403  
DB 441 SerLysGlnPheGluTyrrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460  
QY 1404 ACTTGTTTCAATGCAAGAACCAAGAACTCTCTCATTTGGTTTGGATATCAACAAAGGAA 1463  
DB 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480  
QY 1464 AAAGACATTCAGGAGGCATAAGATATTGTATCATCAAGAGTTTAAGCTTGTATTATTT 1523  
DB 481 LysAlaHisSerGlyIleLysIleLeuTyrrHisLysSerLeuSerLeuPheIlePhe 500  
QY 1524 GGTATTGTTCAATTTGCTGAAAAACACTTCTATTATCAA 1562  
DB 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrrGln 513

## RESULT 11

US-10-176-921-192  
; Sequence 192, Application US/10176921  
; Publication No. US20030027276A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P33301C288  
; CURRENT APPLICATION NUMBER: US/10/176,921  
; CURRENT FILING DATE: 2002-06-20  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 192  
; LENGTH: 513  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-176-921-192

## Alignment Scores:

Pred. No.: 1.98e-273 Length: 513  
Score: 2752.00 Matches: 512  
Percent Similarity: 99.81% Conservative: 0  
Best Local Similarity: 99.81% Mismatches: 1

Query Match: 93.92% Indels: 0

DB: 14 Gaps: 0

US-10-729-807-28 (1-1627) x US-10-176-921-192 (1-513)

QY 24 ATGAAGCGCTTCTGCTTCTGTGTTTCTTTTATAACATTTTCTTCTGCAATTCCTTA 83

DB 1 MetLysArgLeuLeuLeuLeuPheLeuPheIleThrPheSerSerAlaPheProLeu 20

QY 84 GTCGGATGACCGAAAAATGCAAAATATGCAACTGGCTCAGGCATATCTCAACCAAGTTC 143

DB 21 ValArgMetThrGluAsnGluAsnMetGlnLeuAlaGlnAlaTyrrLeuAsnGlnPhe 40

QY 144 TACTCTCTTGAATAGAGGGAATCATCTTGTTCCTTCAAGCAAGAAATAGGAGTCTCATAGT 203

DB 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60

QY 204 GACAAAATTCGGGAAATGCAAGCATTTTGTGATGACAGTCACCTGGAATACTGCACTCA 263

DB 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80

QY 264 AACACCTTTGAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGCCAGATATGCG 323

DB 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrrGly 100

QY 324 TACACCTCCCTGGGTGGAGAAATACACCTCACCACAGATATATAAATATATCTCCG 383

DB 101 TyrThrLeuProGlyTrpArgLysTyrrAsnLeuThrTyrrArgIleIleAsnTyrrThrPro 120

QY 384 GATATGGCACGAGCTGTGTGATGAGGTATCCCAAGAGGTTTAGAAGTGTGGAGCAA 443

DB 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140

QY 444 GTCACCTCCACTAAATTCACCAAGATTTCAAGGGGATTCAGACATCATGATGCTTT 503

DB 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160

QY 504 AGGACTCGAGTCCATGTCGGTGTCTGCTGATTTTGTGCTCCCTGGAGTGTCTTGGC 563

DB 161 ArgThrArgValHisGlyArgCysProArgTyrrPheAspGlyProLeuGlyValLeuGly 180

QY 564 CATGCTTTCTCTCTGTCGGGTCTGGGTGTGACACTCATTTTGTGATGAGATGAAAC 623

DB 181 HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200

QY 624 TCGACCAAGATGAGCAGGATTCAACTTGTGCTGCTGCTCATGAAATTTGCTCAT 683

DB 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220

QY 684 GCACTGGGGCTCTCTCCTCCTCAATGATCAACAGGCTTGATGTTCCCAATTTATGCTCC 743

DB 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrrValSer 240

QY 744 CTGGATCCCGAAAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803

DB 241 LeuAspProArgLysTyrrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyrr 260

QY 804 GGAGTCTGCTTAAGTACCTGCTAAGCCAAAGAACCCACTATACCCCATGCTGTGTAC 863

DB 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280

QY 864 CCTGACTTGACTTTTGAGCTATCACACTTCCGACAGAGATGATGTTCTTTAAAGGC 923

DB 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300

QY 924 AGGCACCTATGAGGAGTCTTATATCATATCACGGATGTTGAGTTTGAATTAATTCCTTCA 983

DB 301 ArgHisLeuTrpArgIleTyrrArgIleThrAspValGluPheGluLeuIleAlaSer 320

QY 984 TTCTGCGCATCTCTGCCAGCTGATCTGCAAGCTGCATCAGAGAACCCAGAGATAGATT 1043

DB 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrrGluAsnProArgAspLysIle 340

QY 1044 CTGGTGTAAAGATGAAACTTCTGATGATCAGAGATATGCTGCTTCCAGATTAT 1103  
Db |||||  
QY 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360  
Db |||||  
QY 1104 CCCAAATCCATCCATACATTAGGTTTTCCAGGACGTGTGAAGAAATAGATGACCGCTC 1163  
Db |||||  
QY 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysIleAspAlaAlaVal 380  
QY 1164 TGTGATTAAGACCAACAGAAACCTACTCTTTGTTGGGCATTTGGTCTGGAGTTTGTAT 1223  
Db |||||  
QY 381 CysAspLysThrThrArgLysThrLysPhePheValGlyIleTrpCysTrpArgPheAsp 400  
QY 1224 GAAATGACCCAAACCATGGAACAAAGGATTCCTCCGACAGAGTGGTAAACACTTTCTCTGGA 1283  
Db |||||  
QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420  
QY 1284 ATCAGTATCCGTGTGTGATGCTGCTTTCCAGTACAAAGGANTCTCTTTTCCAGCGTGA 1343  
Db |||||  
QY 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440  
QY 1344 TCAAGCAATTTGTAATACACATTAAAGCAAGAAATATCCCGAATCATGAGACTAAT 1403  
Db |||||  
QY 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460  
QY 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCTCTTCTTTGTTTGTATATCAACAAAGAA 1463  
Db |||||  
QY 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480  
QY 1464 AAAGCATTCCAGGAGCATAAAGATATTTATCATTAAGAGTTTAAAGCTTTGTTATTTT 1523  
Db |||||  
QY 481 LysAlaHisSerGlyGlyLysLysLysLysLysLysLysLysLysLysLysLysLys 500  
QY 1524 GGTATTTCTTCAATTTGCTGAAACACACTCTTTATTTATCAA 1562  
Db |||||  
QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513

## RESULT 12

US-10-137-865-192  
; Sequence 192, Application US/10137865  
; Publication No. US20030032155A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C154  
; CURRENT FILING DATE: 2002-05-03  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 192  
; LENGTH: 513  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-137-865-192

## Alignment Scores:

Pred. No.: 1.98e-273 Length: 513

Score: 2752.00 Matches: 512  
Percent Similarity: 99.81% Conservative: 0  
Best Local Similarity: 99.81% Mismatches: 1  
Query Match: 93.92% Indels: 0  
DB: 14 Gaps: 0  
US-10-729-807-28 (1-1627) x US-10-137-865-192 (1-513)  
QY 24 ATGAGCGCTTCTGCTTCTGTTGTTCTTTTATACATTTCTTCTGCAATTCCTTCA 83  
Db 1 MetLysArgLeuLeuLeuLeuPheLeuPhePheIleThrPheSerSerAlaPheProLeu 20  
QY 84 GTCGGATACGGAATAAGAAATATGCAATGCTGCTCAGGCATATCTCAACAGTTC 143  
Db 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40  
QY 144 TACTCTCTTGAATPAGAAGGAATCATCTTTGTTTCAAGCAAGATAGAGGTCTCATGAT 203  
Db 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60  
QY 204 GACAAATTCGGGAATGCAAGCATTTTGGATTGACAGTCTGGAAGAACTGAGTCA 263  
Db 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
QY 264 AACACCTCTCAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGGCCAGTATGGC 323  
Db 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
QY 324 TACACCTCTCCTGGTGGAGAAATACAACTCCTACAGATTAATAAATACTATCTCCG 383  
Db 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120  
QY 384 GATATGCGCAGCTGCTGCTGATGAGGCTATCCAAGAGTTTGTAGAGTGTGGAGCAA 443  
Db 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140  
QY 444 GTCACTCCACTTAAATTCACCAAGATTTCAGAGGGGATTGAGACATCATGATTCCTTT 503  
Db 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160  
QY 504 AGGACTCGAGTCCATGCTCGGTCTCGCTATTTTCTGCTATTTTCTGCTGAGGAGTCTGGC 563  
Db 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180  
QY 564 CATGCCCTTCTCTGCTCGGTCTCGGTGCTGACACTCATTTTGTAGTGGAGTGAAGAAC 623  
Db 181 HisAlaPheProProGlyProGlyLeuGlyLysAspThrHisPheAspGluAspGluAsn 200  
QY 624 TGGACCAAGATGGAGCAGGATTCAAATTTGTTTCTTGTGGCTGCTCATGAATTTGGTCA 683  
Db 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220  
QY 684 GCATGGGCTCTCTCATCTCCATGATCAACAGCCTTGATGTTCCCAATATATGTCTCC 743  
Db 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240  
QY 744 CTGGATCCAGAAATACCCACTTTCAGGATGATATCAATGAATCCAGTCCATCTAT 803  
Db 241 LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr 260  
QY 804 GGAGGTCTGCTAAGGTACCTTAAGCCAAAGGAACCCACTATACCCCATGCTGTGAC 863  
Db 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280  
QY 864 CTGACTTGCTTTTGGCTATCAACACTTTCGGCAGAGAGTAAATGTTCTTTAAAGGC 923  
Db 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300  
QY 924 AGCACCTATGAGGATCTATTATGATATCACCGATGTGTAGTTTGAATTAATGCTTCA 983  
Db 301 ArgHisLeuTrpArgLysTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320  
QY 984 TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAGAACCCAGAGATAAGATT 1043

Db 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340  
QY 1044 CTGGTTTTAAAGATGAAACTCTGGATGATCAGAGGATATGCTCTCTGGCAGATTAT 1103  
Db 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360  
QY 1104 CCCAATCCATCATCATAGTTTCCAGACGCTGTGAGAAATAGATGACGCCGTC 1163  
Db 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal 380  
QY 1164 TGTGTAAGACACACAGAACTACTCTCTTGTGGCATTGTGGCTGGAGTTTGAT 1223  
Db 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400  
QY 1224 GAAATGACCCAAACCATGACAAAGGATCCCGCAGAGGTGTGTAACACATTTCTCGA 1283  
Db 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420  
QY 1284 ATCAGTATCCGTTGATGCTGCTTCCAGTACAAAGGATCTCTCTTTTCCAGCGTGA 1343  
Db 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440  
QY 1344 TCAAGCAATTTGAATACAAACATTAAGACAAAGAAATATTACCCGAATCATGAGAACTAAT 1403  
Db 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460  
QY 1404 ACTTGTTTCAATGCAAGAACCAAGAACTCTCTATTTGGTTTTGATATCAACAAGGAA 1463  
Db 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480  
QY 1464 AAAGCAATTCAGGAGGATTAAGATATGCTATCAAGATTAAAGCTTGAAGCTTTATTTT 1523  
Db 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500  
QY 1524 GGTATTGTTCAATTTGCTGTAACAACTCTCTATTATCAAA 1562  
Db 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513

## RESULT 13

US-10-140-474-192  
; Sequence 192, Application US/10140474  
; Publication No. US20030032156A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: F3330R1C162  
; CURRENT APPLICATION NUMBER: US/10/140,474  
; CURRENT FILING DATE: 2002-05-06  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 192  
; LENGTH: 513  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-140-474-192

Alignment Scores: 1.98e-273 Length: 513  
Pred. No.: 2752.00 Matches: 512  
Score: 99.81% Conservative: 0  
Percent Similarity: 99.81% Mismatches: 1  
Best Local Similarity: 99.81% Indels: 0  
Query Match: 93.92% Gaps: 0  
DB: 14

US-10-729-807-28 (1-1627) x US-10-140-474-192 (1-513)

QY 24 ATGAAGCGCTCTCTGCTTCTGTGTTGTTCTTTATAACATTTTCTTCTGCAATTCCTCTTA 83  
Db 1 MetLysArgLeuLeuLeuLeuPheLeuPhePheIleThrPheSerSerAlaPheProLeu 20  
QY 84 GTCGGATGACCGGAAATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACGATTC 143  
Db 21 ValArgMetThrGluAsnGluGluMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40  
QY 144 TACTCTCTTGAATAGAAGGAATCATCTTGTTCCTCAAGCAAGAAATAGGAGTCTCATAGAT 203  
Db 41 TyrSerLeuGluIleGluGlnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60  
QY 204 GACAAATTCGGGAAATGCAAGCATTTTGTGATTGACAGTCTGCTGGAATACTGGACTCA 263  
Db 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
QY 264 AACACCTTTGAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGGCCAGTATGGC 323  
Db 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
QY 324 TACACCTCCCTGGTGGAGAAATACAACTCACCCTACAGAAATATAAATATATCTCCG 383  
Db 101 TyrThrLeuProGlyTrpArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120  
QY 384 GATATGGCAGAGTCTCTGTGATGAGGTATCCAAAGAGGTTTAGAAGTGTGGAGCAA 443  
Db 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140  
QY 444 GTCATCTCCACTAAATTCACCAAGATTTCAAAGGGATTTGCAGACATCATGATGCTCTT 503  
Db 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160  
QY 504 AGGACTCGAGTCCATGGTCTGCTCGCTCTCTGCTATTTTGTGCTCCCTGGAGTGTGGC 563  
Db 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180  
QY 564 CATGCCCTTCTCTCTGCTGGTCTGGGTGTGCTGACACTCATTTTGTGATGAGGATGAAAC 623  
Db 181 HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200  
QY 624 TGGACCAAGATGAGGACAGGATTCAACTTGTGTTTCTTGTGGCTGCTCATGAATTTGTCAT 683  
Db 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220  
QY 684 GCACCTGGGCTCTCTCACCCTCCATGATCAACAGCCCTGATGTTCCCAATATGCTCC 743  
Db 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240  
QY 744 CTGGATCCCAAGAAATACCCACTTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803  
Db 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260  
QY 804 GGAGTCTGCTTAAGGTACTCTGTAAGCAAGAAACCCACTATATACCCCATGCTGTGAC 863  
Db 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280  
QY 864 CTGACTTTCACCTTTTACCGCTATCAACTTCCGACAGAGAGTATGTTCTTTAAGGC 923  
Db 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300  
QY 924 AGGCACCTATGGAGGATCTATTATGATATCAAGGATTTGAGTTTGAATTAATGCTTCA 983

301	Db	ArgHisLeuTrpArgIleTyrTyTAspIleThrAspValGluPheGluLeulleAlaSer	320
984	Qy	TTCTGGCCATCTCTGCCAGCTGATCTCCAAGCTCATACGAGAACCCGAGATAAGATT	1043
321	Db	PhETrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle	340
1044	Qy	CTGGTTTTTAAAGATGAAAACCTTCGTGATGATCATGAGGATATGCTGCTTCGCAGATTAT	1103
341	Db	LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr	360
1104	Qy	CCCAATCCATCCATACATATTAGGTTTTCCAGGAGCTGTGAAGAAATAGATGCAGCGCTC	1163
361	Db	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysIleAspAlaAlaVal	380
1164	Qy	TGTGATAAAGACCACAAGAAAAACCTACTCTCTTGTGGGCATTTGGTGCTCGAGGTTTGAT	1223
381	Db	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTrpArgPheAsp	400
1224	Qy	GAATGACCCCAACCATGGACAAGAATTCCCGCAGAGAGTGTGTAAACACTTTCCTGGA	1283
401	Db	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly	420
1284	Qy	ATCAGTATCCGTGTGTATGCTGCTTCCAGTACAAAGGATTCTTCTTTTTCAGCCGTGGA	1343
421	Db	IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly	440
1344	Qy	TCAAAGCAATTTGTAATCAACATTAAAGACAAAGAATATTACCCGAATCATGAGAACTAAT	1403
441	Db	SerLysGlnPheGlnTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
1404	Qy	ACTTGGTTTCAATGCAAGAAGAACCAAGAATCTCTCATTTGGTTTTGTATTCACACAGGAA	1463
461	Db	ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu	480
1464	Qy	AAAGACATTTCAGGAGGCATAAAGATATTCTATCATAGAGTTTAAAGCTTGTTTATTTTT	1523
481	Db	LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe	500
1524	Qy	GGTATTGTTTCAATTGCTGAAAAACACTTCTATTATCAAA	1562
501	Db	GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln	513

## RESULT 14

```

US-10-142-431-192
; Sequence 192, Application US/10142431
; Publication No. US20030036179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: F3330R1C251
; CURRENT APPLICATION NUMBER: US/10/142,431
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 192
; LENGTH: 513

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QY 924 AGGCACCTATGGAGGATCTATTATGATATACCGGATGTGAGTTGAATTAATTCCTTCA 983
Db 301 ArgHisLeuTrpArgIleTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
QY 984 TTCTGGCCATCTCTGCCAGCTGTCTCTCAAGCTGCATACAGAACCCAGAGATAAGATT 1043
Db 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspIle 340
QY 1044 CTGGTTTTAAAGATGAAACTCTTCGATGATCAGAGATATGCTGTTCGCCAGATTAT 1103
Db 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
QY 1104 CCCTAAATCCATCATACATAGGTTTCCAGGAGCTGTGAGAAATAGATGACCGCTC 1163
Db 361 ProlYsSerIleHisThrLeuGlyPheProGlyArgValLysIleAspAlaAlaVal 380
QY 1164 TGTGATAAGACCAAGAAAACCTACTCTTTTGTGGGCATTTTGTCTGCGAGTTTGAT 1223
Db 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTyrPArgPheAsp 400
QY 1224 GAAATGACCAACCATGGCAAGAGATTCCCGCAGAGAGTGTAACAACACTTTCCTGGA 1283
Db 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
QY 1284 ATCAGTATCGTGTGTGATGCTCTTCCAGTACAAAGGATTCCTCTTTTTCAGCCGTGA 1343
Db 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
QY 1344 TCAAAGCAATTGAATACAAACATTAAAGAACAAATATACCCGAATCATGAGAACTAAT 1403
Db 441 SerLysGlnPheGlnTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
QY 1404 ACTTGTTTCAATGCAAGAACCAAGAACTCCTCATTTGGTTTGTATATCAACAGGAA 1463
Db 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
QY 1464 AAAGCACATTGAGGAGCATAAAGATATTGTATCATAGAGTTTAAAGCTTGTTTATTTT 1523
Db 481 LysAlaHisSerGlyIleLysIleLysLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
QY 1524 GGTATTGTCATTGCTGAAAAACACTTCTATTATCAA 1562
Db 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
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## RESULT 15

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US-10-143-114-192
; Sequence 192, Application US/10143114
; Publication No. US20030036180A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C211
; CURRENT APPLICATION NUMBER: US/10/143,114
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
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; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-143-114-192
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Alignment Scores:
Pred. No.: 1.98e-273 Length: 513
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 93.92% Indels: 0
DB: 14 Gaps: 0
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US-10-729-807-28 (1-1627) x US-10-143-114-192 (1-513)

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QY 24 ATGAAGCGCCTTCCTGCTTCCTGTTGTTCTTTTATAACATTTCTTCGCAATTCCTTCA 83
Db 1 MetLysArgLeuLeuLeuLeuPhePhePheIleThrPheSerSerAlaPheProLeu 20
QY 84 GTCGGATGACGGAATGAAGAAATATCAACTGGCTCAGGCATATCTCAACAGTTC 143
Db 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
QY 144 TACTCTCTTCAATAGNAGGGAATCATCTTGTTCAAAGCAAGATAGAGTCTCATAGAT 203
Db 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
QY 204 GACAAAATTCGGAAATGCAAGCATTTTGTGATTGACAGTGCAGTGGAAAACTGGACTCA 263
Db 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
QY 264 AACACCTTGAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGGCCAGATATGGC 323
Db 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
QY 324 TACACCTCCCTCGGTGGAGAAATCAACCTCACCTACAGATAATAAATACTATCTCCG 383
Db 101 TyrThrLeuProGlyTrpArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120
QY 384 GATATGGCACAGCTGCTGTGGATGAGGCTATCCAAGAAGTTTAGAAGTGTGGAGCAA 443
Db 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140
QY 444 GTCATCCCACTAAATTCACCAAGATTTCAAGGGGATTCAGACATCATTTGATAGGATGAAAC 503
Db 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
QY 504 AGGACTCGAGTCCATGTCGTCTGCTCCTGCTATTTTGTATGCTCCCTGGAGTGTGGC 563
Db 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
QY 564 CATGCTCTTCTCCTGCTCGGGTCTGGGTGGTGACACTCATTTGATAGGATGAAAC 623
Db 181 HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
QY 624 TGGACCAAGGATGAGCAGGAGATTCAACTGTGTTCTTGTGGCTGCTCATGAATTTGGTFCAT 683
Db 201 TrpThrLysAspGlyAlaGlyPheAsnLeuValAlaAlaHisGluPheGlyHis 220
QY 684 GCACTGGGCTCTCTCACTCCAATGATCAAGAGCTTGATGTTGCCAAATATGCTCC 743
Db 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
QY 744 CTGGATCCCAAGAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCAT 803
Db 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260
QY 804 GGAGGTCTGCTTAAGTACTGCTGAAGCCAAAGAAACCCACTATACCCCATGCTGTCGAC 863
Db 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
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QY 864 CCTGACTTGACTTTGGCGCTATCACAACTTTCCGACAGAGTAATGTTCTTTAAAGGC 923  
Db |||||||  
QY 281 ProAspLeuThrPheAspAlaIleThrPheArgArgGluValMetPhePheLysGly 300  
Db |||||||  
QY 924 AGGCACCTATGGAGGATCTATTATGATATCAGGATGTTGAGTTTGAATTAATTGCTTCA 983  
Db |||||||  
QY 301 ArgHisLeuTyrArgIleTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320  
Db |||||||  
QY 984 TTCGGCCATCTCTCCAGCTGATGTGCAAGCTGCATACGAGAACCCAGAGATAAGATT 1043  
Db |||||||  
QY 321 PheTrpProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnProArgAspLysIle 340  
Db |||||||  
QY 1044 CTGGTTTAAAGATGAAGAACTTCTGGGATGATCAGAGATATGCTGCTTGCAGATTAT 1103  
Db |||||||  
QY 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspIle 360  
Db |||||||  
QY 1104 CCCAAATCCATCCATPACATTAGGTTTCCAGGACGTGTGAAGAAATAGATCGACCGTC 1163  
Db |||||||  
QY 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380  
Db |||||||  
QY 1164 TGTGATAAGACACAGAAACCTACTTCTTGTGGGCAATTTGGTGTGGAGGTTTCAT 1223  
Db |||||||  
QY 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400  
Db |||||||  
QY 1224 GAAATGACCCAAACCATGGACAAAGGATTTCCGACAGAGAGTGTAAACACTTTCTCTGA 1283  
Db |||||||  
QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly 420  
Db |||||||  
QY 1284 ATCAGTATCCGTGTTGATGCTCTTTCCAGTACAAAGGATTTCTTTTTCAGCCGTGA 1343  
Db |||||||  
QY 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440  
Db |||||||  
QY 1344 TCAAAGCAATTTGAATACACATTAAGACAAAGATATTACCGAATCATGAGAACTAAT 1403  
Db |||||||  
QY 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460  
Db |||||||  
QY 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCTCATTTGGTTTGTATATCAACAGGAA 1463  
Db |||||||  
QY 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480  
Db |||||||  
QY 1464 AAAGCACATTCAGGAGGCATAAAGATATTGTATCATAGAGTTTAAGCTTGTATTTT 1523  
Db |||||||  
QY 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500  
Db |||||||  
QY 1524 GGTATGTTTCATTTGCTGAAAACACTTCTATTATCAA 1562  
Db |||||||  
QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513  
Db |||||||

Search completed: November 15, 2004, 20:40:52  
Job time : 243.5 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 15, 2004, 21:10:33 ; Search time 775 Seconds  
(without alignments)  
3575.105 Million cell updates/sec

Title: US-10-729-807-10  
Sequence score: 2763  
Sequence: 1 MKRLLLCLEFFITSSAPPL.....SLSLFIFIVLLKNTSIYQ 513

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-O=/cgn2\_1/USPTO\_spool/US10729807/runat 15112004 131728 16871/app query.fasta\_l.711  
-DB=Published Applications NA -OFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blowum62  
-TRANS=human40.cdi -LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODB=LOCAL -OUTFMT=pcr -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -USER=US10729807 @CNG 1.1.480 @runat 15112004 131728 16871  
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARMUP=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:  
4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:  
8: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:  
9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:  
10: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:  
14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:  
15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:  
16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:  
17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:  
18: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:  
19: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:  
20: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:  
21: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

\*

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2763	100.0	1627	17	US-10-729-807-28	Sequence 28, Appl
2	2763	100.0	1845	10	US-09-862-631-1	Sequence 1, Appl
3	2752	99.6	1542	10	US-09-759-130B-172	Sequence 172, App
4	2752	99.6	1542	17	US-10-741-790-172	Sequence 172, App
5	2752	99.6	1647	14	US-10-028-072-191	Sequence 191, App
6	2752	99.6	1647	14	US-10-140-808-191	Sequence 191, App
7	2752	99.6	1647	14	US-10-121-049-191	Sequence 191, App
8	2752	99.6	1647	14	US-10-123-304-191	Sequence 191, App
9	2752	99.6	1647	14	US-10-140-470-191	Sequence 191, App
10	2752	99.6	1647	14	US-10-175-746-191	Sequence 191, App
11	2752	99.6	1647	14	US-10-176-918-191	Sequence 191, App
12	2752	99.6	1647	14	US-10-176-921-191	Sequence 191, App
13	2752	99.6	1647	14	US-10-137-865-191	Sequence 191, App
14	2752	99.6	1647	14	US-10-140-474-191	Sequence 191, App
15	2752	99.6	1647	14	US-10-142-431-191	Sequence 191, App
16	2752	99.6	1647	14	US-10-143-114-191	Sequence 191, App
17	2752	99.6	1647	14	US-10-140-002-191	Sequence 191, App
18	2752	99.6	1647	14	US-10-142-419-191	Sequence 191, App
19	2752	99.6	1647	14	US-10-123-262-191	Sequence 191, App
20	2752	99.6	1647	14	US-10-142-423-191	Sequence 191, App
21	2752	99.6	1647	14	US-10-121-050-191	Sequence 191, App
22	2752	99.6	1647	14	US-10-141-755-191	Sequence 191, App
23	2752	99.6	1647	14	US-10-143-032-191	Sequence 191, App
24	2752	99.6	1647	14	US-10-123-108-191	Sequence 191, App
25	2752	99.6	1647	14	US-10-123-236-191	Sequence 191, App
26	2752	99.6	1647	14	US-10-123-261-191	Sequence 191, App
27	2752	99.6	1647	14	US-10-140-921-191	Sequence 191, App
28	2752	99.6	1647	14	US-10-140-928-191	Sequence 191, App
29	2752	99.6	1647	14	US-10-121-045-191	Sequence 191, App
30	2752	99.6	1647	14	US-10-123-292-191	Sequence 191, App
31	2752	99.6	1647	14	US-10-123-903-191	Sequence 191, App
32	2752	99.6	1647	14	US-10-124-819-191	Sequence 191, App
33	2752	99.6	1647	14	US-10-124-822-191	Sequence 191, App
34	2752	99.6	1647	14	US-10-140-925-191	Sequence 191, App
35	2752	99.6	1647	14	US-10-160-498-191	Sequence 191, App
36	2752	99.6	1647	14	US-10-124-824-191	Sequence 191, App
37	2752	99.6	1647	14	US-10-127-825A-191	Sequence 191, App
38	2752	99.6	1647	14	US-10-127-829A-191	Sequence 191, App
39	2752	99.6	1647	14	US-10-127-835A-191	Sequence 191, App
40	2752	99.6	1647	14	US-10-127-839A-191	Sequence 191, App
41	2752	99.6	1647	14	US-10-127-901A-191	Sequence 191, App
42	2752	99.6	1647	14	US-10-128-693A-191	Sequence 191, App
43	2752	99.6	1647	14	US-10-131-813A-191	Sequence 191, App
44	2752	99.6	1647	14	US-10-131-818A-191	Sequence 191, App
45	2752	99.6	1647	14	US-10-131-823A-191	Sequence 191, App

#### ALIGNMENTS

RESULT 1  
US-10-729-807-28  
; Sequence 28, Application US/10729807  
; Publication No. US20040132158A1  
; GENERAL INFORMATION:  
; APPLICANT: BANDMAN, Olga; HILLMAN, Jennifer L.  
; APPLICANT: TANG, Y. Tom; LAL, Preeti G.  
; APPLICANT: YUE, Henry; AZIMZAI, Yalda  
; APPLICANT: BAUGHN, Mariah R.; LU, Dyrung Alina M.  
; TITLE OF INVENTION: HUMAN PEPTIDASES  
; FILE REFERENCE: PF-0651-1 DIV  
; CURRENT APPLICATION NUMBER: US/10/729,807  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: US 09/889,238  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: PCT/US00/00641  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: US 60/172,247  
; PRIOR FILING DATE: 1999-01-11  
; PRIOR APPLICATION NUMBER: US 60/132,253  
; PRIOR FILING DATE: 1999-05-03



! TYPE: DNA  
! ORGANISM: Homo sapiens  
US-09-862-631-1

Alignment Scores:

Pred. No.: 0 Length: 1845  
Score: 2763.00 Matches: 513  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-10-729-807-10 (1-513) x US-09-862-631-1 (1-1845)

QY 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheSerSerAlaPheProLeu 20  
DB 24 ATGAAGCGCTTCTGCTCTCTGTTGTTCTTTATAACATTTCTTCGATTTCCCTTA 83  
QY 21 ValArgMetThrGluAenGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40  
DB 84 GTCGGGATGACGGAAATGAAGAAATATGCACTGGCTCAGGCATATCTCAACCACTTC 143  
QY 41 TyrSerLeuGluLeuGluGluAsnHisLeuValGlnSerLysAsnArgSerLeuLeuAsp 60  
DB 144 TACTCTCTGAAATAGAGGGAATCATCTTGTTCAGAGCAAGATAGGAGTCTCATAGAT 203  
QY 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
DB 204 GACAAAATTCGGGAAATGCAAGCATTTTTCGATTGACAGTGTGGGAAATCTGGACTCA 263  
QY 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
DB 264 AACACCTCTGAGATCATGAAGACACCCAGGTGTGGGGTGCCTGANGTGGCGAGTATGGC 323  
QY 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleLeuAsnTyrThrPro 120  
DB 324 TACACCTCTCCCTGGTGGAGAAATACACCTCACCTACAGATATATAAATATATACCTCG 383  
QY 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140  
DB 384 GATATGGCAGCAGCTGCTGTGGATGAGCTATCCAAAGAGGTTTAGAAGTGTGGAGCAAA 443  
QY 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160  
DB 444 GTCACCTCCACTAAAATTCACCAAGATTTCAAAGGGGATTCAGACATCATGATGGCTTT 503  
QY 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180  
DB 504 AGGACTCGAGTCCATGGTGGTGTCTCGCTATTTTGATGGTCCCTTGGGAGTGTTCGTC 563  
QY 181 HisAlaPheProProGlyProGlyLeuGlyAspThrHisPheAspGluAspGluAsn 200  
DB 564 CATGCTTTCTCTCTGTCGGGTCCGGGTGTGGGTGTGACACTCATTTTGTGATGAGGATGAAAAC 623  
QY 201 TrpThrLysAspGlyValGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220  
DB 624 TGGACCAAGGATGGAGCAGGATTCACCTGTGTTCCTGTGGCTGTGCTCATGAATTTGGTCTAT 683  
QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240  
DB 684 GCACCTGGGGCTCTCATCTCCATGATCATCAACAGGCTTGATGTTCCCAAAATATATGCTCC 743  
QY 241 LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr 260  
DB 744 CTGGATCCAGAAAATACCCATTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803  
QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280  
DB 804 GGAGGTCTCGCTAAAGTACTCTGTAAGCCAAAGAACCCACTATATACCCCTGCTGTGAC 863  
QY 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300  
DB 864 CCTGACTTGTACTTTTTCACGCTATCATCACTTTCCCGCAGAGAGTATGTTCTTTAAAGC 923

QY 301 AtcHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320  
DB 924 AGGCACCTATGGAGGATCTATTATGATATACCGATGTTGAGTTGAATTAATGCTTCA 983  
QY 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340  
DB 984 TTTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAGAACCCGAGAGATAAGATT 1043  
QY 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360  
DB 1044 CTGGTTTTTAAAGATGAAAACCTTCGATGATCAGAGGATATGCTGCTTTCGAGATTAT 1103  
QY 361 ProLysSerIleHisThrLeuGlyPheProGlyValGlyValLysLysIleAspAlaAlaVal 380  
DB 1104 CCCAAATCCATCATCATATTAGTTTTCCAGGAGCTGTGAAGAAATAGATGCGCCGTC 1163  
QY 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTrpArgPheAsp 400  
DB 1164 TGTGATAAGACCAACAAGAAAAACCTACTTCTTTGTGGGCATTTTGGTCTCGAGGTTTGTAT 1223  
QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly 420  
DB 1224 GAAATGACCCCAACCATGGAAGGATTCCTCCGAGAGAGTGGTAAACACATTTTCTTCTGGA 1283  
QY 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePhePheSerArgGly 440  
DB 1284 ATCAGTATCCGTGTGTGATGCTGCTTCCAGTACAAAGGATTTCTTCTTTTCAGCCGTGA 1343  
QY 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460  
DB 1344 TCAAGCAATTTTGAATACACATTAAAGCAAGAAATATATCCCGAATCATGAGAACTAAT 1403  
QY 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480  
DB 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCTCATTTGTTGTTTGTATATCAACAGGA 1463  
QY 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500  
DB 1464 AAAGCAATTCAGAGGAGCATAAAGATATGATCATCAAGAGTTTAAAGCTTGTATTATTT 1523  
QY 501 GlyIleValHisLeuLeuLysLeuAsnThrSerIleTyrGln 513  
DB 1524 GGTATGTTTCTATTTGCTGAAAAACACTTCTATTATCAAA 1562

RESULT 3

US-09-759-130B-172  
; Sequence 172, Application US/09759130B  
; Publication No. US20030022279A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: McCarthy, Sean A  
; APPLICANT: Fraser, Christopher C  
; APPLICANT: Sharp, John D  
; APPLICANT: Barnes, Thomas S  
; APPLICANT: Kirst, Susan J  
; APPLICANT: Mackay, Charles R  
; APPLICANT: Myers, Paul S  
; APPLICANT: Leiby, Kevin R  
; APPLICANT: Wrighton, Nicolas  
; APPLICANT: Goodearl, Andrew  
; APPLICANT: Holtzman, Douglas A  
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
; FILE REFERENCE: MP100-5350NMIM  
; CURRENT APPLICATION NUMBER: US/09/759,130B  
; PRIOR FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US 09/479,249  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: US 09/559,497  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 09/578,063

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; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/342,364
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 172
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-130B-172

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; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirt, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USSS
; FILE REFERENCE: MP100-5350NMIM
; CURRENT FILING DATE: 2003-12-19
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 09/479,249
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR FILING DATE: 1999-06-14
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR FILING DATE: 2000-07-14
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; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 172
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-790-172

Alignment Scores:
Pred. No.: 0 Length: 1542
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 99.60% Indels: 0
DB: 17 Gaps: 0

US-10-729-807-10 (1-513) x US-10-741-790-172 (1-1542)
Qy 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheLeuThrPheSerSerAlaPheProLeu 20
Db 1 ATGAAGCGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
Qy 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
Db 61 GTCCGGATGACGGAAATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACCAAGTTC 120
Qy 41 TyrSerLeuGluLeuGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 60
Db 121 TACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Qy 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
Db 181 GACAAATTCGGGAATGCAAGCAATTTTGGATTGACAGTGAAGTGAAGAACTGGACATCA 240
Qy 81 AsnThrLeuGluLeuMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
Db 241 AACACCCCTTGAGTATCATGAACACCCAGTGTGGGGTCCCTGATGTGGGGCAGTATGTC 300
Qy 101 TyrThrLeuProGlyTrpArgLysTyrAsnLeuThrTyrArgIleLeuAsnTyrThrPro 120
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Db 301 TACACCTCCTCGGTGGAGAAATACACCTCACCTACAGAAATAATAAACTATACTCCG 360
Qy 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140
Db 361 GATATGGCAGAGCTGCTGTGGATGAGGCTATCAAGAAGGTTTAGAAGTGTGGAGCAA 420
Qy 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
Db 421 GTCACTCCACTAAATTCACAAAGATTTCAAAGGGATTCACAGACATCATGATGCCTTT 480
Qy 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
Db 481 AGGACTCGAGTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Qy 181 HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAsnGluAsn 200
Db 541 CATGCCCTTCTCCTCGTCCGGGTCTGGGTGGTGACACTCATTTTGAAGGATGAAAC 600
Qy 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheValAlaAlaHisGluPheGlyHis 220
Db 601 TGGACCAAGGATGGAGCAGGATTCAACTGTTCTTGTGGCTGCTCATGAATTTGGTCAT 660
Qy 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
Db 661 GCATCGGGCTCTCTCACTCCATGATCAAAACAGCCTTGATGTTCCCAATATATGTCTCC 720
Qy 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260
Db 721 CTGGATCCCAAAATACCCACTTTCTCAGGATGATATCAATGGAAATCCAGATCCATCTAT 780
Qy 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
Db 781 GGAGTCTGCTTAAGTACTGCTTAAGCCAAAGAAACCCACTATACCCCATGCTGTGAC 840
Qy 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
Db 841 CCTGACTTGACTTTTGGCGCTATCACAACTTTCGGCAGAGAAGTAATGTTCTTTAAAGGC 900
Qy 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
Db 901 AGGCACCTATGAGGATCTATTATGATATCAAGATGTTGAGTTGAAATTAATGCTTCA 960
Qy 321 PheTrpProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnProArgAspLysIle 340
Db 961 TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACAGAACCCACAGAGATAGATT 1020
Qy 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
Db 1021 CTGGTTTTTAAAGATGAAACTTCTGGATGATCAGAGGATATGCTGTCTTCCAGATTAT 1080
Qy 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380
Db 1081 CCCAAATCCATCCATACATATTAGTGTTCAGAGAGTGTGAAGAAATAGATGAGCCCTGC 1140
Qy 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400
Db 1141 TGTGATAAGACACAAAGAAACCTACTCTTCTTGTGGCAATTTGGTGTGGAGGTTTGTAT 1200
Qy 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
Db 1201 GAAATGACCCAAACCATCGAACAAAGGATTCGCCAGAGAGTGTGTAACAAACACTTTCTCTGGA 1260
Qy 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePhePheSerArgGly 440
Db 1261 ATCAGTATCCGTTGTGATGCTGCTTCCAGTACAAAGGATTTCTCTTTTTCAGCCGTGGA 1320
Qy 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
Db 1321 TCAAGCAATTTGAATACAACTTGAAGCAAGAAATATATCCCGAATCATGAGAACTAAT 1380
Qy 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
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Db 1381 ACTTGTTTCAATGCAAGAACCAAGAACTCCTCATTGGTTTGTATATCAACAAGAA 1440  
QY 481 LyeAlahHisSerGlyGlylleLysIleLeuTyxHisLysSerLeuPhePhe 500  
Db 1441 AAAGCATTTCAGGAGCATAAAGATATTGTAICATAGAGTTTAACTTGTTTATTTT 1500  
QY 501 GlylleValHisLeuLysAenThrSerIleTyxGln 513  
Db 1501 GGTATTGTTCAATTTGCTGAAACACCTCTATTATCAA 1539

RESULT 5  
US-10-028-072-191  
; Sequence 191, Application US/10028072  
; Publication No. US20030004311A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/028,072  
; PRIOR FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059122  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059184  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059352  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059588  
; PRIOR FILING DATE: 1997-09-19  
; PRIOR APPLICATION NUMBER: 60/059836  
; PRIOR FILING DATE: 1997-09-24  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/062285  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/062287  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/062814  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/062816  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063045  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063082  
; PRIOR FILING DATE: 1997-10-31  
; PRIOR APPLICATION NUMBER: 60/063127  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063327  
; PRIOR FILING DATE: 1997-10-27  
; PRIOR APPLICATION NUMBER: 60/063329  
; PRIOR FILING DATE: 1997-10-27  
; PRIOR APPLICATION NUMBER: 60/063550  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063561  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063704  
; PRIOR FILING DATE: 1997-10-29  
; PRIOR APPLICATION NUMBER: 60/063733  
; PRIOR FILING DATE: 1997-10-29  
; PRIOR APPLICATION NUMBER: 60/063735  
; PRIOR FILING DATE: 1997-10-29  
; PRIOR APPLICATION NUMBER: 60/063738  
; PRIOR FILING DATE: 1997-10-29  
; PRIOR APPLICATION NUMBER: 60/063755  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064248  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/064809  
; PRIOR FILING DATE: 1997-11-07  
; PRIOR APPLICATION NUMBER: 60/065186  
; PRIOR FILING DATE: 1997-11-12  
; PRIOR APPLICATION NUMBER: 60/065846  
; PRIOR FILING DATE: 1997-11-17  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/066453  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/066511  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/066770  
; PRIOR FILING DATE: 1997-11-24  
; PRIOR APPLICATION NUMBER: 60/069212  
; PRIOR FILING DATE: 1997-12-11  
; PRIOR APPLICATION NUMBER: 60/069278  
; PRIOR FILING DATE: 1997-12-11  
; PRIOR APPLICATION NUMBER: 60/069334  
; PRIOR FILING DATE: 1997-12-11  
; PRIOR APPLICATION NUMBER: 60/069694  
; PRIOR FILING DATE: 1997-12-16  
; PRIOR APPLICATION NUMBER: 60/072320  
; PRIOR FILING DATE: 1998-01-23  
; PRIOR APPLICATION NUMBER: 60/073612  
; PRIOR FILING DATE: 1998-02-04  
; PRIOR APPLICATION NUMBER: 60/074086  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: 60/074092  
; PRIOR FILING DATE: 1998-02-09  
; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
; PRIOR APPLICATION NUMBER: 60/078910  
; PRIOR FILING DATE: 1998-03-20  
; PRIOR APPLICATION NUMBER: 60/079294  
; PRIOR FILING DATE: 1998-03-25  
; PRIOR APPLICATION NUMBER: 60/079663  
; PRIOR FILING DATE: 1998-02-27  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/080165  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/081203  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081229  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081695  
; PRIOR FILING DATE: 1998-04-14  
; PRIOR APPLICATION NUMBER: 60/081817  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081819  
; PRIOR FILING DATE: 1998-04-15





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Db 1044 CTGGTTTAAAGATGAACACTCTGGATGATCAGAGGATATGCTGCTTCGACGATTAT 1103
QY 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValIleHisPheAspAlaVal 380
Db 1104 CCCAAATCCATCCATCATATTAGGTTTTCAGGACGCTGTGAAGAAATAGATGACGCGTC 1163
QY 381 CysAspLysThrThrArgLysThrThrPhePheValGlyIleThrPheCysThrArgPheAsp 400
Db 1164 TGTGATGAAGACCAACAGAAACACTACTCTTTGTGGGCAATTTGGTCTGGAGGTTGAT 1223
QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValIleHisPheProGly 420
Db 1224 GAAATGACCAACCATGACCAAGGATTCCTCCGACAGAGTGTGTAACACATTCCTCTGGA 1283
QY 421 IleSerIleArgValAspAlaPheGlnThrLysGlyPhePhePheSerArgGly 440
Db 1284 ATCAGTATCCGTGTTGATGCTGCTTTCCAGTACAAAGGATTCCTCTTTTCAGCCGCTGA 1343
QY 441 SerLysGlnPheGluThrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
Db 1344 TCAACCAATTTGAAATACAACTAAGACAAAGAAATATTACCCGAATCATGAGAACTAAT 1403
QY 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
Db 1404 ACTTGGTTTCAATGCAAGAAACCAAGAACTCTCTCATTTGGTTTGTATCAACAAGGAA 1463
QY 481 LysAlaHisSerGlyGlyIleLysIleLeuThrHisLysSerLeuSerLeuPheIlePhe 500
Db 1464 AAGACACATTCAGAGGCAATAAAGATATTGTATCATAAAGATTTAAAGCTTTGTTATTTT 1523
QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleThrGln 513
Db 1524 GGTATTGTTCAATTTGCTGAAGAAACACTTCTATTATTAACA 1562

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## RESULT 6

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US-10-140-808-191
; Sequence 191, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C182
; CURRENT APPLICATION NUMBER: US/10/140,808
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-808-191

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Alignment Scores: 0
Pred. No.: 2752.00
Score: Length: 1647
Matches: 512

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Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 99.60% Indels: 0
DB: 14 Gaps: 0
US-10-729-807-10 (1-513) x US-10-140-808-191 (1-1647)

QY 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeu 20
Db 24 ATGAAGCGCTTCCTGCTCTGTTTGTCTTTTATAACATTTCTTCTTCGCAITTCCTCTTA 83
QY 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaValTrpLeuAsnGlnPhe 40
Db 84 GTCCGATGACGGAATAATGAAGAAATATGCAACTGGCTCAGCATATCTCAACCAAGTTC 143
QY 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
Db 144 TACTCTCTTCAATAGAGGAATCATCTTGTTCAAAGCAAGAAATAGGAGTCTCATAGAT 203
QY 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
Db 204 GACAAATTCGGGAAATGCAAGCAATTTTGGATTGACAGTGACTGGAAACTGGACTCA 263
QY 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTrpGly 100
Db 264 AACACCTTGGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGCCAGTATGGC 323
QY 101 TyrThrLeuProGlyTrpArgLysThrAsnLeuThrTyrArgIleIleAsnThrPro 120
Db 324 TACACCTCCCTCGGTGGGAAATAACAACCTCACCTACAGATAATAAACTATACTCCG 383
QY 121 AspMetAlaArgAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140
Db 384 GATATGGCAGAGCTGCTGTGGATGAGGCTATCCAAAGAGGTTTAGAAGTGTGGAGCAA 443
QY 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
Db 444 GTCACTCCACTAAATTCACCAAGATTTCAAGGGGATTCAGACACATCATGATGGCTTT 503
QY 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
Db 504 AGGACTCGAGTCCATGGTGGGTGCTCTCGCTATTTTGTGCTGCTTGGAGTGTGGC 563
QY 181 HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
Db 564 CATGCCCTTCTCTCTGCTCGGTCTGGGTCTGGGTGGTGGTGGTGGTGGTGGTGGTGG 623
QY 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
Db 624 TGGACCAAGGATGGAGCAGGATTCACATTTGTTCTTGTGGCTGCTCATGAAATTTGCTCAT 683
QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTrpValSer 240
Db 684 GCACCTGGGCTCTCTCTCACTCCAATGATCAACAGCCTTGATGTTCCTCAAAATATGCTCC 743
QY 241 LeuAspProArgLysThrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTrp 260
Db 744 CTGGATCCCAGAAATATACCCTTTCTCAGGATGATATCAATGGAATTCAGTCCATCTAT 803
QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
Db 804 GGAGGCTCTGCCCTAAGGTCCTGCTAAGCCAAAGAACCCACTATATACCCCATGCTGTGAC 863
QY 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
Db 864 CTGACTTGACTTTTGACGCTATCAACACTTTCCGACAGAAAGTATATGTCTTTAAAGGC 923
QY 301 ArgHisLeuTrpArgIleTrpTrpAspIleThrAspValGluPheGluLeuIleAlaSer 320
Db 924 AGGCACCTATGGAGGATCTATTATGATATCAGGATGTTGAGTTGAATTAATTTGCTTCA 983
QY 321 PheTrpProSerLeuProAlaAspLeuGlnAlaValTrpGluAsnProArgAspLysIle 340

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Db 984 TTCTGCCATCTCTCCAGCTGATCTGCAAGCTGCATACAGAACCCAGAGATAAGATT 1043  
 QY 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360  
 Db 1044 CTGGTGTAAAGATGAAGAACTCTGGATGATCAGAGGATATGCTGTCTGCCAGATTAT 1103  
 QY 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal 380  
 Db 1104 CCCAATCCATCCATACATTAGTGTTCAGAGCTGTGTGAAGAAATAGATCAGCCGTC 1163  
 QY 381 CysAspLysThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400  
 Db 1164 TGTGATAAGACCAAGAAACCTACTCTTTGTGGGCATTTGTGTGGAGTTTGTAT 1223  
 QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420  
 Db 1224 GAAATGACCCCAACCATGACAAAGATTCCCGCAGAGAGTGTGTAACACATTTCTCTGGA 1283  
 QY 421 IleSerIleArgValAspAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440  
 Db 1284 ATCAGTATCCGTGTGTGATGCTCTTCCAGTACAAAGGATCTCTTTTCAGCCGTGGA 1343  
 QY 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460  
 Db 1344 TCAAGACCAATTTGAATACAACTTAAGACAAAGAAATATTACCCGAATCATGAGAACTAAT 1403  
 QY 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480  
 Db 1404 ACTTGGTTCAATGCAAGAACCAAGAACTCCTCATTTGGTTTGTATCATCAACAAAGGAA 1463  
 QY 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLysLeuPheIlePhe 500  
 Db 1464 AAAGCACATTCAGGAGGCATAAAGATATTGTATCATAGAGTTTAAGCTGTGTATTTT 1523  
 QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513  
 Db 1524 GGTATTGTTCATTTGCTGAAAACACTTCTATTATCA 1562

## RESULT 7

US-10-121-049-191  
 ; Sequence 191, Application US/10121049  
 ; Publication No. US2003002239A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeForge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3330R1C17  
 ; CURRENT APPLICATION NUMBER: US/10/121,049  
 ; CURRENT FILING DATE: 2002-04-12  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 191  
 ; LENGTH: 1647  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-121-049-191

## Alignment Scores:

Pred. No.:	0	Length:	1647
Score:	2752.00	Matches:	512
Percent Similarity:	99.81%	Conservative:	0
Best Local Similarity:	99.81%	Mismatches:	1
Query Match:	99.60%	Indels:	0
DB:	14	Gaps:	0

US-10-729-807-10 (1-513) x US-10-121-049-191 (1-1647)

QY	1	MetLysArgLeuLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeu	20
Db	24	ATGAAGCGCTTCTGCTTCTGTTTTGTTCTTTATAACATTTCTTCTGCAATTTCCCTTA	83
QY	21	ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrIleuAsnGlnPhe	40
Db	84	GTCCGGATGACGGAAATATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACAGTTC	143
QY	41	TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp	60
Db	144	TACTCTCTTGAAATAGAGGGGAAATCATCTTGTTCAAGCAAGAAATAGGAGTCTCATAGAT	203
QY	61	AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer	80
Db	204	GACAAATTTGGGAAATGCAAGCATTTTTCGATTGACAGTCACTGGAAAACTGGACTCA	263
QY	81	AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100
Db	264	AACACCTTGTAGATCATGAAGACACCCAGGTGTGGGTGCTGTGTGGCCAGTATGGC	323
QY	101	TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro	120
Db	324	TACACCTTCCCTGGGTGGAGAAATACAACTCCTACAGAAATTAATAACTATCTACTCG	383
QY	121	AspMetAlaArgAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys	140
Db	384	GATATGGCAGGCTGCTGTGGATGAGGCTATCCAAAGAGGTTTAGAAGTGTGGAGCAA	443
QY	141	ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe	160
Db	444	GTCATCCACTAAAATTCACCAAGATTTCAAAGGGGATTGCAGACATCATGATTCCTTT	503
QY	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180
Db	504	AGGACTCGAGTCCATGGTGGTGTCTCGCTATTTGATGTGCTTGGGAGTGTGTGGC	563
QY	181	HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn	200
Db	564	CATGCTTTCTCTCTGCTGGTCTGGGTGTGGTGTGACACTCATTTTGTATGAGGATGAAAAC	623
QY	201	TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis	220
Db	624	TGGACCAAGGATGGAGCAGGATTCAACTTGTTCGTGGCTGTCTCATGATGAGGATGAAAC	683
QY	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
Db	684	GCATGGGGCTCTCTCACTCCAAATGATCAAAAGCCTTGAAGTTCCTCCAAATTAATGTCTCC	743
QY	241	LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr	260
Db	744	CTGGATCCAGAAATACCCACTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT	803
QY	261	GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp	280
Db	804	GGAGTCTGCTTAAGGTACTGTCTAAGCCAAAGGAACCCACTATACCCCATCGCTGTGAC	863
QY	281	ProAspLeuThrPheAspAlaIleThrThrPheArgGluValMetPhePheLysGly	300
Db	864	CCTGACTTGTACTTTTGACGCTATCACAACTTTCGACAGAGAAATATGTCTTTAAAGGC	923
QY	301	ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer	320
Db	924	AGGCACCTATGAGGATCTATTATGATATCAGGATGTTGAGTTTGAATTAAATTTGCTTCA	983

Qy	321	PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle	340
Db	984	TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAGAACCCTCCAGATAAGATT	1043
Qy	341	LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr	360
Db	1044	CTGGTTTTAAAGATGATAAACTTCTGGATGATCAGAGGATATGTGTTCTGGCAGATTAT	1103
Qy	361	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal	380
Db	1104	CCCAAAATCCATACATATTAGTGTTCAGGACGTGTGAAGAAAAATAGATGCAGCGCTC	1163
Qy	381	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysLrpAlaGpPheAsp	400
Db	1164	TGTGATGAAGACCAACAGAAAAAACCCTACTCTTTGTGGGCAATTTGGTGCTGGAGGTTTGAT	1223
Qy	401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly	420
Db	1224	GAATGACCCAAACCATGGACAAAGGATTCCTCGCAGAGAGTGTGTAAACACTTTCCTGGA	1283
Qy	421	IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly	440
Db	1284	ATCAGTATCCGTGTGTGCTGCTTTCAGTACAAAGAGATTCTTCTTTTTCAGCCGTGGA	1343
Qy	441	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
Db	1344	TCAAAGCAATTTGAAATCAACATTTAAGACAAAGAAATATTACCCGAAATCATGAGAACTTAAT	1403
Qy	461	ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu	480
Db	1404	ACTTGGTTTTCAATGCAAAAGAACCAAGAACTCCCTCATTTGGTTTTGATATCAACAGGAA	1463
Qy	481	LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe	500
Db	1464	AAAGCATTTCAGAGGCATAAAGATATTGTATCATTAAGAGTTTAAGCTGTTTATTTTT	1523
Qy	501	GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln	513
Db	1524	GGTATTGTTCTATTTCGTGAAGAAACACTTCTATTATCAAA	1562

## RESULT 8

```

US-10-123-904-191
; Sequence 191, Application US/10123904
; Publication No. US2003022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA

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Qy	301	ArgHisLeuThrArgIleTyrTrpAspIleThrAspValGluPheGluLeuIleAlaSer	320
Db	924	AGGCACCTATGCGAGGATCTATTATGATATCAGGATGTGTGAGTTTGAAATTAAATGCTTCA	983
Qy	321	PheTrpProSerLeuProAlaAspLeuGlnAlaIaTyrGluAenProAtrAspLysIle	340
Db	984	TTCTGGCCATCTCTGGCCAGCTGATCTGCAGCTGCATACGAGAACCCGAGAGATAAGATT	1043
Qy	341	LeuValPheLysAspGluAAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr	360
Db	1044	CTGGTTTTTAAAGATGAAAACTTCTGGATGATCAGAGATATGCTGTCTGCCAGATTAT	1103
Qy	361	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal	380
Db	1104	CCCAATCCCATACATATAGGTTTTCCAGGACGTGTGAAGAAAAATAGATGCACCCGTC	1163
Qy	381	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTrpAtrPheAsp	400
Db	1164	TGTGATAAGACCACAAGAAAAACCTACTTCTTTGTGGGCATTTGGTGCTGGAGGTTTGAT	1223
Qy	401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly	420
Db	1224	GAATATGACCCAAACCATATGGACAAAGAGATTCCCGCAGACAGTGGTAAACACATTTCTCTGGA	1283
Qy	421	IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly	440
Db	1284	ATCAGTATCCGTGTGTATGTGCTTTCCAGTACAAAGAGATTCTTCTTTTCAGCCGGTGA	1343
Qy	441	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
Db	1344	TCAAAGCAATTTGAATACAAACATTAAAGACAAAGAAATATTACCCGAATCATGAGAACTAAT	1403
Qy	461	ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu	480
Db	1404	ACTTGGTTTTCAATGCCAAGAACCAAGAGAACTCCCTCATTTGGTTTGTATATCAACAAGGAA	1463
Qy	481	LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe	500
Db	1464	AAAGCACATTGAGGAGCATAAAGATATTGTATCATTAAGATTAAAGCTGTTTATTTTTT	1523
Qy	501	GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln	513
Db	1524	GGTATCTGTCATTGGCTGAAAAACATCTCATTTATCAAA	1562

## RESULT 9

```

US-10-140-470-191
; Sequence 191, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550

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864 CCTGCTTGAATTTTTCAGCGTATCACAACTTTCGACAGAGTAATGTTCTTTAAAGGC 923  
301 ArgHisLeuTrpArgIleTyrAspIleThrAspValGluPheGluLeuAlaSer 320  
924 AGGACCTATGGAGGATCTATTATGATATACCGATGTTGAGTTGAATTAATGCTTCA 983  
321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340  
984 TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAGAACCCAGAGATAAGATT 1043  
341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360  
1044 CTGGTTTTTAAAGATGAAGAACTTCTGATGATCAGAGATATGCTGCTTGCAGATTAT 1103  
361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380  
1104 CCCAATCCATCCATACATTAGGTTTTCCAGGACGCTGGAAGAAATAGATGCAGCCGTC 1163  
381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400  
1164 TGTGATAGACCAACAGAAAAACCTACTTCTTTGTGGGCAATTTGGTGCTGGAGGTTTGT 1223  
401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420  
1224 GAATGACCCAAACCATGGACAAAGGATTTCCGCGAGAGTGGTGAACACACTTTCTTCTGGA 1283  
421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440  
1284 ATCAGTATCCGTGTGTGCTGCTTTCCAGTACAAAGGATTTCTTTTTCAGCCGTGGA 1343  
441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460  
1344 TCAAGCAATTTGAATCAACATTAAGCAAAAGAAATATTACCCGGAATCATGAGAACTAAT 1403  
461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480  
1404 ACTTGGTTTCAATCAAGAACCAAGAACTCTTCATTTGTTTGTATATCAACAGAA 1463  
481 LysAlaHisSerGlyGlyIleLysIleLysThrHisLysSerLeuSerLeuPheIlePhe 500  
1464 AAGCACATTCAGGAGGCATTAAGATATTGATATCAAGAGTTTAAGCTTGTATTATTTT 1523  
501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513  
1524 GGTATTGTTTCAATTTGCTGAAACCACTTCTATTATCA 1562

RESULT 10

US-10-175-746-191  
; Sequence 191, Application US/10175746  
; Publication No. US20030027270A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C353  
; CURRENT APPLICATION NUMBER: US/10/175,746

; CURRENT FILING DATE: 2002-06-19  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 191  
; LENGTH: 1647  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-175-746-191  
Alignment Scores:  
Pred. No.: 0 Length: 1647  
Score: 2752.00 Matches: 512  
Percent Similarity: 99.81% Conservatives: 0  
Best Local Similarity: 99.81% Mismatches: 1  
Query Match: 99.60% Indels: 0  
DB: 14 Gaps: 0  
US-10-729-807-10 (1-513) x US-10-175-746-191 (1-1647)  
QY 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeu 20  
Db 24 ATGAAGCGCCTTCTGCTTCTGTTTCTTTTATATACATTTCTTCTGCAATTCCTTCA 83  
QY 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40  
Db 84 GTCGGATGACGGAAATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACCACTTC 143  
QY 41 TyrSerLeuGluLeuGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60  
Db 144 TACTCTCTTGAATAGAGGGAATCATCTTTTCAAAGCAAGAAATAGGAGTCTCATAGAT 203  
QY 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
Db 204 GACAAAATTCGGGAATTCGAAGCAATTTTGGATGTGACGTGACTGGAAACTGGACTCA 263  
QY 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
Db 264 AACACCTTCAGATCATGAAGACACCCAGGTTGGGGTGGCTGATGTGGGCCAGTATGGC 323  
QY 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120  
Db 324 TACACCTCTCCCTGGTGGAGAAATACAACCTCACTACAGATAATAAACTATACCTCCG 383  
QY 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140  
Db 384 GATATGGCAGCTGCTGTGGATGAGCTATCCAAAGAGTTTAGAAGTGTGGAGCAA 443  
QY 141 ValThrProLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160  
Db 444 GTCACCTCACTAAAATTCACCAAGATTTCAAAGGGATTCAGACATCATGATGCTTTT 503  
QY 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180  
Db 504 AGGACTGAGTCCATGCTGGTGGTCTGGTGTCTGCTATTTTATGTTGCTTGGGAGTGTGGC 563  
QY 181 HisAlaPheProGlyProGlyLysLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200  
Db 564 CATGCCCTTCTCTCTGGTCCGGGTCTGGGTGTGGTGTGACACTCATTTTGTATGAGATGAAAC 623  
QY 201 TrpThrLysAspGlyAlaGlyPheAsnLeuValAlaAlaHisGluPheGlyHis 220  
Db 624 TGGACCAAGGATGGAGCAGGATTCAACTTGTGTTCTTGTGGTGTGCTCATGAATTTGGTCA 683  
QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240  
Db 684 GCATCTGGGCTCTCTCACTCCAAATGATCAACACGCTTGTATGTTCCCAAAATATGTCTCC 743  
QY 241 LeuAspProArgLysTyrProLeuSerSerGlnAspIleAsnGlyIleGlnSerIleTyr 260  
Db 744 CTGGATCCCAAGAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803  
QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280



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Db 804 GGAGGTCTCGCTAAGTACCTGTAAGCAAGAAAGCAACCCACTATACCCCATCGCTGTGAC 863
QY 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
Db 864 CTGACTTCTGACCTTTTGGCGCTATCAACATTTCCGCGAGAGAGTATGTCTTTTAAAGCG 923
QY 301 ArgHisLeuThrArgIleThrArgPheThrAspValGluPheGluLeuLeuAlaSer 320
Db 924 AGGCACCTATGAGGAGTCTATTATGATATCAGGATGTGAGTTTGAATTAATGTCTTCA 983
QY 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaThrGluAsnProArgAspLysIle 340
Db 984 TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAGAACCCAGAGATAGATT 1043
QY 341 LeuValPheLysAspGluAsnThrMetIleArgGlyThrAlaValLeuProAspTyr 360
Db 1044 CTGGTTTTTAAAGATGAAAACTTCTGGATGATCAGAGGATATGCTGTCTTGCAGATTAT 1103
QY 361 ProLysSerIleHisThrLeuGlyPheProGlyValGlyValLysLysIleAspAlaAlaVal 380
Db 1104 CCCAATCCATCCATACATAGTTTTCAGAGCGTGTGAGAAATATAGATGAGCCGTC 1163
QY 381 CysAspLysThrThrArgLysThrThrPhePheValGlyIleTrpCysTrpArgPheAsp 400
Db 1164 TGTGATAAGACACACAAAGAAACCTACTTCTTTGTGGCATTTGGTGTGAGGTTTGAT 1223
QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
Db 1224 GAAATGACCCAAACCATGACAAAGGATTTCCCGCAGAGAGTGGTAAACACATTTTCTCTGA 1283
QY 421 IleSerIleArgValAspAlaAlaPheGlnThrLysGlyPhePhePhePheSerArgGly 440
Db 1284 ATCAGTATCCGTTGGTGAATGCTCTTCCAGTACAAAGGATTTCTCTTTTCAGCCGTGA 1343
QY 441 SerLysGlnPheGluThrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
Db 1344 TCAAGACATTTGATACAAACATTAAGACAAAGATATTACCAGATCATGAGAACTAAT 1403
QY 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
Db 1404 ACTTGTTTCAATGCAAGAAACCAAGAACTCTCTCAATTTGGTTTGTATATCAACAAGGAA 1463
QY 481 LysAlaHisSerGlyGlyIleLysIleLeuThrHisLysSerLeuSerLeuPheIlePhe 500
Db 1464 AAAGCACATTCAGAGGCAATAAGATATTGTATCATAGAGTTTAAAGCTTTTATTTT 1523
QY 501 GlyIleValHisLeuLysAsnThrSerIleTyrGln 513
Db 1524 GGTATTGTTCAITTTGCTGAAGAAACACTTCTATTATCAAA 1562

RESULT 11
US-10-176-918-191
; Sequence 191, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
```

```
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RLC382
; CURRENT APPLICATION NUMBER: US/10176,918
; PRIOR APPLICATION DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-176-918-191

Alignment Scores:
Pred. No.: 0 Length: 1647
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 99.60% Indels: 0
DB: 14 Gaps: 0

US-10-729-807-10 (1-513) x US-10-176-918-191 (1-1647)
QY 1 MethLysArgLeuLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeu 20
Db 24 ATGAAGCGCTTCTGCTTCTGTTTTTGTCTTTTAAACATTTTCTTCGATTTCCCTTA 83
QY 21 ValArgMetThrGluAsnGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
Db 84 GTCCGGATGACGGAATAATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACCATGTC 143
QY 41 TyrSerLeuGluIleLeuGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
Db 144 TACTCTCTTGAATAGAGGGAATCATCTTGTCAAAGCAAGANTAGGAGTCTCATAGAT 203
QY 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
Db 204 GACAAAATTCGGGAAATGCAAGCATTTTTTGGATTGACAGTCAGCTGGAATACTGGACTCA 263
QY 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
Db 264 AACACCTTTGAGATCATGAAGACACCCAGGTGTGGGTGCTGCTGATGTGGGCCAGTATGC 323
QY 101 TyrThrLeuProGlyTrpArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120
Db 324 TACACCTCTCCCTGGGTGGAGAAAATACAACTCCTACAGATATAATAACTATATCTCCG 383
QY 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140
Db 384 GATATGGCACGAGCTGCTGTGGATGAGGCTATCCAAAGAGGTTTAGAAGTGTGGAGCAAA 443
QY 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
Db 444 GTCACTCCACTAAATTTCCAAAGGAGATTGCAGACATCATGATGTGCTTT 503
QY 161 ArgThrArgValHisGlyValArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
Db 504 AGGACTCGAGTCCATGGTGGTGTCTCTGCTATTATTGATGCTCCCTTGGAGTGTGCTGC 563
QY 181 HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
Db 564 CATGCTTTCTCTCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 623
QY 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
Db 624 TGGACCAAGGATGAGACAGGATTCAACTTGTGTTTCTTGTGGCTGCTCATGAATTTGCTCAT 683
QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
Db 684 GCATGGGGCTCTCTCACTCAATGATCAACAGGCTTGTATGTTCCCAATTTATGTCTCC 743
QY 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260
Db 744 CTGGATCCCAAGAAATACCCACTTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803
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Qy 261 GlyClyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
Db 804 GGAGGCTGCTAGGTAAGTCTGTAAGCAAGAACCCATATACCCCTGCTGTGAC 863
Qy 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
Db 864 CCGACTTGACTTTTGCGCTATCACAACTTTCGCGAGAGATATGTTCTTTAAAGGC 923
Qy 301 ArgHisLeuThrArgIleThrThrAspIleThrAspValGluPheGluLeuIleAlaSer 320
Db 924 AGGCACCTATGAGGATCTATTATGATATACCGATGTTGAGTTGAATTAATGCTTCA 983
Qy 321 PheTrpProSerLeuProAlaAspLeuGlnAlaLysValGluAsnProArgAspLysIle 340
Db 984 TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTCATACGAGAACCCCGAGAGATAAGATT 1043
Qy 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
Db 1044 CTGGTTTTTAAGATGAACCTCTGGATGATCAGAGATATGCTGCTTGGCCAGATTAT 1103
Qy 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380
Db 1104 CCCAAATCCATCCATACATTAGGTTTCCAGAGCTGTGAAGAAATAGATGCAGCCGTC 1163
Qy 381 CysAspLysThrThrArgLysThrThrPhePheValGlyIleThrCysTrpArgPheAsp 400
Db 1164 TGTGATTAAGACCAACAAGAAACCTACTTCTTGTGGGCAATTTGGTGTGGAGTTTGAT 1223
Qy 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
Db 1224 GAATGACCCCAACCATGGACCAAGGATTCCTCGCAGAGATGGTAAACACTTTCCTGGA 1283
Qy 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
Db 1284 ATCAGTATCGCTGTGTGATGCTGCTTTCAGTACAAAGGATTTCTTCTTTTTCAGCCGTTGA 1343
Qy 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
Db 1344 TCAAGCAATTTGTAATACACATTAAGCAAAAGATATATCCCGAAATCATGAGAACTAAT 1403
Qy 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
Db 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCTCTCAATTTGGTTTGTATATCAACAAGAA 1463
Qy 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
Db 1464 AAAGCAATTCAGGAGGACATAAAGATATTTGTATCATAAAGAGTTTAAAGCTTTGTTATTTT 1523
Qy 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
Db 1524 GGTATTGTTTCAATTTGCTGAAACACACTTCTATTATTCNA 1562

RESULT 12
US-10-176-921-191
; Sequence 191, Application US/10176921
; Publication No US20030027276A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
```

```
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C288
; CURRENT APPLICATION NUMBER: US/10/176,921
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-921-191

Alignment Scores:
Pred. No.: 0 Length: 1647
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 99.60% Indels: 0
DB: 14 Gaps: 0

US-10-729-807-10 (1-513) x US-10-176-921-191 (1-1647)
```

```
Qy 1 MetLysArgLeuLeuLeuLeuLeuLeuPhePheIleThrPheSerSerAlaPheProLeu 20
Db 24 ATGAAGCGCCTTCGCTCTGTTTGTCTTTATAACATTTCTTCGCAATTTCCCTTA 83
Qy 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
Db 84 GTCGGATGACGGAATATGAAGAAATATGCACTGGCTCAGGCATATCTCAACAGTTC 143
Qy 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
Db 144 TACTCTCTGAAATAGAGGGAATCATCTTGTTCAAAGCAAGATAGAGTCTCATAGAT 203
Qy 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
Db 204 GACAAAATTCGGGAAATGCAAGCAATTTTGGATGTAGAGTCTGGAAAACTGGACTCA 263
Qy 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
Db 264 AACACCTCTGAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGCCAGTATGGC 323
Qy 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120
Db 324 TACACCTCTCCCTGGGTGGAGAAAATACAACTCACCTACAGAAATAATAAATACTACTCCG 383
Qy 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140
Db 384 GATATGGCAGAGCTGCTGTGGATGAGGCTATCCAAAGGTTTAGAAGTGTGGAGCAAA 443
Qy 141 ValThrProLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
Db 444 GTCACCTCCACTAAATTCACCAAGATTTCAAAGGGGATTCAGAGACATCATGATTTGCCTT 503
Qy 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
Db 504 AGGACTCGAGTCCATGGTGGTGTGCTCTATTTTGTATGCTCCCTTGGAGTGTCTGGC 563
Qy 181 HisAlaPheProProGlyProGlyLeuGlyValAspThrHisPheAspGluAspGluAsn 200
Db 564 CATGCCCTTCTCTCTGCTCCGGTCTGGGTGGTGACACTCATTTTGTATGAGGATGAAAC 623
Qy 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaHisGluPheGlyHis 220
Db 624 TGGACCAAGATGGAGCAGGATTCACACTTGTCTTCTGTGGCTGCTCATGAATTTGGTCAT 683
Qy 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
Db 684 GCACCTGGGGCTCTCTCTACTCCATGATCAAAACAGCCCTTGATGTTCCCAAAATATGTCCTCC 743
```

```
QY 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260
DB 744 CTGATCCAGAAAATACCCACTTTCTCAGGATGATATCAATGGAAATCCAGTCCATCAT 803
QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
DB 804 GGAGGTCTGCTTAAGTACTCTTAAGCCAAAGAACCCACTATATCCCATCCCTGTGAC 863
QY 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
DB 864 CTTGACTTGTCTTTCAGCGCTATCAAACTTTCCGACAGAGTAATGTCTTTTAAAGGC 923
QY 301 ArgHisLeuTrpArgIleTyrTrpAspIleThrAspValGluPheGluLeuIleAlaSer 320
DB 924 AGGCACCTATGAGGATCTTATATGATATCATCGGATGTTGAGTTTGAATTAATTCCTCA 983
QY 321 PheTrpProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnProArgAspLysIle 340
DB 984 TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAGAACCCAGAGATAAGATT 1043
QY 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
DB 1044 CTGGTTTTTAAAGATGAAAACCTTCGGATGATCAGAGGATATGCTGTCTTGCAGATTAT 1103
QY 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaIleVal 380
DB 1104 CCCAAATCCATCCATACATTAGGTTTTCAGGACGTTGTAAGAAATAGATGACCCGTC 1163
QY 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400
DB 1164 TGTGATAGACACCAAGAAAACCTTCTTTTGGGCAATTTGGTCTGGAGGTTTGAT 1223
QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly 420
DB 1224 GAATGACCCAAACCATGACAAAGGATTCGCGCAGAGAGTGTGTAACCACTTTTCTCGGA 1283
QY 421 IleSerIleArgValAspAlaIlePheGlnTyrLysGlyPhePhePheSerArgGly 440
DB 1284 ATCAGTATCCGTGTGATGCTCTTTCCAGTACAAAGGATTTCTTTTTCAGCCGTGGA 1343
QY 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
DB 1344 TCAGAGCAATTTGAATACAACTTAAGACAAAGAAATATTACCGAATCATGAGAACTAAT 1403
QY 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGln 480
DB 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCTCTCATTTTGGTTTTGTATATCAACAAGGAA 1463
QY 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
DB 1464 AAAGCACTTCAGAGGCAATAAGATATTGTATCATAGAGTTAAGCTTGTATTATTTT 1523
QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
DB 1524 GGTAATTGTTCAATTTGCTGAAAAACACTTCTATTATCAAA 1562
```

## RESULT 13

```
US-10-137--865-191
; Sequence 191, Application US/10137865
; Publication No. US20030032155A1
```

## GENERAL INFORMATION:

```
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
```

```
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C154
; CURRENT APPLICATION NUMBER: US/10/137,865
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-137-865-191
```

## Alignment Scores:

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Pred. No.: 0 Length: 1647
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 99.60% Indels: 0
DB: 14 Gaps: 0
```

US-10-729-807-10 (1-513) x US-10-137-865-191 (1-1647)

```
QY 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeu 20
DB 24 ATGAAGCGCTTCTGCTTCTGTTTGTCTTTTATTAACATTTTCTCTGCATTTCCCTTA 83
QY 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
DB 84 GTCCCGATGACCGAAATGAAGAAATATGCAACTGCGCTCAGCATATCTCAACAGTTC 143
QY 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
DB 144 TACTCTTGAATAGAGGGAATCATCTTGTTCAAAGCAAGAAATAGGAGTCTCATAGAT 203
QY 61 AspLysIleArgGluMetGlnAlaPheGlyLeuThrValThrGlyLysLeuAspSer 80
DB 204 GACAAAATTCGGGAAATGCAAGCAATTTTGTGATTTGACAGTCACTGGAAAACTGGACTCA 263
QY 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
DB 264 AACACCTTTGAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGCCAGTATGCG 323
QY 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120
DB 324 TACACCTCTCTGGGTGGAGAAAATACAACTCACCTACAGAAATAATAAATACTATCTCCG 383
QY 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGlnValTrpSerLys 140
DB 384 GATATGACAGAGTCTGCTGTGATGAGGCTATCCAAAGAGGTTTAGAAGTGGAGCAAA 443
QY 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
DB 444 GTCATCTCCACTAAATTCACCAAGATTTCAAAGGGATTTGCAGACATCATGATGCTTTT 503
QY 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
DB 504 AGGACTCGAGTCCATGCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 563
QY 181 HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAsn 200
DB 564 CATGCCCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 623
QY 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheValAlaAlaHisGluPheGlyHis 220
DB 624 TGGACCAAGGATGAGCAGGATTTCAACTTGTCTTCTGTGCTCTCTCTCTCTCTCTCTCAT 683
QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
```



Db 624 TGGACCAAGGATGGAGCAGGATTCACACTGTTCTTGTGGCTGCTCATGAATTTGGTCAT 683  
 QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240  
 Db 684 GCACCTGGGGCTCTCTCACTCCATGATCAACAGCCTTGATGTTCCCAAAATATGTCCTCC 743  
 QY 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260  
 Db 744 CTGGATCCCAAGAAATACCCACTTTCTCAGGATGATATCAATGGAAATCCAGTCCATCAT 803  
 QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280  
 Db 804 GGAGTCTGGCTTAAGTACCTCTAAGCCAAAGAACCCACTATACCCCATGCCCTGTGAC 863  
 QY 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300  
 Db 864 CTTGACTTGGCTTATGAGCTATCAACTTTCCGACAGAAAGTAAATGCTTTTAAAGGC 923  
 QY 301 ArgHisLeuTyrArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320  
 Db 924 AGGCACCTATGAGGATCTATTATGATATCACGGATGTGAGTTTGAATTAATTCCTTCA 983  
 QY 321 PheTyrProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnProArgAspLysIle 340  
 Db 984 TTCTGGCCATCTCTGCCAGCTGATCTGCNAGCTGCTATACGAGAACCCACGAGATTAAGATT 1043  
 QY 341 LeuValPheLysAspGluAsnPheTyrMetIleArgGlyTyrAlaValLeuProAspTyr 360  
 Db 1044 CTGGTTTTTAAAGATGAAACCTCTCTGGATGATCAGAGGATATGCTGTCTTCCAGATTAT 1103  
 QY 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal 380  
 Db 1104 CCCAAATCCATCATACATATAGTGTTCAGACGCTGTCAAGAAATATAGTACGACCGTC 1163  
 QY 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTyrArgPheAsp 400  
 Db 1164 TGTGATAAGCACCAAGAAACCTACTTCTTTTGGGCAATTTGGTCTGGAGTTTGAT 1223  
 QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420  
 Db 1224 GAATGACCCAAACCATGACAAAGGATTTCCCGCAGAGAGTGTGTAACACACTTTCTCTGA 1283  
 QY 421 IleSerIleArgValAspAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440  
 Db 1284 ATCAGTATCCGTGTTGATGCTGTTTCCAGTACAAAGGATTTCTTTTTCAGCCGTGA 1343  
 QY 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460  
 Db 1344 TCAAGCAATTTGAATACAACTTAAGAACAAAGAAATATACCGAATCATGAGAACTAAT 1403  
 QY 461 ThrTyrPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480  
 Db 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCTCTCATTTGTTTTCATATCAACAAAGAA 1463  
 QY 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500  
 Db 1464 AAAGCACATTCAGAGGCATAAAGATATTGTATCATAAAGAGTTTAAAGCTTGTATTATTTT 1523  
 QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513  
 Db 1524 GGTATTGTTTCTTGTGAAACAACTTCTATTATTATCA 1562

## RESULT 15

US-10-142-431-191  
 ; Sequence 191, Application US/10142431  
 ; Publication No. US20030036179A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeFoige, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3330R1C251  
 ; CURRENT APPLICATION NUMBER: US/10/142,431  
 ; CURRENT FILING DATE: 2002-05-10  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 191  
 ; LENGTH: 1647  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; US-10-142-431-191

Alignment Scores:  
 Pred. No.: 0 Length: 1647  
 Score: 2752.00 Matches: 512  
 Percent Similarity: 99.81% Conservative: 0  
 Best Local Similarity: 99.81% Mismatches: 1  
 Query Match: 99.60% Indels: 0  
 DB: 14 Gaps: 0

US-10-729-807-10 (1-513) x US-10-142-431-191 (1-1647)

QY 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeu 20  
 Db 24 ATGAAGCGCTTCTGCTTCTGTTTGTCTTTATATAACATTTTCTTCTGCAATTCCTTTA 83  
 QY 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40  
 Db 84 GTCCGGATGACGGAATAATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACCAAGTTC 143  
 QY 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60  
 Db 144 TACTCTCTTGAATTAAGAGGGAATCATCTTGTTCAAAGCAAGAAATAGGAGTCTCATAGAT 203  
 QY 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
 Db 204 GACAAATTCGGGAAATGCAAGCATTTTGTGATTGACAGTGAAGTGAAGAACTGGACTCA 263  
 QY 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
 Db 264 AACACCCCTTGAGATCATGAAGACACCCAGGTGTGGGGTGCCTGATGTGGCCAGTATGGC 323  
 QY 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120  
 Db 324 TACACCTCTCCCTGGGTGGAGAAAAATACAACTTCCTACAGATATAATAACTATATCTCCG 383  
 QY 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140  
 Db 384 GATATGGCAGAGTGTCTGTGGATGAGCTATCCAAAGAGGTTTAGAAGTGTGGAGCAAA 443  
 QY 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160  
 Db 444 GTCACTCCACTAAATTCACCAAGATTTCAAAGGGGATTTGCAGACATCATGATTGCTTT 503  
 QY 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180  
 Db 504 AGGACTCGAGTCCATGCTGGTGTCTCTCGTATTTTGTGGTCCCTTGGAGGTGCTTGGC 563  
 QY 181 HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200  
 Db 564 CATGCCCTTTCTCTCGTGGTCTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 623

```
Qy 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
Db |||
Db 624 TGGACCAAGGATGGAGCAGGATCAACTTGTCTTGTGGCTGCTCATGAATTTGGTCAT 683
Qy 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
Db |||
Db 684 GCACCTGGGGCTCTCTCACTCCAATGATCAAAACAGCCTTGATGTTCCCAAAATATGTCTCC 743
Qy 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260
Db |||
Db 744 CTGGATCCAGAAATACCCCACTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803
Qy 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
Db |||
Db 804 GGAGGTCTGCCCTAAGTACCTGTAGCCAAAGGACCCACTATACCCCATGCCCTGTGAC 863
Qy 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
Db |||
Db 864 CCTGACTTGACTTTTGAAGCTATCACAACTTTCGCGAGAGAAGTAATGTTCTTTAAGGC 923
Qy 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
Db |||
Db 924 AGGCACCTATGGAGGATCTATTATGATATCAGGATGTTAGATTGAATTAATTTGCTTCA 983
Qy 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340
Db |||
Db 984 TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAGAACCCCGAGAGATAAGATT 1043
Qy 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360
Db |||
Db 1044 CTGGTTTTTAAAGATGAAACTTCTGGATGATCAGAGATATGCTGTTGCCAGATTAT 1103
Qy 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380
Db |||
Db 1104 CCCAATCCATCCATCATATTAGTTTTCAGGAGCTGTGAAGAAAAATAGATGCGCCGTC 1163
Qy 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTyrArgPheAsp 400
Db |||
Db 1164 TGTGATAAGACCAACAAAGAAACCTACTTCTTTGTGGCATTTGGTCTGGAGGTTTGAT 1223
Qy 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly 420
Db |||
Db 1224 GAAATGACCCAAACCAATGGCAAAAGGATTCGCCGAGAGAGTGGTAAACACTTTCTCTGGA 1283
Qy 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
Db |||
Db 1284 ATCAGTATCCGTGTTGATGCTGTTTCCAGTACAAGGATTCCTTTTCAGCCGTGGA 1343
Qy 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
Db |||
Db 1344 TCAAAGCAATTTGAATACACATTAAAGCAAAAGATATTACCCGAAATCATGAGAACTAAT 1403
Qy 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
Db |||
Db 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCCTCATTTGGTTTGTATATCAACAAGAA 1463
Qy 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
Db |||
Db 1464 AAAGCAGATTCAGAGGCATAAAGATATTGTATCATAGAGTTTAAGCTTGTATTATTTT 1523
Qy 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
Db |||
Db 1524 GGTATTGTTCAATTGCTGAAAAACACTTCTATTATCAAA 1562
```

Search completed: November 16, 2004, 00:46:28

Job time : 804 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 15, 2004, 21:08:13 ; Search time 4696 Seconds  
(without alignments)  
3980.746 Million cell updates/sec

Title: US-10-729-807-10

Perfect score: 2763

Sequence: 1 MKRLLLCLEFFIFSSAPPL.....SLSLFIRGIVHLLKNVSIYQ 513

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/cgm2 1/USPTO.spool/US10729807/runat 15112004 131727 16851/app query.fasta\_1.711  
-DB=EST -QSWT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptp -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10729807 @CGN 1 1 3437 @runat 15112004 131727 16851 -NCPU=3  
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1322	47.8	731	5 BX102293	BX102293 BX102293
2	1243.5	45.0	1735	3 AK020292	AK020292 Mus muscu
3	1159	41.9	2223	3 AK089234	AK089234 Mus muscu
4	1154	41.8	2074	3 AK089516	AK089516 Mus muscu
5	1154	41.8	2426	3 AK089381	AK089381 Mus muscu
6	1149	41.6	755	4 BG189775	BG189775 RST8821 A
7	1146	41.5	2427	3 AK089336	AK089336 Mus muscu
8	1107	40.1	1784	3 CR603756	CR603756 full-length
9	1032.5	37.4	1798	3 AK089309	AK089309 Mus muscu

10	1030.5	37.3	2013	3 AK049552	AK049552 Mus muscu
11	1024.5	37.1	1800	3 AK090051	AK090051 Mus muscu
12	1023.5	37.0	1519	3 AK089523	AK089523 Mus muscu
13	1023.5	37.0	1798	3 AK089452	AK089452 Mus muscu
14	984.5	35.6	1449	9 AY420752	AY420752 Mus muscu
15	983.5	35.6	1452	9 AY420750	AY420750 Homo sapi
16	979.5	35.5	1453	3 AK089509	AK089509 Mus muscu
17	915	33.1	1416	9 AY418899	AY418899 Homo sapi
18	910	32.9	1850	3 CR645708	CR645708 Tetraodon
19	905	32.8	1419	9 AY418901	AY418901 Mus muscu
20	865	31.3	1330	9 AY420747	AY420747 Homo sapi
21	862.5	31.2	894	5 BU120858	BU120858 603144842
22	839.5	30.4	683	6 BY753385	BY753385 BY753385
23	821	29.7	632	5 BU402270	BU402270 604137994
24	819	29.6	1027	7 CN065546	CN065546 D09 Ag2 p
25	808	29.2	1261	9 AY420749	AY420749 Mus muscu
26	797	28.8	2895	3 CR608838	CR608838 full-length
27	792.5	28.7	1452	9 AY420751	AY420751 Pan trogl
28	770	27.9	771	7 CN052608	CN052608 Salamande
29	769	27.8	871	7 CN067389	CN067389 J10 Ag2 p
30	765.5	27.7	843	7 CN062082	CN062082 Ag2_p35 H
31	764.5	27.7	854	7 CN066791	CN066791 H10 Ag2 p
32	764.5	27.7	903	6 CA471366	CA471366 AGENCOURT
33	757.5	27.4	869	5 BU281887	BU281887 603602842
34	752.5	27.2	909	1 AU050632	AU050632 AU050632
35	747	27.0	832	7 CN060762	CN060762 A04 Ag2 p
36	746	27.0	746	1 AI436025	AI436025 th80g12.x
37	745.5	27.0	846	7 CN064495	CN064495 Ag2_p7 D8
38	743	26.9	928	5 BU382223	BU382223 603857156
39	741	26.8	593	4 BM440043	BM440043 pgr.in.pk0
40	737	26.7	411	1 AA424347	AA424347 zv90e12.r
41	731.5	26.5	4346	3 BC047278	BC047278 Mus muscu
42	730	26.4	716	5 BU200410	BU200410 604158850
43	728.5	26.4	910	7 CN068049	CN068049 l12 Ag2 p
44	723	26.2	935	7 CO647474	CO647474 ILDMIGEN
45	720	26.1	561	5 BX918107	BX918107 BX918107

#### ALIGNMENTS

RESULT 1

BX102293

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BX102293 731 bp mRNA linear EST 06-FEB-2003  
BX102293 Soares NHMPu\_S1 Homo sapiens cDNA clone IMAGE9980231887 ;  
IMAGE:767086, mRNA sequence.

BX102293.1 GI:27845222

EST.

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 731)

Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,

Radelof,U., Schneider,D. and Korn,B.

Human Unigeneset - RZPD3

Unpublished (2003)

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany

RZPD; IMAGE9980231887.

RZPDLIB; I.M.A.G.E. cDNA Clone Collection;

Human Unigeneset - RZPD3 (RZPDLIB No.972)

http://www.rzpd.de/CloneCards/cgi-

bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 101

Fax: +49 30 32639 111

www.rzpd.de

This clone is available royalty-free from RZPD;

contact RZPD (clone@rzpd.de) for further information. Seq primer:

M13r, Primer sequence: TTTCACAGGAAACAGCTATGAC.

FEATURES  
source

## Location/Qualifiers

1. 731  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clones="IMAGp980231887 ; IMAGE:767086"  
/tissue\_type="Pooled human melanocyte, fetal heart, and pregnant uterus"  
/lab\_host="DH10B"  
/clone\_lib="Soares NHMPu S1"  
/note="Organ: mixed (see below); Vector: p7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBHM, pregnant uterus NBHPU, and fetal heart NBH19W) were mixed, and ss circles was made in vitro. Following HAP purification, this DNA reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of 1.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

## ORIGIN

## Alignment Scores:

Pred. No.: 7.42e-143 Length: 731  
Score: 1322.00 Matches: 241  
Percent Similarity: 99.59% Conservative: 1  
Best Local Similarity: 99.18% Mismatches: 1  
Query Match: 47.85% Indels: 0  
DB: 5 Gaps: 0

US-10-729-807-10 (1-513) x BX102293 (1-731)

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Db 181 TGGAGGATCTATTATGATATACGGATGTTGAGTTTGAATTAATTCCTTCATCTCGCCA 240  
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Db 241 TCTCTGCCAGCTGAUCTGACGTGATACGAGAACCCAGAGATAAGATTCCTGGTTTTT 300  
Qy 344 LysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyrProLysSer 363  
Db 301 AAAGATGAAACTTCCTGGATGATCAGAGATATGCTGCTTGCAGATTATCCCAATCC 360  
Qy 364 IleHisThrLeuGlyPheProGlyArgValLysIleAspAlaValCysAspLys 383  
Db 361 ATCCATACATTAGGTTTCCAGACGCTGCAAGAAATAGATGCACCGCTCTGTGATAAG 420  
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Qy 464 GlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGluLysAlaHis 483  
Db 661 CAATGCANAGAACCAAGAACTCTCTATTGGTTTGTATATCAACAAGGAAAAAGCAT 720  
Qy 484 SerGlyGly 486  
Db 721 TCAGGAGGC 729  
RESULT 2  
AK020292  
LOCUS  
DEFINITION  
Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130404C19 product:matrix metalloproteinase 10, full insert sequence.  
AK020292.1 GI:12860834  
VERSION  
HTC; CAP trapper.  
KEYWORDS  
Mus musculus (house mouse)  
SOURCE  
Mus musculus  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1  
Carninci, P. and Hayashizaki, Y.  
REFERENCE  
TITLE  
High-efficiency full-length cDNA cloning  
JOURNAL  
Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE  
99279253  
PUBMED  
10349636  
2  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
REFERENCE  
TITLE  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL  
Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE  
20493374  
PUBMED  
11042159  
3  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujisawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
REFERENCE  
TITLE  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
JOURNAL  
Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE  
20530913  
PUBMED  
11076861  
4  
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium  
REFERENCE  
TITLE  
Functional annotation of a full-length mouse cDNA collection  
JOURNAL  
Nature 409, 685-690 (2001)  
PUBMED  
11076861  
5  
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
REFERENCE  
TITLE  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL  
Nature 420, 563-573 (2002)  
PUBMED  
12011735  
6 (bases 1 to 1735)  
7  
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuta, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hirakawa, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koyu, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, K., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,



Db	1122	AGTCAGTCTCGGCAGTCCGAGGAAATGAAGTCACGAGGCTACCCAAAGGGGATCCAC	1181
Qy	366	ThrLeuGlyPheProGlyArgValLysLysIleAspAlaValCysAspLysThr	385
Db	1182	ACTCTCGTTCCTCCACCGTGAAGAAGATTGATCAGCTGTTTGGAAAGGAGAAG	1241
Qy	386	ArgLysThrTyPhePheValGlyLeuTrpCysTrpArgPheAspGluMetThrGlnThr	405
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Qy	406	MetAspLysGlyPheProGlnArgValLysHisPheProGlyLysSerIleArgVal	425
Db	1302	ATGCATAAAGGCTCCCAAGACACATACAGATCATTTTCAGGAATTGAGCCACAAGTT	1361
Qy	426	AspAlaIlePheGlnTyLysGlyPhePhePhePheSerArgGlySerLysGlnPheGlu	445
Db	1362	GATGCTGTGTACACGAATTGGGTTTTTTTATTTCTCCGAGTATCATCAGTTTCGAG	1421
Qy	446	TyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsnThrTrpPheGlnCys	465
Db	1422	TTTGACCCCAATGCCAGGAGCGTGACACATACTGAAGAGCAACACTGGCTGCTGTC	1481
RESULT 3			
AK089234			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
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Db      88  CTGAAGACACTTCCATTACTGATCTTCTCCACACACAGCTTGCCAAATGCTTCCAGTA 147
Qy      21  ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
Db      148  CTGAACACCTGGAA--GAGAAATATATAAACTGCTGAGAAATTACCTACGAAATTC 204
Qy      41  TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60
Db      205  TACAACCTTA-----CCAAGCAATCAATTCGGTCTTCGAGGAATGCCACGATGTTGCA 258
Qy      61  AspLysIleArgGluMetGlnAlaPheGlyLeuThrValThrGlyLysLeuAspSer 80
Db      259  GAGAGCTCTAAAGATGAGCGCTCTCTACAGCTAGCAGAGACTGGGAAGTTAGATGCA 318
Qy      81  AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
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Qy      101  TyrThr-----LeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyr 118
Db      379  CTAACCCAGGGAAGTCCCAAGTGGACACACACTAACTGACCTACAGGATTATAAACCAT 438
Qy      119  ThrProAspMetAlaArgAlaValAlaAspGluAlaIleGlnGluGlyLeuGluValTrp 138
Db      439  AGCCGACAGCTCTCAAGGCTGAAGTGAACAGCAATGGAGAGCTTTTCACGCTCGG 498
Qy      139  SerLysValThrProLeuLysPheThrLysSerLysGlyIleAlaAspIleMetIle 158
Db      499  AGTGTAGCATGCCCTGACCTTCCAGGATCTTACAGGAGAACTACAGGAGAAAGCAGACATCAACATT 558
Qy      159  AlaPheArgThrArgValHisGly---ArgCysProArgTyrPheAspGlyProLeuGly 177
Db      559  GCTTTCGTCTCAAGACACCATGGTGCACATTTCTCCA-----TTTGATGGACCCCAATGGA 612
Qy      178  ValLeuGlyHisAlaPheProGlyProGlyLeuGlyGlyValPheAsnThrHisPheAspGlu 197
Db      613  ATCCCTTGCCATGCCCTTCAACAGCCCAAGGATTTGGAGAGAGTCTCATTTTGATTTCA 672
Qy      198  AspGluAsnTrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGlu 217
Db      673  GAAGAAACCTGGACTCAAGATTCCTCAAAATTTACAACTATTCTCGTGGCTGCTCATGAA 732
Qy      218  PheGlyHisAlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsn 237
Db      733  TTTGGACATCTTTGGGACTCTCTCACTCCACTGATCCTGGTGGCTTGTATGATACCCAAAC 792
Qy      238  TyrValSerLeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGln 257
Db      793  TATGCTTACAGGGAACCCAGCCTATTCACTACCTCAAGATGATATCAATGGCATTCAG 852
Qy      258  SerIleTyrGlyLeuProLysValProAlaLysProLysGluProThrIleProHis 277
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Qy      278  AlaCysAspProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhe 297
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Qy      298  PheLysGlyArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeu 317
Db      970  TTTAAAGACAAAGTACTTCTGGAGCGGCCTCTCAGCTGAGACAGTTGACCTCAATTTC 1029
Qy      318  IleAlaSerPheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsn---Pro 336
Db      1030  ATATCTCTGTCTGGCCCTCTTACCCACCGCTTTCAGGCTGCTTATGAAGATTTTGAC 1089
Qy      337  ArgAspLysIleLeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaVal 356
Db      1090  AGAGACCTAGTTTCTCTATTAAAGGACAGACTGCTGCTCAAGTGGCTATGACCTG 1149
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Db      1264  TGGAGATATGACATCAAAAGAGATCCATGACCCAGCTTACCCCAAAAGACATACCAAGC 1323
Qy      417  HisPheProGlyIleSerIleArgValAspAlaPheGlnTyrLysGlyPhePhePhe 436
Db      1324  ATGTTCCAGGAGTAAACTGTAGATCGATGCTGATGCTTTTCTCGCAGGACTCCTCTTCTCCTC 1383
Qy      437  PheSerArgGlySerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIle 456
Db      1384  TTCCTTCAGTGACCAACAATATTTTGCATTTTAATTTTGTTCAGTCACAGAGTCACTAGATT 1443
Qy      457  MetArgThrAsnThrTrpPheGlnCys 465
Db      1444  GCAGAGCAATTTATGCTTAACCTGT 1470

RESULT 4
LOCUS AK089516 2074 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F730044H20 product:matrix metalloproteinase 8, full insert sequence.
ACCESSION AK089516
VERSION AK089516.1 GI:26354565
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

```

REFERENCE  
AUTHORS

6 (bases 1 to 2074)  
 Adachi, J., Aizawa, K., Akimura, T., Atakawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, I., Hirozane, T.,  
 Hori, F., Imoani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, I.,  
 Sugabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A.,  
 Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission

TITLE  
JOURNAL

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp.  
 URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216)

## COMMENT

cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics  
 Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome  
 Trust/MRC building Addenbrookes Hospital Cambridge) whose  
 assistance we gratefully acknowledge.  
 Please visit our web site for further details.  
 URL: <http://genome.gsc.riken.jp/>  
 URL: <http://fantom.gsc.riken.jp/>.

## FEATURES

Location/Qualifiers  
 1..2074

source

/organism="Mus musculus"  
 /mol\_type="mRNA"  
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## ORIGIN

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US-10-729-807-10 (1-513) x AK089516 (1-2074)

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 41 TyrSerLeuGluLeuGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuLeuAsp 60  
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 61 AspLysLeuArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
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 81 AsnThrLeuGluLeuMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
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 369 CTAACCCCGAAGAGTCCCAAGTGGACACACACTAACCTGACTACAGGATTATAAACCAT 428  
 119 ThrProAspMetAlaArgAlaAlaValAspGluAlaLeuGlnGluGlyLeuGluValTyr 138  
 429 ACGCCACAGCTGTACAGGCTGAAGTGAACAGCAATGAGAAAGCTTTTTCACGCTCTGG 488  
 139 SerLysValThrProLeuLysPheThrLysLeuSerLysGlyLysLeuAlaAspLeuMet 158  
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 159 AlaPheArgThrArgValHisGly---ArgCysProArgTyrPheAspGlyProLeuGly 177  
 549 GCTTTCGCTCTCAAGAGACCATGCTGCAATTCCTCA-----TTTGATGGACCAATCGA 602  
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 603 ATCTTGTCCCATGCCCTTCAACAGCCCAAGGATTATGGAGAGATGCTCAATTTGATGCA 662  
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US-10-729-807-10 (1-513) x AK089381 (1-2426)

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Dd		149	TCTGAACACACCTGGAA--GAGAAAAATAAATACTGCTGGAATTAGCTACGAAAATTC	205
QY		41	TyrSerLeuGliulleGlieGluYlsHisLeuValGlnSerLysAsnArgSerLeuilleAsp	60
Dd		206	TACAACCTA-----CCAAGCAATCAATTCGGTCTTCGAGAATGCCAGATGTGCA	259
QY		61	AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer	80
Dd		260	GAGAAGCTTTAAAGAGATGACGCGTCTCTTCAGCTTAGCAGAGACTGGGAAGTTAGATGCA	319
QY		81	AsnThrLeuGliulleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100
Dd		320	GCTACATGGGATATGGAATGCTCGATGGAGTGCTGACTCTGGTGAATTTCTTG	379
QY		101	TyrThr-----LeuproGlyTyrArgLysTyrAsnLeuthrTyrAtgIlelleAsnTyr	118
Dd		380	CТААСССССАГАAGTCCCAGTGGACACACACTAACCTGACTACAGATTTATTAACCAT	439
QY		119	ThrProaspMetalArgAlaAlaValaspGluAlalleGlnGluGlyLeuGluValTrp	138
Dd		440	ACGCCACAGCTGTCAAGGGCTGAAGTTGAAAAACAGCAATTTGAGAAAGCTTTTTCACTCTGG	499
QY		139	SerLysValThrProLeuLysPheThryllysIleSerLysGlyIleAlaAspIleMettile	158
Dd		500	AGTGTAGCATGCCCCCTGACCTTCACCGAGATCTTACGAGGAGAGACAGACATCAACATT	559
QY		159	AlaPheArgThrArgValHisGly---ArgCysProArgTyrPheAspGlyProLeuGly	177
Dd		560	GCCTTCGTCTCAAGAGACCATTGGTGACAATTCCTCA-----TTTGATGGACCCCAATGGA	613
QY		178	ValLeuGlyHisAlaPheProGlyProGlyLeuGlyAspThrHisPheAspGlu	197
Dd		614	ATCCTTGCCCATGCTTTTCAAACAGGCCAAGGTATTGAGGAGAGATGCTCATTTTGATTCA	673
QY		198	AspGluAsnTrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGlu	217
Dd		674	GAGAAACGTGGACTCAAGATTCCAAAAATTACAACTATTTCGTGGGTGCTCATGAA	733
QY		218	PheGlyHisAlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsn	237
Dd		734	TTTGGACATCTTTGGGACTCTCTCACTCCACTGATCCTGGTGCTTGATGTACCCAAAC	793
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Dd		794	TATGCTTTACAGGAACCCACACACTATATCTACTCTCACATGATATCAATGGCATTCAG	853
QY		258	SerIleTyrGlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHis	277
Dd		854	ACAATCTATGGACCTTCAGACAAC---CCCATCCACCTACTGGGCCACGACACCCAAA	910
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Dd		911	GCCTGTGACCCCCACCTGAGATTTGATGCTACTACCACACTCCCTGGGGAGATTTACTTC	970
QY		298	PheLysGlyArgHisLeuTyrArgIleTyrTyrAspIleThrAspValGluPheGluLeu	317
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QY		337	ArgAspLysIleLeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaVal	356

Db	1091	AGAGACCTAGTTTTCTTAAAGGCAGACAGTACTGGGCTCTAAGTGCGCTATGACCTG	1150
Qy	357	LeuProAspTyrProLysSerIleHisThrLeuGlyPheProGlyArgValLysIle	376
Db	1151	CAGCAAGGTTACCCAGAGATATATCCAACTATGGATTCCCAAGGAGTGTCCAAGGCATT	1210
Qy	377	AspAlaAlaValCysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCys	396
Db	1211	GATGCAGCTGTT-----TCCATAACGGGAAGACATACTCTTCTATAAACACACCTAGTGC	1264
Qy	397	TrpArgPheAspGluMetThrGlnThrMetAspLysGlyPhePheProGlnArgValLys	416
Db	1265	TGGAGATATGACAAATCAAGAAGATCCATGAACCCAGGTTACCCAAAAGCATACCAAGC	1324
Qy	417	HisPheProGlyIleSerIleArgValAspAlaPheGlnTyrLysGlyPhePhePhe	436
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Qy	437	PheSerArgGlySerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIle	456
Db	1385	TTCTTCAGTGGACCAATAATTTTGCATTTAATTTTGTCAAGTCACAGAGTCATAGATT	1444
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SOURCE	Homo sapiens (human)
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REFERENCE	1 (bases 1 to 755)
AUTHORS	Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Panzig, J. and Ducar, M.
TITLE	Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL	Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE	21227151
PUBMED	11329013
COMMENT	Contact: Scott J. Cain

**Auerisys, Inc.**  
3201 Carnegie Ave., Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596

FEATURES  
source  
Location/Qualifiers  
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## ORIGIN

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## ORIGIN

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US-10-729-807-10 (1-513) x AK089336 (1-2427)	

US-10-729-807-10 (1-513) x AK089336 (1-2427)

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		91	CTG	AAG	ACAC	TCTCC	ATTA	CTGAT	CTCT	CCACAC	CAGCTT	GC	AAATG	CTTCC	CAGTA	150						
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		151	CCT	GAA	CACTG	GAA--	GAG	AAA	AAATATA	AAAA	CTGCT	GAGA	AAATAC	TCTAC	TAC	GAAA	ATTC	207				
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		208	TACA	ACTTA	-----	CCA	AGCA	ATCA	ATTCC	GGTCTTC	GAGGA	ATGCC	CAGATGG	TTGCA	261							
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		262	GAGA	AGCTTAA	GAGATG	CAAG	CGCTTCT	CAGCTT	AGCAG	AGACTG	GGA	AGTTAG	ATGCA	321								
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		562	TGCT	TTCTG	CTCAAG	ACCATGGT	GACA	ATTCTCA	-----	TTTGATG	GACCCAA	TGG	615									
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1 (bases 1 to 1784)				
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.				
Full-length cDNA libraries and normalization				
Unpublished				
Contact : Feng Liang Email : fliang@lifetech.com URL : <a href="http://fulllength.invitrogen.com/">http://fulllength.invitrogen.com/</a> Invitrogen Corporation 1600 Paraday Avenue				
2 (bases 1 to 1784)				
Genoscope.				
Direct Submission				
Submitted (20-JUL-2004)				
Genoscope - Centre National de Séquençage				



TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes  
MEDLINE Genome Res. 10 (10), 1617-1630 (2000)  
PubMed 20499374  
FBI 11042159

## AUTHORS

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwara, S., Inoue, K., Todawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
Yoneda, Y., Ishikawa, T., Orawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multipillar sequencer  
Genome Res. 10 (11), 1757-1771 (2000)

## JOURNAL

20530913

## MEDLINE

11076861

## FBI

## AUTHORS

4 The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.

## TITLE

Functional annotation of a full-length mouse cDNA collection

## JOURNAL

Nature 409, 685-690 (2001)

## REFERENCE

## AUTHORS

5 The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 1798)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
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Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, R., Ohno, M., Ohsato, N.,  
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A.,  
Muramatsu, M., and Hayashizaki, Y.

## TITLE

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,  
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

## COMMENT

cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics  
Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome  
Trust/MRC Building Addenbrookes Hospital Cambridge) whose  
assistance we gratefully acknowledge.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
Location/Qualifiers

## FEATURES

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## Qy

## Db

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## Db

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## Qy

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## Qy

## Db



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 Qy 335 AsnProArgAspLysIleLeuValPheLysAspGluAsnPheTyrMetIleArgGlyTyr 354  
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 DEFINITION Mus musculus 7 days embryo whole body cDNA, RIKEN full-length enriched library, clone:C430029P05 product:collagenase-like A, full insert sequence.  
 ACCESSION AK049552  
 VERSION 1 GI:26340287  
 KEYWORDS HTC; CAP trapper.  
 SOURCE Mus musculus (house mouse)  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1  
 AUTHORS Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE  
PUBMED  
REFERENCE

## AUTHORS

## TITLE

## JOURNAL

MEDLINE  
PUBMED  
REFERENCE

## AUTHORS

## TITLE

## JOURNAL

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## AUTHORS

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MEDLINE  
PUBMED  
REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

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2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374  
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3 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913  
 11076861

4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (Bases 1 to 2013)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurahara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saitoh, H., Saitoh, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://phantom.gsc.riken.jp/

Location/Qualifiers

1. .2013

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High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253  
10349636

2  
REFERENCE  
AUTHORS  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
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20499374  
11042159

3  
REFERENCE  
AUTHORS  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
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REFERENCE  
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The RIKEN Genome Exploration Research Group Phase II Team and the  
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Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

5  
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Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 1800)

JOURNAL  
REFERENCE  
AUTHORS  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
Hayaehida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
Okazaki, Y., Saigo, R., Saichou, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A.,  
Muramatsu, M. and Hayashizaki, Y.  
Direct Submission  
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,  
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

TITLE  
JOURNAL  
COMMENT  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
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FEATURES  
source



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LOCUS			
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ACCESSION			
VERSION			
KEYWORDS			







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LOCUS

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1452)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1452)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,P., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
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135 LeuGluValTrpSerLysValThrProLeuLysPheThrLysSerLysGlyValAla 154
436 TTGCAGCCCTGGAGTAGCGCGTCCCTCTGAGCTTTGTGAGATTAACCTCAGGAGACG 495
155 AspileMetIleAlaPheArgThrArgValHisGlyArgCysProArgTyr---PheAsp 173
496 GATATTATGATATCTTTTGAATAATGGAGATCACGGG-----GATTCCATCCATTCGAT 549
174 GlyProLeuGlyValLeuGlyHisAlaPheProGlyProGlyLeuGlyGlyAspThr 193
550 GGGCCCTCGGGGACTCTAGCCCATGCAATTTGCTCTGGAGAAGCCCTGGGAGAGATACA 609
194 HisPheAspGluAspGluAsnTrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuVal 213
610 CATTTCCACAATGCTGAGAGAGTGAGCTATGGGAACGAATGGTTTAAATTTGTTTACCGTT 669
214 AlaAlaHisGluPheGlyHisAlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeu 233
670 GCTGCTCATGAATTTGGCCATGCGCTGGCCCATTCACAGACCCATCAGCACTG 729
234 MetPheProAsnTrpValSerLeuAspProGlySerProGlySerGlnAspAspIle 253
730 ATGTACCACCACTTATAAGTACAAGATCCCTATGGATTCCACCTCCCAAGATGATGTG 789
254 AsnGlyIleGlnSerIleTyrGly-----GlyLeuProLysValPro 267
790 AAGGGATCAGGATTAACGACCTCGGAAGATATTCCTGGGGAAGCCACTCTGCC 849
268 AlalysPro---LysGluProThrIleProHisAlaCysAspProAspLeuThrPheAsp 286
850 CATGCCCCCATCACAAAGCCATCCATCCCTGACCTCTGTGACTCCAGCTCATCCTTGAC 909
287 AlaIleThrThrPheArgArgGluValMetPhePheLysGlyArgHisLeuTrpArgIle 306
910 GCTGTGACAATGCTGGGAGGAGCTCCTCTCTCAAGACCGGATTTCTGGAGACGG 969
307 TyrTyrAspIle---ThrAspValGluPheGluLeuIleAlaSerPheTrpProSerLeu 325
970 CAGTTTCACCTTCGGACAGGAATTCGGCCAGCACTATTACCAGTCTCTCCCCAGCTC 1029
326 ProAlaAspLeuGlnAlaAlaTyrGlu---AsnProArgAspLysIleLeuValPheLys 344
1030 ATGTCCAAATGTGGATGCAGCTTACGAAAGTGGCTGAGAGGGGCACTGCTTACTTCTCAA 1089
345 AspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyrProLysSerIle 364
1090 GGTCCCCACTACTGGATAACAAGAGGATTCCAA---ATGCAAGGTCTCTCTCGGACTATT 1146
365 HisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaValCysAspLysThr 384
1147 TATGACTTTGGATTTCCAGGCAGCTGCAGCAATAGATGCTGTCTACCTCAGGGAG 1206
385 ThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAspGluMetThrGln 404
1207 CCACAGAAGACCCCTTTCTTTGTGGGAGATCAATACTACAGTACGACGAAAGGAAAGG 1266
405 ThrMetAspLysGlyPheProGlnArgValValLysHisPheProGlyIleSerIleArg 424
1267 AAAATGGAAGAAAGACTATCCAAAGAAATACTGAAGAAGAAATTTTCAGGAGTAAATGGCCAA 1326
425 ValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGlySerLysGlnPhe 444
1327 ATCATGCTGCTGAGATTAATATGGCTACATTTACTTCTTTTCAGGACCAAAACATAC 1386
445 GluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsnThrTrpPheGln 464
1387 AAGTATGACACAGAGAGGAGATGTGGTTAGTGTGGTGAATCTAGTCTCTGGATTGGT 1446
465 Cys 465

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 13:11:00 ; Search time 1693 Seconds

(without alignments)  
35019.163 Million cell updates/sec

Title: US-10-729-807-28

Perfect score: 1627

Sequence: 1 gcttcagctgaagaagaga.....aattctgttcaaatagaa 1627

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hic: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gss1: \*  
9: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	726.2	44.6	731	5	BX102293	BX102293 BX102293
2	641.6	39.4	755	4	BG189775	BG189775 RST8821 A
3	482.2	29.6	746	1	AI436025	AI436025 th80g12.x
4	437.8	26.9	683	6	BY753385	BY753385 BY753385
5	409.4	25.2	411	1	AA424347	AA424347 zv90e12.r
6	392	24.1	1735	3	AK020292	AK020292 Mus muscu
7	386	23.7	2074	3	AK089516	AK089516 Mus muscu
8	386	23.7	2223	3	AK089234	AK089234 Mus muscu
9	385.8	23.6	561	5	EX918107	EX918107 BX918107
10	384.4	23.6	2426	3	AK089381	AK089381 Mus muscu
11	383	23.5	675	6	BY750280	BY750280 BY750280
12	381.6	23.5	1784	3	CR603756	CR603756 full-leng
13	375	23.0	2427	3	AK089336	AK089336 Mus muscu
14	369.2	22.7	382	1	AA424513	AA424513 zv90e12.s
15	360.8	22.2	1798	3	AK089309	AK089309 Mus muscu
16	357.6	22.0	1800	3	AK090051	AK090051 Mus muscu
17	356	21.9	1519	3	AK089523	AK089523 Mus muscu
18	356	21.9	1798	3	AK089452	AK089452 Mus muscu
19	353	21.7	894	5	EU120858	EU120858 603144842
20	349.2	21.5	1453	3	AK089509	AK089509 Mus muscu
21	343.8	21.1	2013	3	AK049552	AK049552 Mus muscu
22	320.6	19.7	1330	9	AY420747	AY420747 Homo sapi
23	316.6	19.5	632	5	BU402270	BU402270 604137994
24	314.2	19.3	1416	9	AY418899	AY418899 Homo sapi

25	309.2	19.0	454	1	AA716836	AA716836 vu62a11.r
26	309.2	19.0	1419	9	AY418901	AY418901 Mus muscu
27	304.2	18.7	869	5	BU281887	BU281887 603602842
28	302.8	18.6	593	4	BM440043	BM440043 Bgrln.pko
29	298.6	18.4	572	1	AI643892	AI643892 vu62a11.x
30	288	17.7	771	7	CN052608	CN052608 Salamande
31	282.2	17.3	854	7	CN066791	CN066791 H10_Ag2.p
32	279	17.1	1416	9	AY418900	AY418900 Pan trogl
33	278.6	17.1	716	5	BU200410	BU200410 604158850
34	277.8	17.1	926	6	CA487316	CA487316 AGENCOURT
35	275.4	16.9	1027	7	CN065546	CN065546 D09_Ag2.p
36	274.4	16.9	1449	9	AY420752	AY420752 Mus muscu
37	271.2	16.7	832	7	CN060762	CN060762 A04_Ag2.p
38	270.2	16.6	935	7	CO647474	CO647474 ILLUMIGEN
39	266.4	16.4	871	7	CN067389	CN067389 J10_Ag2.p
40	264.6	16.3	843	7	CN062082	CN062082 Ag2_p35.H
41	264.4	16.3	784	9	AY402829	AY402829 Pan trogl
42	263.8	16.2	895	6	CA489750	CA489750 AGENCOURT
43	263	16.2	360	6	BY779280	BY779280 BY779280
44	262.8	16.2	784	9	AY402828	AY402828 Homo sapi
45	262	16.1	295	1	AI273586	AI273586 ql60g12.x

## ALIGNMENTS

### RESULT 1

BX102293

LOCUS

DEFINITION

IMAGE:767086, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BX102293 Soares NHMPu\_S1 Homo sapiens cDNA clone IMAGE767086, mRNA sequence.  
IMAGE:767086, mRNA sequence.  
BX102293.1 GI:27845222  
EST.  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 731)  
Ebert, L., Heil, O., Hennig, S., Neubert, P., Partsch, E., Peters, M.,  
Radelof, J., Schneider, D. and Korn, B.  
Human UnigeneSet - RZPD3  
Unpublished (2003)  
Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; IMAGE9980231887.  
Human UnigeneSet - RZPD3 (RZPDLIB No.972)  
http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de  
This clone is available royalty-free from RZPD;  
contact RZPD (clone@rzpd.de) for further information. Seq primer:  
M13r, Primer sequence: TTTCACACAGGAACAGCTATGAC.

### FEATURES

source

1. 731  
Location/Qualifiers  
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/db\_xref="taxon:9606"  
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/tissue type="Pooled human melanocyte, fetal heart, and  
pregnant uterus"  
/lab host="DH10B"  
/clone\_lib="Soares NHMPu\_S1"  
/notes="Organ: mixed (see below); Vector: p773D-Pac  
(Pharmacia) with a modified polylinker; Site: 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three  
normalized libraries (melanocyte 2NBHM, pregnant uterus

NbHPU, and fetal heart NBH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."

## ORIGIN

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Query Match      44.6%; Score 726.2; DB 5; Length 731;
Best Local Similarity 99.6%; Pred. No. 4.1e-188;
Matches 728; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 753 AGAAATACCCACTTTCTCAGGATGATATCAATGAAATCCAGTCCATCTATGGAGGCTCG 812
DB 1 AGAAATACCCACTTTCTCAGGATGATATCAATGAAATCCAGTCCATCTATGGAGGCTCG 60

QY 813 CCTAAGTCTCTGCTTAAGCCAAAGAACCCACTATACCCCATGCTGTGACCCCTGACTTG 872
DB 61 CCTAAGGAACCTGCTAAGCCAAAGAACCCACTATACCCCATGCTGTGACCCCTGACTTG 120

QY 873 ACTTTTGACGCTATCACAACCTTTCGCGAGAGAAGTAATGTTCTTTAAAGGAGGACCTTA 932
DB 121 ACTTTTGACGCTATCACAACCTTTCGCGAGAGAAGTAATGTTCTTTAAAGGAGGACCTTA 180

QY 933 TGGAGGATCTATATGATATACCGGATGTTGAGTTGTAATTAATGTTCTTCTGGCCA 992
DB 181 TGGAGGATCTATATGATATACCGGATGTTGAGTTGTAATTAATGTTCTTCTGGCCA 240

QY 993 TCTCTGCCAGTGTCTGCAAGCTGCATACGAGAACCCAGAGATAAGATTCTGTTTTT 1052
DB 241 TCTCTGCCAGTGTCTGCAAGCTGCATACGAGAACCCAGAGATAAGATTCTGTTTTT 300

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DB 301 AAAGATGAACCTTCTGAGATACAGAGGATATGCTGTCTTCCAGATTTATCCCAATGCC 360

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DB 361 ATCCATACATTAGGTTTCCAGGACGCTGTGAAGAAATAGATGACGCGTCTGTGATAAG 420

QY 1173 ACCAAGAAACCTACTCTTTTGTGGCATTTTGTGCTGGAGTTTGTGAAATGACC 1232
DB 421 ACCAAGAAACCTACTCTTTTGTGGCATTTTGTGCTGGAGTTTGTGAAATGACC 480

QY 1233 CAACCATGCAAGGATTTCCCGCAGAGATGTTAAACACTTTCCTGGATCAGTATC 1292
DB 481 CAACCATGCAAGGATTTCCCGCAGAGATGTTAAACACTTTCCTGGATCAGTATC 540

QY 1293 CGTGTGATGCTGTTTCCAGTACAAAGGATTTCTTTTTCAGCGTGGATCAAGCAA 1352
DB 541 CGTGTGATGCTGTTTCCAGTACAAAGGATTTCTTTTTCAGCGTGGATCAAGCAA 600

QY 1353 TTGAAATACAACTTAAGACAAAGATTAATACCCGAATCATGAGAACTAATCTTGGTTT 1412
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QY 1413 CAATGCAAGAACCAAGAACTCTCTCATTTGGTTTGTATATCAACAGGAAAGACAT 1472
DB 661 CAATGCAAGAACCAAGAACTCTCTCATTTGGTTTGTATATCAACAGGAAAGACAT 720

QY 1473 TCAGGAGGCAT 1483
DB 721 TCAGGAGGCAT 731

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RESULT 2  
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 LOCUS  
 DEFINITION RSP8821 Athersys RAGE Library Homo sapiens cdna, mRNA sequence.  
 ACCSSION BG189775  
 VERSION BG189775.1 GI:13711462  
 KEYWORDS EST.

## SOURCE

## ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 755)

## REFERENCE

## AUTHORS

Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, J., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.

Creation of genome-wide protein expression libraries using random activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

Contact: Scott J. Cain

Athersys, Inc.

3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 361 9596

Email: scain@atersys.com

High quality sequence stop: 551.

Location/Qualifiers

1..755

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/cell\_line="HT1080"

/clone\_lib="Athersys RAGE Library"

/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

## ORIGIN

Query Match 39.4%; Score 641.6; DB 4; Length 755;

Best Local Similarity 94.2%; Pred. No. 7.8e-165;

Matches 710; Conservative 0; Mismatches 39; Indels 5; Gaps 4;

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QY 646 TCAACTTGTCTTCTGTGCTCTCATGAATTTGGTCATGCACTGGGGCTCTCTCACTCCA 705
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QY 706 ATGATCAAAACAGCCTTGATGTTCCAAATTAATGTTCTCCCTGGATCCCAAGAAATACCCAC 765
DB 67 ATGATCAAAACAGCCTTGATGTTCCAAATTAATGTTCTCCCTGGATCCCAAGAAATACCCAC 126

QY 766 TTTCTCAGGATGATATCAATGGATCCAGTCCATCATATGAGGTTCTGCTAAGTACTTG 825
DB 127 TTTCTCAGGATGATATCAATGGATCCAGTCCATCATATGAGGTTCTGCTAAGTACTTG 186

QY 826 CTAAGCCAAAGAACCCACTATACCCATGCTGTGACCCCTGACTTGACTTTTCACGCTA 885
DB 187 CTAAGCCAAAGAACCCACTATACCCATGCTGTGACCCCTGACTTGACTTTTCACGCTA 246

QY 886 TCACAACTTTCCGAGAGAGTAAGTCTTTTAAAGGACGACCTATGAGGATCTATT 945
DB 247 TCACAACTTTCCGAGAGAGTAAGTCTTTTAAAGGACGACCTATGAGGATCTATT 306

QY 946 ATGATATCAGGATGTTGAGTTTGAATTAATGTTCTTCCATCTGCGCATCTGCGCAGCTG 1005
DB 307 ATGATATCAGGATGTTGAGTTTGAATTAATGTTCTTCCATCTGCGCATCTGCGCAGCTG 366

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DB 367 ATCTGCAAGCTGCATACAGAAACCCAGAGATAAGATTCTGTGTTTTTAAAGATGAAACT 426

QY 1066 TCTGGATGATCAGAGGATATGCTGTCTTGGCAGATTAATCCCAATTCATTCATCATTAG 1125
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QY 1126 GTTTTCCAGGCGTGTGAAGAAAATAGATGCAGCGCTGTGTATAGACCAAGAAAA 1185
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QY 1246 AAGGATCCCGCAGAGAGTGTTAAACACATTTCTCTGGAATGATGCGTGTGGTGTGCTG 1305
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QY 1306 CTTTCCAGTACAAAGATCTCTCTTTTCCAGCGCTGATCAAGCAATTTGATACAAACA 1365
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Db 722 TTAACAGGAATTTTCCCGATCTTCATACC 755

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LOCUS
DEFINITION
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3' similar to SW:CG3_MOUSE P28862 STROMELYSIN-1 PRECURSOR ;, mRNA
sequence.
ACCESSION
AI436025
VERSION
AI436025.1 GI:4307295
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 746)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapb@emil.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1092 Std Error: 0.00
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High quality sequence stop: 448.
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Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NhMpu, and fetal heart NhH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

Query Match 29.6%; Score 482.2; DB 1; Length 746;
Best Local Similarity 96.0%; Pred. No. 5.5e-121;
Matches 504; Conservative 0; Mismatches 20; Indels 1; Gaps 1;

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(Pharmacia) with a modified polylinker; Site: 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NhMpu, and fetal heart NhH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

```

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QY 1104 CCCAATCCATCCATCATAGTTAGTTTCCAGGACGTGTGAAGAAAATAGATGCAGCGTC 1163
Db 743 CCCAATCCATCCATCATAGTTTCCAGGACGTGTGAAGAAAATAGATGCAGCGTC 684
QY 1164 TGTGATAAGACCAAGAAAAAACCCTACTCTTTGTGGGCATTTGGTGTCTGGAGTTTGTAT 1223
Db 683 TGTGATAGCCCCCAAGAAANACCCTACTCTTTGTGGGCATTTGGTGTCTGGAGTTTGTAT 624
QY 1224 GAAATGACCCAAACCATGGACAAA--GGATTCCCGCAGAGAGTGTTAAACACACTTCTCTGG 1282
Db 623 GAAATGACCCAAACCATGGACAAAAGGGGTTCCCGCAGAGAGTGTTAAACACACTTCTCTGG 564
QY 1283 AATCAGTATCCGTTGTGATGCTCTTTCCAGTACAAAGGATCTCTCTTTTTCAGCCGTGG 1342
Db 563 AATCAGTATCCGTTGTGATGCTCTTTCCAGTACAAAGGATCTCTCTTTTTCAGCCGTGG 504
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Db 503 ATCAAAGCAATTTGATACGACATTAAAGCAAGATATTTACCCGAATCATGAGAACTAA 444
QY 1403 TACTTGGTTTCAATGCAAGAACCAAGAACTCTCTCTTTTGTGATATCAACAGGA 1462
Db 443 TACTTGGTTTCAATGCAAGAACCAAGAACTCTCTCTTTTGTGATATCAACAGGA 384
QY 1463 AAAAGCACATTTCAGGAGGATTAAGATATTTGATATCAAGAGTTTAAAGCTTGTATTATTT 1522
Db 383 AAAAGCACATTTCAGGAGGATTAAGATATTTGATATCAAGAGTTTAAAGCTTGTATTATTT 324
QY 1523 TGGTATTTGTTCAATTTGCTGAAAAACACTTCTATTTATCAATAAATTCATAGACTAAAT 1582
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QY 1583 AAACCTCAACAGGCTTTTAAATATAAATTCGTTCAAAATAGAA 1627
Db 263 AAACCTCAACAGGCTTTTAAATATAAATTCGTTCAAAATAGAA 219

RESULT 4
BY53385
LOCUS
DEFINITION
BY53385 RIKEN full-length enriched, osteoclast-like cell Mus
musculus cDNA clone 1420007I11 5', mRNA sequence.
ACCESSION
BY53385
VERSION
BY53385.1 GI:27184783
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
1 (bases 1 to 683)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Oshio, N., Saito, R., Suzuki, H., Yamana, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
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Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
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Site 2: Eco RI; Equal amounts of plasmid DNA from three
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NBHPU, and fetal heart NBH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

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DB 361 ATCCATACATTAGTGTTCAGACCTGTCAGAAATAGTCGACCGCTC 411

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LOCUS Mus musculus adult male cecum cDNA, RIKEN full-length enriched
DEFINITION library, clone:9130404C19 product:matrix metalloproteinase 10, full-
insert sequence.
ACCESSION AKO20292.1 GI:12860834
VERSION HTG; CAP trapper.
KEYWORDS Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 Carninci,P. and Hayashizaki,Y.
AUTHORS Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes
MEDLINE Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 20499374
AUTHORS

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Location/Qualifiers

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3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
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Suni,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
MEDLINE 11076861
PUBMED
4 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
FUNCTIONAL annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1735)
Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
Hirakawa,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
Saito,H., Saito,K., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
Tajima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.jp,
URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.jp/) for further
details.
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues. First strand cDNA was primed with a primer
[5' GAGAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse transcriptase
and subsequently enriched for full-length by cap-trapper. cDNA went
through one round of normalization to Rot = 10.0 and subtraction to
Rot = 185.2. Second strand cDNA was prepared with the primer
adapter of sequence [5'
GAGAGAGAGATCTCGAGATTAATAATTAATCCCTCCCCCCCC 3']. cDNA was cleaved
with BamHI and XhoI. Vector: a modified pBluescript KS(+) after
bulk excision from Lambda FLC 1. Cloning sites, 5' end: SalI; 3'
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Location/Qualifiers

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ORIGIN

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LOCUS Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN
DEFINITION full-length enriched library, clone:F73004H20 product:matrix
metallopeptidase 8, full insert sequence.
ACCESSION AK089516
VERSION AK089516.1 GI:26354565
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

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TITLE	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
JOURNAL	Functional annotation of a full-length mouse cDNA collection		
REFERENCE	Nature 409, 685-690 (2001)		
AUTHORS	5		
TITLE	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
JOURNAL	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
REFERENCE	Nature 420, 563-573 (2002)		
AUTHORS	6 (bases 1 to 2074)		
TITLE	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.		
JOURNAL	Direct Submission		
REFERENCE	Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)		
AUTHORS	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.		
TITLE	Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.		
JOURNAL	Please visit our web site for further details.		
COMMENT	URL: http://genome.gsc.riken.jp/		
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QY      1348  AGCAATTTGAATACAAATTAAGACAAAGATATTACCCGATCATGAGTACTATATCTT 1407
Db      1390  AATATTGCAATTTAATTTGTCAGTCAAGTCACTAGAGTTCGAAGAGCAATTTAT 1449
QY      1408  GGTTCATG 1417
Db      1450  GGTAACTG 1459

RESULT 8
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LOCUS      2223 bp      mRNA      linear      HTC 03-APR-2004
DEFINITION Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630050H05 product:matrix metalloproteinase 8, full insert sequence.
ACCESSION AK089234.1 GI:26354353
VERSION    AK089234.1
KEYWORDS   HTC; CAP trapper.
SOURCE     Mus musculus (house mouse)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1
  Carninci,P. and Hayashizaki,Y.
  High-efficiency full-length cDNA cloning
  Meth. Enzymol. 303, 19-44 (1999)
  99279253
  10349636
2
  Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
  Genome Res. 10 (10), 1617-1630 (2000)
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  11042159
3
  Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,I., Harada,A., Yamamoto,K., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.
  RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipillar sequencer
  Genome Res. 10 (11), 1757-1771 (2000)

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MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
CDS

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4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6
(bases 1 to 2223)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoaka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,K., Ohno,M., Ohsato,N., Okazaki,Y., Saito,D., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC Building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
1. 2223
  /organism="Mus musculus"
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```



## ORIGIN

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DB	332	TTATGGAATATGCTCGATGTGGATGCCCTGACCTCTGGTGATTTCTTGCTTAAACCCAGGA	391	
QY	333	--CCTGGGTGGAAAAATACAACCTCACCTACAGAAATAATAACATATATCCTGGATATGG	390	
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QY	391	CACGAGCTGCTGGATGAGGCTATCCAAGAGTTTGAAGTGTGGAGCAAAAGTCACTC	450	
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QY	511	GAGTCATGGTGGTCTCGCTATTTTATGGTCCCTTGGAGTGTCTTGGCCATGTCCT	570	
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QY	631	AGGATGGAGCAGGATTCACCTGTTTCTTGTGGCTGCTCATGAATTTGGTTCATGCATGG	690	
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DEFINITION BX918107 Sus Scrofa library (scan) Sus scrofa cDNA clone scan0036d.c.23 5prim, mRNA sequence.  
ACCESSION BX918107  
VERSION BX918107.1 GI:41134926  
KEYWORDS EST.  
SOURCE Sus scrofa (pig)  
ORGANISM Sus scrofa  
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REFERENCE 1 (bases 1 to 561)  
AUTHORS Bonnet,A., Tosser-Klopp,G., Benne,F., Cabau,C., Villegier,S., Soares,M., Donald,F. and Hathey,F.  
TITLE A Pig Normalised Multi-Tissue cdna Library  
JOURNAL Unpublished (2003)  
COMMENT Contact: Tosser-Klopp G  
Genetique Animale  
Institut National de la Recherche Agronomique  
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan cedex, FRANCE  
Tel: 33 (0) 5.61.28.51.14  
Fax: 33 (0) 5.61.28.53.08  
Email: tosser@toulouse.inra.fr  
Sequence cleaned of vector, adaptor and repetitions. Contact us at sigenassupport@jouy.inra.fr to obtain the chromatogram of this sequence.

FEATURES	source
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## ORIGIN

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of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 22354683  
 MEDLINE  
 PUBMED  
 COMMENT

Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,  
 Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,  
 Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,  
 Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,  
 Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,  
 Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,  
 Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission

Computational Analysis of Full-length Mouse cDNAs Compared with  
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics  
 Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome  
 Trust/MRC Building Addenbrookes Hospital Cambridge) whose  
 assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp/>) for  
 further details.

## FEATURES

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## ORIGIN

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 ACCESSION  
 CR603756  
 VERSION  
 CR603756.1 GI:50484563  
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 HTC; CNSLT\_cDNA.  
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 REFERENCE  
 1 (bases 1 to 1784)  
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished  
 JOURNAL  
 JOURNAL  
 REMARK  
 Contact: Feng Liang Email: [fliang@lifetech.com](mailto:fliang@lifetech.com) URL :  
<http://fulllength.invitrogen.com/> Invitrogen Corporation 1600  
 Faraday Avenue  
 Genoscope.  
 REFERENCE  
 2 (bases 1 to 1784)  
 Direct Submission  
 Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : [secref@genoscope.cns.fr](mailto:secref@genoscope.cns.fr))  
 - Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
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 QY 103 AAGAAATATGCAACTGGCTCAGGCATATCTCAACAGTTCTACTCTCTTGAATAGAG 162  
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RESULT 13  
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LOCUS Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN  
DEFINITION full-length enriched library, clone:F73008D09 product:matrix  
metallopeptidase 8, full insert sequence.  
ACCESSION AK089336  
VERSION AK089336.1 GI:26105213  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253  
10349636

2  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20493374  
11042159

3  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

4  
The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

5  
The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 2427)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
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Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tgami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

# TITLE

## JOURNAL

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

## COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/.

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sequence.
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REFERENCE 1 (bases 1 to 382)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
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WashU-Merck EST Project 1997
Unpublished (1997)
CONTACT: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNLML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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NhMPu, and fetal heart NhH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
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(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NhMPu, and fetal heart NhH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Katsunai,T., Tashiro,H., Itoh,M.,
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Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
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JOURNAL Nature 420, 563-573 (2002)
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AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
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```

Muramatsu, M. and Hayashizaki, Y.

Submitted (16-Apr-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Chemical Research, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/.

## FEATURES

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

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- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB Length	ID	Description
1	2763	100.0	513	3	AA90293	Human pep
2	2763	100.0	513	5	AAE14392	Aae14392 Human mat
3	2752	99.6	513	4	AAU12267	Aau12267 Human PRO
4	2752	99.6	513	4	AAU00469	Aau00469 Human TAN
5	2752	99.6	513	6	ABO17711	Abol7711 Novel hum
6	2752	99.6	513	6	ABU80965	Abu80965 Human PRO
7	2752	99.6	513	6	ABU66665	Abu66665 Human PRO
8	2752	99.6	513	6	ABO32578	Abos32578 Secreted
9	2752	99.6	513	6	ABU59746	Abus59746 Novel sec
10	2752	99.6	513	6	ABO24936	Abos24936 Human sec
11	2752	99.6	513	6	ABU66941	Abu66941 Human sec
12	2752	99.6	513	6	ADA45711	Ada45711 Novel hum
13	2752	99.6	513	6	ADA76142	Ada76142 Human PRO
14	2752	99.6	513	6	ADA18792	Ada18792 Human PRO
15	2752	99.6	513	6	ADA61415	Ada61415 Homo sapi
16	2752	99.6	513	6	ADB19200	Adb19200 Novel hum
17	2752	99.6	513	6	ADB27741	Adb27741 Human PRO
18	2752	99.6	513	6	ADA86220	Ada86220 Novel hum
19	2752	99.6	513	6	ADA86220	Ada86220 Novel hum
20	2752	99.6	513	6	ADA47570	Ada47570 Human PRO
21	2752	99.6	513	6	ADA67365	Ada67365 Human PRO
22	2752	99.6	513	6	ADB30372	Adb30372 Human PRO
23	2752	99.6	513	6	ADA85668	Ada85668 Novel hum
24	2752	99.6	513	6	ADA96880	Ada96880 Human PRO
25	2752	99.6	513	6	ADA79184	Ada79184 Human PRO

## ALIGNMENTS

## RESULT 1

AA90293  
ID AAY90293 standard; protein; 513 AA.

XX AC AAY90293;

XX DT 24-OCT-2000 (first entry)

XX DE Human peptidase, HPEP-10 protein sequence.

XX KW Human; peptidase; cell proliferative disorder; arteriosclerosis;  
KW psoriasis; myelofibrosis; cancer; autoimmune disorder; Crohn's disease;  
KW inflammatory disorder; AIDS; anaemia; allergy; asthma; atherosclerosis;  
KW Grave's disease; multiple sclerosis; scleroderma; infection; diabetes;  
KW metabolic disorder; Addison's disease; cystic fibrosis; diagnosis;  
KW glycogen storage disease; obesity; therapy; HPEP-10.

XX OS Homo sapiens.

XX PN WO200042201-A2.

XX PD 20-JUL-2000.

XX PF 11-JAN-2000; 2000WO-US000641.

XX PR 11-JAN-1999; 99US-0172247P.

XX PR 03-MAY-1999; 99US-0132253P.

XX PR 27-MAY-1999; 99US-0136653P.

XX PA (INCY-) INCYTE PHARM INC.

XX PI Bandman O, Hillman JL, Tang YT, Azimzai Y, Baughn MR, Lal P;

XX PI Yue H, Lu DAM;

XX DR WPI; 2000-482832/42.

XX DR N-PSDB; AAA37666.

XX PT An isolated polypeptide for diagnosis, prevention and treatment of cell  
XX proliferative, autoimmune/ inflammatory and metabolic disorders comprises  
XX a sequence encoding a human peptidase.

XX PS Claim 2; Page 100-101; 131pp; English.

XX CC This sequence represents a human peptidase, designated HPEP-10. The  
XX invention relates to 18 human peptidases designated HPEP-1 to HPEP-18,  
XX respectively. The peptidases can be used for treating a disease or  
XX condition associated with decreased expression or over expression of  
XX functional human peptidases. The diseases that can be diagnosed,

26	2752	99.6	513	6	ADA87323	Novel hum
27	2752	99.6	513	6	ADB16525	Human PRO
28	2752	99.6	513	6	ADA91617	Novel hum
29	2752	99.6	513	6	ADB14680	Human PRO
30	2752	99.6	513	6	ADB18641	Novel hum
31	2752	99.6	513	6	ADA93856	Human PRO
32	2752	99.6	513	6	ADB19752	Novel hum
33	2752	99.6	513	6	ADB13064	Human PRO
34	2752	99.6	513	6	ABO43244	Novel hum
35	2752	99.6	513	6	ADA74318	Human PRO
36	2752	99.6	513	6	ADB24551	Human PRO
37	2752	99.6	513	6	ADA82075	Human PRO
38	2752	99.6	513	6	ADA75038	Human PRO
39	2752	99.6	513	6	ADA85116	Novel hum
40	2752	99.6	513	6	ADA84564	Human PRO
41	2752	99.6	513	6	ADB29820	Human PRO
42	2752	99.6	513	6	ADA80348	Human PRO
43	2752	99.6	513	6	ADA75590	Human PRO
44	2752	99.6	513	6	ADA66815	Human PRO
45	2752	99.6	513	6	ADB25111	Human PRO

CC prevented and treated include cell proliferative disorders (such as  
CC arteriosclerosis, psoriasis, myelofibrosis, and cancers),  
CC autoimmune/inflammatory disorders (such as AIDS, anaemia, allergies,  
CC Crohn's disease, asthma, atherosclerosis, Grave's disease, multiple  
CC sclerosis, and scleroderma), infections, and metabolic disorders (such as  
CC Addison's disease, diabetes, cystic fibrosis, glycogen storage diseases  
CC and obesity)  
XX  
XX Sequence 513 AA;

Query Match 100.0%; Score 2763; DB 3; Length 513;  
Best Local Similarity 100.0%; Pred. No. 3.4e-262;  
Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRLLLCCLFFITSSAPPLVRMTENENMOLAQYLNQFYSLEIEGHLVQSKRSLID 60  
DB 1 MKRLLLCCLFFITSSAPPLVRMTENENMOLAQYLNQFYSLEIEGHLVQSKRSLID 60  
QY 61 DKIREMQAFFGLTVTGKLDNTLEIMKTPRCGVPDVGQYGLPGWRKYNLTIRIINYP 120  
DB 61 DKIREMQAFFGLTVTGKLDNTLEIMKTPRCGVPDVGQYGLPGWRKYNLTIRIINYP 120  
QY 121 DMARAANDVDEAIOEGLEWWSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180  
DB 121 DMARAANDVDEAIOEGLEWWSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180  
QY 181 HAPPPGGLGGTHFDEENWTKGAGNLFVAAHFGHALGSHSNDQALMFPNYS 240  
DB 181 HAPPPGGLGGTHFDEENWTKGAGNLFVAAHFGHALGSHSNDQALMFPNYS 240  
QY 241 LDPRKYPUSODDINGIQSYGGLPKVPAPKPEPTIPHACDPLTDFAITTFRREVMFFKG 300  
DB 241 LDPRKYPUSODDINGIQSYGGLPKVPAPKPEPTIPHACDPLTDFAITTFRREVMFFKG 300  
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360  
DB 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360  
QY 361 PKSIHTLGFPGRVKKIDAACVCKTRKTYFFVGIWCRFDEMTQMDKGFQORVVKHFFG 420  
DB 361 PKSIHTLGFPGRVKKIDAACVCKTRKTYFFVGIWCRFDEMTQMDKGFQORVVKHFFG 420  
QY 421 ISIRVDAAFQYKGFYFFSRSQKFEVNIKTNTIMRTNTWFOCKEPKNSSFGDINKE 480  
DB 421 ISIRVDAAFQYKGFYFFSRSQKFEVNIKTNTIMRTNTWFOCKEPKNSSFGDINKE 480  
QY 481 KAHSGGKILYHKLSLFTFGIVHLLKNTSIYQ 513  
DB 481 KAHSGGKILYHKLSLFTFGIVHLLKNTSIYQ 513

RESULT 2  
ID AAE14392  
XX AAE14392 standard; protein; 513 AA.  
XX AAE14392;  
XX 16-OCT-2002 (first entry)  
XX Human matrix metalloproteinase MMP1.  
XX Matrix metalloproteinase; MMP; extracellular matrix; ECM;  
XX embryonic development; morphogenesis; reproduction; tissue repair;  
XX mental disorder; Alzheimer's disease; multiple sclerosis; obesity;  
XX Parkinson's disease; motoneuron disease; metabolic disease; retinopathy;  
XX type 2 diabetes; cardiovascular; dyslipidaemia; adipogenesis; neuropathy;  
XX nephropathy; proliferative disease; cancer; psoriasis;  
XX prostate hyperplasia; hormonal disorder; alopecia; Crohn's disease;  
XX central nervous system disorder; CNS; inflammatory condition; arthritis;  
XX periodontal disease; wound healing; human; MMP1.  
OS Homo sapiens.

PN WO200190326-A2.  
XX 29-NOV-2001.  
XX 22-MAY-2001; 2001WO-US016563.  
XX 22-MAY-2000; 2000US-0206119P.  
XX (PHAA ) PHARMACIA & UPJOHN CO.  
XX Holmgren E, Kihlen M, Wood T, Ekblom J;  
XX WPI; 2002-083105/11.  
XX N-PSDB; AAD23963.  
XX New matrix metalloproteinases (MMP) genes and polypeptides, useful for  
XX treating diseases or for screening modulators of MMP to treat such  
XX diseases, e.g. mental disorders, Parkinson's disease, cancers or  
XX inflammatory conditions.  
XX Claim 31; Page 59; 94pp; English.

CC The invention relates to genes encoding matrix metalloproteinases (MMP).  
CC The MMP genes are useful for producing MMP polypeptides and for screening  
CC modulators of MMP. The MMPs are useful for breaking down extracellular  
CC matrix (ECM), which is essential for processes including embryonic  
CC development, morphogenesis, reproduction, or tissue repair and  
CC remodelling. The MMPs are particularly useful for identifying compounds  
CC that modulate the activity of genes to treat pathologies, e.g. mental  
CC disorders, Alzheimer's disease, multiple sclerosis, Parkinson's disease  
CC or motoneuron disease. The MMP polypeptides and genes, as well as their  
CC modulators, are useful for treating metabolic diseases and disorders  
CC (e.g. type 2 diabetes, obesity, cardiovascular, dyslipidaemias,  
CC adipogenesis, retinopathies, neuropathies or nephropathies).  
CC proliferative diseases and cancers (e.g. breast, colon or lung cancer,  
CC tumour growth, tumour invasion, psoriasis or prostate hyperplasia),  
CC hormonal disorders (e.g. male/female hormonal replacement, polycystic  
CC ovarian syndrome or alopecia), central nervous system (CNS) disorders,  
CC inflammatory conditions (e.g. Crohn's disease or arthritis), periodontal  
CC diseases or wound healing. The present sequence is human matrix  
CC metalloproteinase MMP1

XX Sequence 513 AA;

Query Match 100.0%; Score 2763; DB 5; Length 513;  
Best Local Similarity 100.0%; Pred. No. 3.4e-262;  
Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRLLLCCLFFITSSAPPLVRMTENENMOLAQYLNQFYSLEIEGHLVQSKRSLID 60  
DB 1 MKRLLLCCLFFITSSAPPLVRMTENENMOLAQYLNQFYSLEIEGHLVQSKRSLID 60  
QY 61 DKIREMQAFFGLTVTGKLDNTLEIMKTPRCGVPDVGQYGLPGWRKYNLTIRIINYP 120  
DB 61 DKIREMQAFFGLTVTGKLDNTLEIMKTPRCGVPDVGQYGLPGWRKYNLTIRIINYP 120  
QY 121 DMARAANDVDEAIOEGLEWWSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180  
DB 121 DMARAANDVDEAIOEGLEWWSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180  
QY 181 HAPPPGGLGGTHFDEENWTKGAGNLFVAAHFGHALGSHSNDQALMFPNYS 240  
DB 181 HAPPPGGLGGTHFDEENWTKGAGNLFVAAHFGHALGSHSNDQALMFPNYS 240  
QY 241 LDPRKYPUSODDINGIQSYGGLPKVPAPKPEPTIPHACDPLTDFAITTFRREVMFFKG 300  
DB 241 LDPRKYPUSODDINGIQSYGGLPKVPAPKPEPTIPHACDPLTDFAITTFRREVMFFKG 300  
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360  
DB 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360  
QY 361 PKSIHTLGFPGRVKKIDAACVCKTRKTYFFVGIWCRFDEMTQMDKGFQORVVKHFFG 420



Db 361 PKSIHTLGFPRVKIDAAVCDKTRKTYFVGIWCRWFDEMOTMDKGFQVRVXHPG 420  
QY 421 ISIRVDAAFQYKGFPSRSGKOFENYKTKNITRIMRTNTWFOCKEPKNSSGFDINKE 480  
Db 421 ISIRVDAAFQYKGFPSRSGKOFENYKTKNITRIMRTNTWFOCKEPKNSSGFDINKE 480  
QY 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513  
Db 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513  
RESULT 3  
AAU12267  
ID AAU12267 standard; protein; 513 AA.  
XX  
AC AAU12267;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE Human PRO5992 polypeptide sequence.  
XX  
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;  
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;  
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;  
KW A-peptide; factor VIIA; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO200140466-A2.  
XX  
PD 07-JUN-2001.  
XX  
PF 01-DEC-2000; 2000WO-US032678.  
XX  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 09-DEC-1999; 99US-0170262P.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 03-MAR-2000; 2000US-0187202P.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 05-JUN-2000; 2000US-0209832P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.  
XX (GETH ) GENENTECH INC.  
PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX WPI; 2001-408281/43.  
DR N-PSDB; AAS21339.  
XX  
XX Isolated , secretory and transmembrane PRO polypeptide used to detect  
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO  
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,  
PT breast, prostate, cervical.  
XX  
XX Claim 12; Fig 192; 813pp; English.  
PS  
XX AAU12172-AAU12446 represent novel human secretory and transmembrane PRO  
CC polypeptides. The PRO polypeptides are useful to detect other PRO  
CC polypeptides, to link bioactive molecules to cells expressing PRO  
CC polypeptides, to modulate biological activities of cells expressing PRO  
CC polypeptides, and to detect the presence of mammalian lung, colon,  
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
CC polypeptide expression in a cell sample to that in a control sample. Some  
CC of the 275 sequences are also useful to stimulate the release of tumour  
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or  
CC differentiation of chondrocytes, the proliferation or gene expression in  
CC pericyte cells, the release of proteoglycans from cartilage, the  
CC proliferation of inner ear utricular supporting cells or of T-  
CC lymphocytes, the release of a cytokine from peripheral blood monocytes  
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO  
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal  
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor  
CC VIIA. The PRO polypeptides can be used in assays to identify molecules  
CC involved in binding interactions. The polynucleotides encoding PRO  
CC polypeptides can be used to generate probes, antisense RNA/DNA,  
CC transgenic or knock out animals and can be used in gene therapy  
XX  
SQ Sequence 513 AA;  
Query Match 99.6%; Score 2752; DB 4; Length 513;  
Best Local Similarity 99.8%; Pred. No. 4.1e-261;  
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MKRLLLLLFFITFSSAPFLVRMTENENNNQAAQAYLNQFYSLEIEGHNHVSQKNSRLID 60  
Db 1 MKRLLLLLFFITFSSAPFLVRMTENENNNQAAQAYLNQFYSLEIEGHNHVSQKNSRLID 60  
QY 61 DKIREMQAFGLTVTKLDSNTLEIMTKPRCGVPDVGQGYTLPGWRKYNLYRIINYP 120  
Db 61 DKIREMQAFGLTVTKLDSNTLEIMTKPRCGVPDVGQGYTLPGWRKYNLYRIINYP 120  
QY 121 DMARAAVDEAIQEGLEVWSKVTPFKFTKISKGIADIAMIATRVRVHRCRPRYDGLGVLG 180  
Db 121 DMARAAVDEAIQEGLEVWSKVTPFKFTKISKGIADIAMIATRVRVHRCRPRYDGLGVLG 180  
QY 181 HAPPPGPGIGGDTHFDEDEENWTKDAGFNLFLVAAHEFGHALGSLHSDQATALMFPNYS 240  
Db 181 HAPPPGPGIGGDTHFDEDEENWTKDAGFNLFLVAAHEFGHALGSLHSDQATALMFPNYS 240  
QY 241 LDPRKYPVLSQDDINGIQSIYGGLPKVPAPKEPTIPHACDPDLTDAITTFREVMFPKG 300  
Db 241 LDPRKYPVLSQDDINGIQSIYGGLPKVPAPKEPTIPHACDPDLTDAITTFREVMFPKG 300  
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFMWIRGIVLDPY 360  
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFMWIRGIVLDPY 360  
QY 361 PKSIHTLGFPRGVKKIDAAVCDKTRKTYFFVGIWCRWFDEMTQTMKGFQVRVXHPG 420  
Db 361 PKSIHTLGFPRGVKKIDAAVCDKTRKTYFFVGIWCRWFDEMTQTMKGFQVRVXHPG 420

QY 421 ISIRVDAAFQYKGFPPSRGSKQFEYNKTKNITRIMRTNTWFOCKEPKNSFGFDINKE 480  
 DB 421 ISIRVDAAFQYKGFPPSRGSKQFEYNKTKNITRIMRTNTWFOCKEPKNSFGFDINKE 480  
 QY 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513  
 DB 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513

RESULT 4  
 AAU00469  
 ID AAU00469 standard; protein; 513 AA.  
 XX  
 AC AAU00469;  
 XX  
 DT 04-JUL-2001 (first entry)  
 XX  
 DE Human TANGO 210 protein.  
 XX  
 KW Human; TANGO 210; clone jthke034a06; TANGO 364; TANGO 366; INTERCEPT 394;  
 KW INTERCEPT 400; TANGO 405; cellular process regulator; gene therapy;  
 KW MMP-8; matrix metalloproteinase-8; proteinase activity;  
 KW extracellular matrix; kidney disorder; bone marrow disorder;  
 KW skin disorder; vascular hypertension; metastatic cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..17  
 FT /label= Signal peptide  
 FT /note= "Specifically claimed"  
 FT Protein 18..513  
 FT /label= Mature TANGO\_210 protein  
 FT /note= "Specifically claimed"  
 FT Domain 18..488  
 FT /note= "Optionally in alternative form #1 this domain is  
 FT extracellular or in alternative form #2 this domain is  
 FT intracellular. Specifically claimed"  
 FT Domain 489..506  
 FT /label= Transmembrane domain  
 FT /note= "Specifically claimed"  
 FT Domain 507..513  
 FT /note= "Optionally in alternative form #1 this domain is  
 FT intracellular or in alternative form #2 this domain is  
 FT extracellular. Specifically claimed"  
 XX  
 FN WO200118016-A1.  
 XX  
 PD 15-MAR-2001.  
 XX  
 PF 30-JUN-2000; 2000WO-US018174.  
 XX  
 PR 10-SEP-1999; 99US-00393996.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Fraser CC, Sharp JD, Wrighton N, Myers PS, Goodearl ADJ;  
 XX  
 DR WPI; 2001-183280/18.  
 DR N-PSDB; AAS01367.  
 XX  
 PT Isolated nucleic acid molecules encoding proteins useful as modulating  
 PT agents in regulating a variety of cellular processes are used for  
 PT treating e.g. cancer and autoimmune disorders.  
 XX  
 PS Claim 9; Fig 1A-ID; 326pp; English.  
 XX  
 CC The present sequence representing human TANGO 210 protein is isolated  
 CC from cDNA clone jthke034a06 from a human foetal skin cDNA library. It is  
 CC 1 of 6 novel human proteins which include TANGO 364 (AAU00471), TANGO 366  
 CC (AAU00472), INTERCEPT 394 (AAU00473), INTERCEPT 400 (AAU00476), and TANGO  
 CC 405 (AAU00479). Novel sequences for murine TANGO 210 (AAU00470),  
 CC INTERCEPT 400 (AAU00477), TANGO 405 (AAU00480) and a rat INTERCEPT 400

CC (AAU00478) sequence are also described. The nucleic acids encoding these  
 CC novel proteins are useful as modulating agents in regulating a variety of  
 CC cellular processes and can be used to express the proteins in a host cell  
 CC in gene therapy applications. Human TANGO 210 shows sequence homology to  
 CC human MMP-8 (matrix metalloproteinase-8). TANGO 210 exhibits proteinase  
 CC activity used to degrade one or more proteinaceous components of the  
 CC extracellular matrix and can be used to regulate, diagnose or treat  
 CC kidney, bone marrow or skin disorders e.g. vascular hypertension, acute  
 CC renal failure and metastatic cancers. Note: This sequence has residues  
 CC 309-513 missing in the sequence ID listing but the complete sequence is  
 CC found in Fig1A-ID  
 XX  
 XX Sequence 513 AA;

Query Match 99.6%; Score 2752; DB 4; Length 513;  
 Best Local Similarity 99.8%; Pred. No. 4.le-261;  
 Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLCLFFITPSSAPPLVRMTENEENMQLAQAYLNQFYSLIEGHNHLVQSKNRSLLID 60  
 DB 1 MKRLLLCLFFITPSSAPPLVRMTENEENMQLAQAYLNQFYSLIEGHNHLVQSKNRSLLID 60  
 QY 61 DKIREMAFFGLTVTGKLDNTLEIMKTPRCGVPDVQGYGTYLPGWKYNYLTYRIINYP 120  
 DB 61 DKIREMAFFGLTVTGKLDNTLEIMKTPRCGVPDVQGYGTYLPGWKYNYLTYRIINYP 120  
 QY 121 DMARAADVEAIOEGLEVSKVTPKFTKISKGIADIMIAFTRVHGRCPRYDFDGLGVIG 180  
 DB 121 DMARAADVEAIOEGLEVSKVTPKFTKISKGIADIMIAFTRVHGRCPRYDFDGLGVIG 180  
 QY 181 HAFPPGGLGGDTHFDEDEENWTKDAGFNLFVAAHEFGHALGSHSDQTALMFPNYS 240  
 DB 181 HAFPPGGLGGDTHFDEDEENWTKDAGFNLFVAAHEFGHALGSHSDQTALMFPNYS 240  
 QY 241 LDPKPYLSQDDINGIOSIYGLPKVPAKPEPTIPACDDPLDFDAITTFRRVMPFKG 300  
 DB 241 LDPKPYLSQDDINGIOSIYGLPKVPAKPEPTIPACDDPLDFDAITTFRRVMPFKG 300  
 QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAVENPRDKILVFXDENFWMIIRGVAVLDPY 360  
 DB 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAVENPRDKILVFXDENFWMIIRGVAVLDPY 360  
 QY 361 PKSHTLGLFPGRVKKIDAAVCDTKTRKTYFFVGVICWRFDEMTQTMDFKFFQVRVKKHPPG 420  
 DB 361 PKSHTLGLFPGRVKKIDAAVCDTKTRKTYFFVGVICWRFDEMTQTMDFKFFQVRVKKHPPG 420  
 QY 421 ISIRVDAAFQYKGFPPSRGSKQFEYNKTKNITRIMRTNTWFOCKEPKNSFGFDINKE 480  
 DB 421 ISIRVDAAFQYKGFPPSRGSKQFEYNKTKNITRIMRTNTWFOCKEPKNSFGFDINKE 480  
 QY 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513  
 DB 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513

## RESULT 5

ABO17711  
 ID ABO17711 standard; protein; 513 AA.  
 XX  
 AC ABO17711;  
 XX  
 DT 26-AUG-2003 (first entry)  
 XX  
 DE Novel human secreted and transmembrane protein PRO5992.

XX Human; secreted and transmembrane protein; PRO; antiinflammatory;  
 KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;  
 KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;  
 KW TNF-alpha release; cell proliferation; cell differentiation;  
 KW gene expression modulator; proteoglycan release; cytokine release;  
 KW tumour; inflammatory disease; organ failure; atherosclerosis;  
 KW cardiac injury; infertility; birth defect; premature aging; AIDS;  
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;



CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.  
CC This is the amino acid sequence of a novel human secreted and  
CC transmembrane PRO polypeptide  
XX  
SQ Sequence 513 AA;

Query Match 99.6%; Score 2752; DB 6; Length 513;  
Best Local Similarity 99.8%; Pred. No. 4.1e-261;  
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MKRLLLCLEFITTSSAPFLVRMTENENMQLAQAYLNQFYSLEIEGHNHLVQSKNRSLLID 60  
Db |||||  
QY 61 DKIREMAFGLTVGKLDNTLEIMKTPRGVPDVGQGYTLPGWRKYNLTYYRIINYP 120  
Db |||||  
QY 121 DMARAAVDEAIOEGLEWVSKVTPPLKFTKISGDIADIMAFRTRVHGRCPRYFDGPLGVIG 180  
Db |||||  
QY 181 HAPPPGCLGDTDFEDENWTKDAGFNFLVAHFEFGHALGSHSNDQTALMFPNNYS 240  
Db |||||  
QY 241 LDPKPYLSQDINGISYIGGLPKVPKPKPEPTIPHACDPLDFTDAITTFRRVMPFKG 300  
Db |||||  
QY 301 RHLWRIYDITDFEFELIASFWPSLPADLQAAAYENPRDKILVFDENFWMIRGVAVLPDY 360  
Db |||||  
QY 361 PKSIHTLGFPGRRKKIDAAVCDKTRTKTYFFVGICWRFDEMTQTMKGFPQVRVYKHPG 420  
Db |||||  
QY 421 ISIRVDAAFQYKGFSSRSRGSQFEYNIKTNIITRIKNTNFWQCKEPKNSFGFDINKE 480  
Db |||||  
QY 481 KAHSGGIKLYHKSLSLFIQVHLLKNTSIYQ 513  
Db |||||

RESULT 6

ID ABU80965 standard; protein; 513 AA.  
XX AC ABU80965;  
XX DT 23-JUN-2003 (first entry)  
XX DE Human PRO polypeptide #96.  
XX KW Human; PRO polypeptide; secreted and transmembrane protein;  
KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;  
KW bone disorder; cartilage disorder; rheumatoid arthritis; obesity;  
KW sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia;  
KW hearing loss; coagulation disorder; stroke; heart attack; cardiac;  
KW antidiabetic; anorectic; vulnery; antiarthritic; osteopathic;  
KW antirheumatic; auditory; cerebroprotective; angiogenic.  
OS Homo sapiens.  
XX US2003004311-A1.  
XX PD 02-JAN-2003.  
XX PF 19-DEC-2001; 2001US-00028072.  
XX

PR 18-JUN-1997; 97US-0049911P.  
PR 26-AUG-1997; 97US-0056974P.  
PR 17-SEP-1997; 97US-0059113P.  
PR 17-SEP-1997; 97US-0059115P.  
PR 17-SEP-1997; 97US-0059117P.  
PR 17-SEP-1997; 97US-0059122P.  
PR 18-SEP-1997; 97US-0059184P.  
PR 18-SEP-1997; 97US-0059263P.  
PR 19-SEP-1997; 97US-0059352P.  
PR 19-SEP-1997; 97US-0059588P.  
PR 24-SEP-1997; 97US-0059836P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 17-OCT-1997; 97US-0062285P.  
PR 17-OCT-1997; 97US-0062287P.  
PR 17-OCT-1997; 97US-0063755P.  
PR 24-OCT-1997; 97US-0062814P.  
PR 24-OCT-1997; 97US-0062816P.  
PR 24-OCT-1997; 97US-0063045P.  
PR 24-OCT-1997; 97US-0063108P.  
PR 24-OCT-1997; 97US-0063127P.  
PR 27-OCT-1997; 97US-0063327P.  
PR 27-OCT-1997; 97US-0063329P.  
PR 28-OCT-1997; 97US-0063550P.  
PR 28-OCT-1997; 97US-0063561P.  
PR 29-OCT-1997; 97US-0063704P.  
PR 29-OCT-1997; 97US-0063733P.  
PR 29-OCT-1997; 97US-0063735P.  
PR 29-OCT-1997; 97US-0063738P.  
PR 03-NOV-1997; 97US-0064248P.  
PR 07-NOV-1997; 97US-0064809P.  
PR 12-NOV-1997; 97US-0065186P.  
PR 17-NOV-1997; 97US-0065846P.  
PR 21-NOV-1997; 97US-0065634P.  
PR 24-NOV-1997; 97US-0066453P.  
PR 24-NOV-1997; 97US-0066511P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 11-DEC-1997; 97US-0069212P.  
PR 11-DEC-1997; 97US-0069278P.  
PR 11-DEC-1997; 97US-0069334P.  
PR 16-DEC-1997; 97US-0069694P.  
PR 23-JAN-1998; 98US-0072320P.  
PR 04-FEB-1998; 98US-0073612P.  
PR 09-FEB-1998; 98US-0074086P.  
PR 09-FEB-1998; 98US-0074092P.  
PR 12-MAR-1998; 98US-0077791P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 25-MAR-1998; 98US-0079294P.  
PR 27-MAR-1998; 98US-0079663P.  
PR 27-MAR-1998; 98US-0079728P.  
PR 31-MAR-1998; 98US-0080165P.  
PR 12-JUN-1998; 98WO-US012456.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 16-SEP-1998; 98WO-US019177.  
PR 17-SEP-1998; 98WO-US019330.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 05-OCT-1999; 99WO-US023089.  
 PR 29-NOV-1999; 99WO-US028214.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 30-NOV-1999; 99WO-US028409.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 02-DEC-1999; 99WO-US028564.  
 PR 02-DEC-1999; 99WO-US028565.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 20-DEC-1999; 99WO-US030999.  
 PR 30-DEC-1999; 99WO-US031243.  
 PR 30-DEC-1999; 99WO-US031274.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000277.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US0003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 18-FEB-2000; 2000WO-US004342.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 01-MAR-2000; 2000WO-US005601.  
 PR 02-MAR-2000; 2000WO-US005746.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI; 2003-352836/33.  
 DR N-PSDB; ACA67089.  
 XX  
 PT New isolated PRO polypeptide useful for treating diabetes, rheumatoid  
 PT arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or  
 PT heart attack.  
 XX  
 PS Claim 12; Fig 192; 643pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human PRO  
 CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
 CC polypeptides are secreted and transmembrane proteins. The PRO  
 CC polypeptides and polynucleotides are useful for preparing a medicament  
 CC useful in the treatment of diabetes, bone and/or cartilage disorders  
 CC (e.g. rheumatoid arthritis, sports injuries, osteoarthritis), obesity,  
 CC hyper- or hypo-insulinaemia, hearing loss, and coagulation disorders  
 CC (e.g. stroke, heart attack). Anti-PRO antibodies are useful in diagnostic  
 CC assays for PRO, by detecting its expression in specific cells, tissues or  
 CC serum, and for affinity purification of PRO from recombinant cell culture  
 CC or natural sources. ABU0870-ABU81144 represent the human PRO  
 CC polypeptides of the invention. Note: The sequence data for this patent  
 CC was obtained in electronic format directly from the USPTO web site at  
 CC seqdata.uspto.gov/psipsiDentry.html  
 XX  
 SQ Sequence 513 AA;  
 Query Match 99.6%; Score 2752; DB 6; Length 513;  
 Best Local Similarity 99.8%; Pred. No. 4.1e-261; Indels 0; Gaps 0;  
 Matches 512; Conservative 0; Mismatches 1;  
 QY 1 MKRLLLCFFITFSSAPFLVRMTENEENMQAAYLNQFYSLEIEGHNHVSQKNSRLID 60  
 Db 1 MKRLLLCFFITFSSAPFLVRMTENEENMQAAYLNQFYSLEIEGHNHVSQKNSRLID 60  
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 Db 61 DKIREMQAFGLTVTKLDSNLTLEIMKTPRCGVPDVGQGYTLPGWRKKNLYRIINYP 120  
 QY 121 DMARAADVAEIOEGLEVWSKVTPLETKISGDIADIMIAFRTRVHGRCPRYFDGLGVLG 180

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 Db 181 HAFPPGPGGLGGDTFDEDEENWTKGAGFNLFVAAHEFGHALGLSHSNDQTALMFPNYS 240  
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 Db 241 LDPRKYPISQDDINGIQSIYGLPKVPAPKPKPTIPHACDPLDTFDAITTFREVMFFPKG 300  
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 Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAENPRDKILVFKDENFWMIRGIYAVLPDY 360  
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 Db 361 PKSIHTLGFPGRVKKIDAAVCDKTRKTYFFVGIWCRPDEMTQTMKGFPQORVVKHFFPG 420  
 QY 421 ISIRVDAAFQYKGFPPFSGSGSKQFYNIKTNITRMTNTWFOCKEKNSSSFGFDINKE 480  
 Db 421 ISIRVDAAFQYKGFPPFSGSGSKQFYNIKTNITRMTNTWFOCKEKNSSSFGFDINKE 480  
 QY 481 KAHSGGKILYHKLSLSLFIIGVHLLKNTSIYQ 513  
 Db 481 KAHSGGKILYHKLSLSLFIIGVHLLKNTSIYQ 513  
 RESULT 7  
 ABU66665  
 ID ABU66665 standard; protein; 513 AA.  
 XX  
 AC ABU66665;  
 XX  
 DT 23-MAY-2003 (first entry)  
 XX  
 DE Human PRO polypeptide #96.  
 XX  
 KW Human; PRO polypeptide; secreted and transmembrane protein;  
 KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;  
 KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003036180-A1.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PP 09-MAY-2002; 2002US-00143114.  
 PR 31-MAR-1997; 97WO-US005230.  
 PR 12-JUN-1998; 98WO-US012456.  
 PR 14-JUL-1998; 98WO-US014552.  
 PR 28-AUG-1998; 98WO-US017888.  
 PR 10-SEP-1998; 98WO-US018824.  
 PR 14-SEP-1998; 98WO-US019093.  
 PR 14-SEP-1998; 98WO-US019094.  
 PR 14-SEP-1998; 98WO-US019177.  
 PR 16-SEP-1998; 98WO-US019330.  
 PR 17-SEP-1998; 98WO-US019437.  
 PR 07-OCT-1998; 98WO-US021141.  
 PR 29-OCT-1998; 98WO-US022991.  
 PR 29-OCT-1998; 98WO-US022992.  
 PR 20-NOV-1998; 98WO-US024855.  
 PR 01-DEC-1998; 98WO-US025108.  
 PR 05-JAN-1999; 99WO-US000106.  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 10-MAR-1999; 99WO-US005190.  
 PR 20-APR-1999; 99WO-US008615.  
 PR 14-MAY-1999; 99WO-US010733.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 08-SEP-1999; 99WO-US020594.

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PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 03-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030939.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003365.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US020321.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032878.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006566.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001WO-US0172035.
PR 01-JUN-2001; 2001US-008017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882836.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX (GETH ) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart FA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-332040/31.
DR N-PSDB; ACA03698.
XX
PT New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
PT typing, and in chromosome identification.
XX
PS Claim 12; Fig 192; 660pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, and for
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The PRO polypeptides are useful for
CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
CC human blood, for stimulating the proliferation or differentiation of
CC chondrocytes, and detecting the presence of tumours. The polynucleotide
CC sequences encoding PRO polypeptides are useful as hybridisation probes,
CC in chromosome and gene mapping, in the generation of antisense RNA and
CC DNA, in the preparation of PRO polypeptides, for generating transgenic
CC animals or knockout animals, for the genetic analysis of individuals with
CC genetic disorders, and in gene therapy. AB066570-AB066844 represent the
CC human PRO polypeptides of the invention. Note: The sequence data for this
CC patent was obtained in electronic format directly from the USPTO web site
CC at seqdata.uspto.gov/psipsDIDentry.html
XX
SQ Sequence 513 AA;
Query Match 99.6%; Score 2752; DB 6; Length 513;
Best Local Similarity 99.8%; Pred. No. 4.le-261;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MKRLILLCLFFITFSSAPPLVRMTENEENMQLAQAYLNQFYSLEIEGNHLVQSKRSLID 60
Db 1 MKRLILLCLFFITFSSAPPLVRMTENEENMQLAQAYLNQFYSLEIEGNHLVQSKRSLID 60
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Db 241 LDPRKYPISQDDINGIOSIYGLPKVPAKPKETIPHACDPDLTFFDAITTFREVMFPKG 300
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Qy 361 PKSIHTLGGPGRVKKIDAAVCDKTRKTYFVGLWCWRFDEMTOTMDKGPQRVVKHPPG 420
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 421 ISIRVDAAFQYKGFPPFSGSKQFYNKTKNITRMTNTWFOCKEPKNSSGFDINKE 480  
 481 KAHSGGKILYHKLSLSLFIPIGVHLLKNTSIYQ 513  
 481 KAHSGGKILYHKLSLSLFIPIGVHLLKNTSIYQ 513  
 RESULT 8  
 ABO32578  
 ID ABO32578 standard; protein; 513 AA.  
 XX AC ABO32578;  
 XX DT 17-SEP-2003 (first entry)  
 XX DE  
 XX DE Secreted polypeptide-related protein #40.  
 XX KW Human; TANGO; INTERCEPT; secreted polypeptide; immune disorder;  
 KW hormonal disorder; proliferative disorder; cancer; thyroid disorder;  
 KW diabetes; multiple sclerosis; lupus; neurological disorder; anaemia;  
 KW Alzheimer's disease; Parkinson's disease; cardiovascular disorder;  
 KW myocardial infarction; congestive heart disease; blood platelet disorder;  
 KW thrombocytopenia; blood vessel; atherosclerosis; vasculitis.  
 XX OS Homo sapiens.  
 XX XX  
 XX FN US2003022279-A1.  
 XX PD  
 XX PF 30-JAN-2003.  
 XX XX  
 XX PF 12-JAN-2001; 2001US-00759130.  
 XX XX  
 XX PR 14-JUN-1999; 99US-00333159.  
 XX PR 29-JUN-1999; 99US-00342364.  
 XX PR 10-SEP-1999; 99US-00393996.  
 XX PR 19-OCT-1999; 99US-00420707.  
 XX PR 07-JAN-2000; 2000US-00479249.  
 XX PR 27-APR-2000; 2000US-00559497.  
 XX PR 24-MAY-2000; 2000US-00578063.  
 XX PR 16-JUN-2000; 2000US-00596194.  
 XX PR 23-JUN-2000; 2000US-00602871.  
 XX PR 30-JUN-2000; 2000US-00608452.  
 XX XX  
 XX PA (FRAS/) FRASER C C.  
 XX PA (BARN/) BARNES T M.  
 XX PA (SHAR/) SHARP J D.  
 XX PA (KIRS/) KIRST S J.  
 XX PA (MYER/) MYERS P S.  
 XX PA (LEIB/) LEIBY K R.  
 XX PA (HOLT/) HOLTZMAN D A.  
 XX PA (MCCA/) MCCARTHY S A.  
 XX PA (WRIG/) WRIGHTON N.  
 XX PA (MACK/) MACKAY C R.  
 XX PA (GOOD/) GOODEARL A D J.  
 XX XX  
 XX PI Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KB;  
 XX PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;  
 XX XX  
 XX DR WPI; 2003-456290/43.  
 XX DR N-PSDB; ACD66739, ACD66740.  
 XX XX  
 XX PT New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,  
 XX PT TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or  
 XX PT treating disorders such as cancer, diabetes or atherosclerosis, and in  
 XX PT forensic biology.  
 XX XX  
 XX PS Claim 9; Fig 15A-15D; 482pp; English.  
 XX XX  
 XX CC The invention relates to secreted polypeptide-related proteins and  
 XX CC nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The  
 XX CC nucleic acids, proteins and antibodies specific to the proteins are  
 XX CC useful in screening assays, predictive medicine (e.g. diagnostic assays,

CC prognostic assays, monitoring clinical trials and pharmacogenetics) and  
 CC prophylactic and therapeutic methods. The sequences are used in  
 CC diagnosing, preventing or treating proliferative disorders (e.g.  
 CC cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune  
 CC disorders (e.g. multiple sclerosis or lupus), neurological disorders  
 CC (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular  
 CC disorders (e.g. myocardial infarction or congestive heart disease), blood  
 CC platelet disorders (e.g. thrombocytopenia or anaemia) and disorders  
 CC involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic  
 CC acids may also be used in chromosome mapping, tissue typing and forensic  
 CC biology, and as surrogate markers. This sequence represents a secreted  
 CC polypeptide-related protein of the invention. Note: The sequence data for  
 CC this patent was obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html  
 XX XX  
 XX SQ Sequence 513 AA;  
 Query Match 99.6%; Score 2752; DB 6; Length 513;  
 Best Local Similarity 99.8%; Pred. No. 4.1e-261;  
 Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MKRLLLLCLFITSSAFPLVRMTENEENMQLAQAYLNQFYSLEIEGHNHLSQSKRSLID 60  
 DB 1 MKRLLLLCLFITSSAFPLVRMTENEENMQLAQAYLNQFYSLEIEGHNHLSQSKRSLID 60  
 QY 61 DKIREMQAFGLTVTGKLDNSTLEIMKTPRCGVPDVGQYTLPGWRKYNLTIRIINTP 120  
 DB 61 DKIREMQAFGLTVTGKLDNSTLEIMKTPRCGVPDVGQYTLPGWRKYNLTIRIINTP 120  
 QY 121 DMARAANDVAIQEGLVMSKVTPFKTKISKGIADIMIAFRTRVHGRCPRYFDGGLVIG 180  
 DB 121 DMARAANDVAIQEGLVMSKVTPFKTKISKGIADIMIAFRTRVHGRCPRYFDGGLVIG 180  
 QY 181 HAPFPGGLGGDTHFDEDEENWTKDAGFNLFVAHAHEFGHALGSHSNDQTALMPENYVS 240  
 DB 181 HAPFPGGLGGDTHFDEDEENWTKDAGFNLFVAHAHEFGHALGSHSNDQTALMPENYVS 240  
 QY 241 LDPKRYPLSQDDINGIQSIYGLPKVPKPKPTPIHACDDPLTDAITTFRRVWFFKG 300  
 DB 241 LDPKRYPLSQDDINGIQSIYGLPKVPKPKPTPIHACDDPLTDAITTFRRVWFFKG 300  
 QY 301 RHLWRIYYDITDVEPELIASFWSLPADLQAAVENPRDKILVFKDENFMIRGAVLPDY 360  
 DB 301 RHLWRIYYDITDVEPELIASFWSLPADLQAAVENPRDKILVFKDENFMIRGAVLPDY 360  
 QY 361 PKSHTLGPGRVKKIDAAVCDKTRKTYFFVGIWCFWDFDENTQMDKGFPPORVVKHPPG 420  
 DB 361 PKSHTLGPGRVKKIDAAVCDKTRKTYFFVGIWCFWDFDENTQMDKGFPPORVVKHPPG 420  
 QY 421 ISIRVDAAFQYKGFPPFSGSKQFYNKTKNITRMTNTWFOCKEPKNSSGFDINKE 480  
 DB 421 ISIRVDAAFQYKGFPPFSGSKQFYNKTKNITRMTNTWFOCKEPKNSSGFDINKE 480  
 QY 481 KAHSGGKILYHKLSLSLFIPIGVHLLKNTSIYQ 513  
 DB 481 KAHSGGKILYHKLSLSLFIPIGVHLLKNTSIYQ 513  
 RESULT 9  
 ABO59746  
 ID ABO59746 standard; protein; 513 AA.  
 XX AC ABO59746;  
 XX DT 13-MAY-2003 (first entry)  
 XX DE  
 XX DE Novel secreted and transmembrane protein PRO5992.  
 XX KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
 KW cardiac insufficiency disorder; cancer; tumour; immune response;  
 KW adrenal cortical capillary endothelial growth; c-fos induction;  
 KW vascular endothelial growth factor inhibition; VEGF inhibition;  
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;

KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosum; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
XX chondrocyte redifferentiation; sports injury; arthritis.

OS Homo sapiens.

PN US2003017563-A1.

XX 23-JAN-2003.

XX 07-MAY-2002; 2002US-00140808.

XX 31-MAR-1997; 97WO-US005230.

PR 12-JUN-1998; 98WO-US012456.

PR 28-AUG-1998; 98WO-US017888.

PR 10-SEP-1998; 98WO-US018824.

PR 14-SEP-1998; 98WO-US019093.

PR 14-SEP-1998; 98WO-US019094.

PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.

PR 07-OCT-1998; 98WO-US021141.

PR 29-OCT-1998; 98WO-US022991.

PR 20-NOV-1998; 98WO-US024855.

PR 01-DEC-1998; 98WO-US025108.

PR 05-JAN-1999; 99WO-US000106.

PR 08-MAR-1999; 99WO-US005028.

PR 10-MAR-1999; 99WO-US005190.

PR 20-APR-1999; 99WO-US008615.

PR 14-MAY-1999; 99WO-US010733.

PR 02-JUN-1999; 99WO-US012252.

PR 01-SEP-1999; 99WO-US020111.

PR 08-SEP-1999; 99WO-US020594.

PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.

PR 15-SEP-1999; 99WO-US021547.

PR 03-OCT-1999; 99WO-US023089.

PR 29-NOV-1999; 99WO-US028214.

PR 30-NOV-1999; 99WO-US028313.

PR 30-NOV-1999; 99WO-US028409.

PR 01-DEC-1999; 99WO-US028301.

PR 01-DEC-1999; 99WO-US028634.

PR 02-DEC-1999; 99WO-US028551.

PR 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.

PR 20-DEC-1999; 99WO-US030999.

PR 22-DEC-1999; 99WO-US030720.

PR 30-DEC-1999; 99WO-US031243.

PR 05-JAN-2000; 99WO-US031274.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000277.

PR 06-JAN-2000; 2000WO-US000376.

PR 11-FEB-2000; 2000WO-US000365.

PR 18-FEB-2000; 2000WO-US000431.

PR 18-FEB-2000; 2000WO-US000432.

PR 22-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US004914.

PR 24-FEB-2000; 2000WO-US005004.

PR 01-MAR-2000; 2000WO-US005501.

PR 02-MAR-2000; 2000WO-US005746.

PR 02-MAR-2000; 2000WO-US005841.

PR 10-MAR-2000; 2000WO-US006319.

PR 15-MAR-2000; 2000WO-US006884.

PR 20-MAR-2000; 2000WO-US007377.

PR 21-MAR-2000; 2000WO-US007532.

PR 30-MAR-2000; 2000WO-US008439.

PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.

PR 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-2000; 2000WO-US015264.

PR 28-JUL-2000; 2000WO-US020710.

PR 11-AUG-2000; 2000WO-US022031.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.

PR 01-DEC-2000; 2000WO-US032678.

PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.

PR 28-FEB-2001; 2001US-00796498.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-MAR-2001; 2001WO-US006666.

PR 09-MAR-2001; 2001US-00802706.

PR 14-MAR-2001; 2001US-00808689.

PR 22-MAR-2001; 2001US-00816744.

PR 05-APR-2001; 2001US-00828366.

PR 10-MAY-2001; 2001US-00854208.

PR 10-MAY-2001; 2001US-00854280.

PR 18-MAY-2001; 2001US-00860216.

PR 25-MAY-2001; 2001US-00866028.

PR 25-MAY-2001; 2001US-00866034.

PR 25-MAY-2001; 2001WO-US017092.

PR 01-JUN-2001; 2001US-00872035.

PR 01-JUN-2001; 2001WO-US017800.

PR 05-JUN-2001; 2001US-00874503.

PR 14-JUN-2001; 2001US-00882636.

PR 19-JUN-2001; 2001US-00886342.

PR 20-JUN-2001; 2001WO-US019692.

PR 21-JUN-2001; 2001US-00887879.

PR 22-JUN-2001; 2001WO-US020116.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-JUL-2001; 2001WO-US021735.

PR 18-JUL-2001; 2001US-00908827.

PR 06-AUG-2001; 2001US-00924419.

PR 09-AUG-2001; 2001US-00927796.

PR 16-AUG-2001; 2001US-00931836.

PR 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;

Garritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-148238/14.

N-PSDB; ABX89236.

Two hundred and seventy five nucleic acids encoding PRO polypeptides,  
useful for treating pericyte-associated tumors, diabetes and various bone  
and/or cartilage disorders, e.g. arthritis.

Claim 12; Fig 192; 659pp; English.

The invention describes an isolated human PRO polypeptide. The PRO  
polypeptides are useful in detecting PRO polypeptides in a sample, in  
linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
in modulating at least one biological activity of a cell expressing a PRO  
polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
stimulate adrenal cortical capillary endothelial growth, and PRO536,  
PRO943, PRO828, PRO826, PRO1068 or PRO535, PRO826, PRO819, PRO1126,  
PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
useful for treating conditions or disorders where angiogenesis would be  
beneficial, e.g. wound healing and antagonist of this polypeptide are  
useful for treating cancerous tumors. PRO812 inhibits vascular  
endothelial growth factor (VEGF) stimulated proliferation of endothelial  
cells and is thus useful for inhibiting endothelial cell growth in  
mammals which would be beneficial in inhibiting tumour growth. PRO826,  
PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
stimulated T-lymphocytes and are therapeutically useful for enhancing

CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
CC rod photoreceptor cells) and therefore are useful for treating retinal  
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
CC and therefore are useful for treating kidney disorders associated with,  
CC decreased mesangial cell function such as Berger disease or other  
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
CC proliferation and/or redifferentiation of chondrocytes in culture and are  
CC thus useful for treating sports injuries, and arthritis. This is the  
CC amino acid sequence of a novel human PRO protein  
XX  
SQ Sequence 513 AA;

Query Match 99.6%; Score 2752; DB 6; Length 513;  
Best Local Similarity 99.8%; Pred. No. 4,1e-261;  
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLGLFFITFSSAPLVMTENEENMQAAYLNQFYSLTEGHNHLSVSKRSLLID 60  
Db 1 MKRLLLGLFFITFSSAPLVMTENEENMQAAYLNQFYSLTEGHNHLSVSKRSLLID 60  
QY 61 DKIREMQAFFGLTVTGKLDNLTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINTP 120  
Db 61 DKIREMQAFFGLTVTGKLDNLTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINTP 120  
QY 121 DMARAADVAEIOEGLEWMSKVTPKFTKISGIADIMIAFRTRVHGRCPRYDGLVGLG 180  
Db 121 DMARAADVAEIOEGLEWMSKVTPKFTKISGIADIMIAFRTRVHGRCPRYDGLVGLG 180  
QY 181 HAPPPGGLGGTHFDEENWTKDAGFNLFVAHAEFGHAGLSHNDQTALMPFNYS 240  
Db 181 HAPPPGGLGGTHFDEENWTKDAGFNLFVAHAEFGHAGLSHNDQTALMPFNYS 240  
QY 241 LDPRKPLSQDDINGITQSYGGLPKVPKPKPTTIPHACDPLDTDAITTFRRVYMFVK 300  
Db 241 LDPRKPLSQDDINGITQSYGGLPKVPKPKPTTIPHACDPLDTDAITTFRRVYMFVK 300  
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWIRGYAVLPDY 360  
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWIRGYAVLPDY 360  
QY 361 PKSIHTLGPGRVKKIDAAVCCKTKTKYFFVGIWCWREDEMTQMDKGFPORVVKHPPG 420  
Db 361 PKSIHTLGPGRVKKIDAAVCCKTKTKYFFVGIWCWREDEMTQMDKGFPORVVKHPPG 420  
QY 421 ISIRVDAAFQYKGFYFFSRGSKQFEYNIKTKNITRIMTRNTWFOCKEPKNSFGFDINKE 480  
Db 421 ISIRVDAAFQYKGFYFFSRGSKQFEYNIKTKNITRIMTRNTWFOCKEPKNSFGFDINKE 480  
QY 481 KAHSGGKILYHKSLSLFTFGIVHLLKNTSIYQ 513  
Db 481 KAHSGGKILYHKSLSLFTFGIVHLLKNTSIYQ 513  
RESULT 10  
ABO24936  
ID ABO24936 standard; protein; 513 AA.  
XX  
AC ABO24936;  
XX  
DT 05-SEP-2003 (first entry)  
XX  
DE Human secreted/transmembrane protein (PRO) #96.  
XX  
KW Human; PRO; secreted protein; transmembrane protein; tumour; cytostatic;  
KW gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood;  
KW proteoglycan; cartilage; cytokine; peripheral blood mononuclear cell;  
KW PBMC; Glucose uptake; FFA; skeletal muscle cell; adipocyte cell;  
KW chondrocyte cell proliferation; chondrocyte cell differentiation;  
KW pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell;  
KW endothelial cell; A-peptide; factor VIIA.

XX  
OS Homo sapiens.  
XX US2003036179-A1.  
XX 20-FEB-2003.  
XX  
PF 10-MAY-2002; 2002US-00142431.  
XX  
XX 31-MAR-1997; 97WO-US005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 05-JAN-2000; 99WO-US031274.  
PR 06-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 11-FEB-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.

PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030352.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 09-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 18-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
PR 22-JUN-2001; 2001WO-US020116.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.  
PR 09-AUG-2001; 2001US-00927796.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.  
XX

(GETH ) GENENTECH INC.

PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
DR WPI; 2003-466355/44.  
DR N-PSDB; ACD41890.

XX New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or  
PT PRO4978, useful in molecular biology, chromosome and gene mapping, in  
PT generating antisense RNA and DNA, and in gene therapy.

XX Claim 12; Fig 192; 659pp; English.

XX The invention relates to an isolated nucleic acid comprising at least 80%  
CC sequence identity to a PRO (secreted and transmembrane protein) cDNA  
CC comprising a nucleic acid (a) encoding a PRO polypeptide, or its  
CC extracellular domain (with or without its associated signal peptide),  
CC which comprises any of the 275 120-850 residue amino acid sequences,  
CC given in the specification; (b) comprising any of the 275 300-3500  
CC nucleotide sequences, given in the specification; or (c) comprising the  
CC full-length coding sequence of the nucleotide sequences given in the  
CC specification, or of the DNA deposited under any of the American Type  
CC Culture Collection (ATCC) Accession Numbers listed in the specification.  
CC Also included are a vector comprising the novel nucleic acid, a host cell  
CC comprising the vector, producing a PRO polypeptide, the isolated PRO  
CC polypeptide detailed above, a chimeric molecule comprising the PRO  
CC polypeptide of fused to a heterologous amino acid sequence, an anti-PRO  
CC antibody, detecting a PRO polypeptide in a sample suspected of containing  
CC the PRO polypeptide, linking a bioactive molecule to a cell expressing a  
CC PRO polypeptide, modulating at least one biological activity of a cell  
CC expressing a PRO polypeptide, stimulating the release of tumour necrosis  
CC factor-alpha (TNF-alpha) from human blood, (or) proteoglycans from  
CC cartilage or cytokine from peripheral blood mononuclear cells (PBMC)),  
CC modulating the uptake of glucose or FFA by skeletal muscle cells or  
CC adipocyte cells, stimulating the proliferation or differentiation of

CC chondrocyte cells (or proliferation of or gene expression in pericyte  
CC cells), stimulating the proliferation of inner ear utricular supporting  
CC cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the  
CC binding of A-peptide to factor VIIA, or differentiation of adipocyte  
CC cells, detecting the presence of a tumour in a mammal and an  
CC oligonucleotide probe derived from any of the nucleotide sequences given  
CC in the specification. The polynucleotide is useful in molecular biology,  
CC including uses as hybridisation probes, in chromosome and gene mapping,  
CC in generating antisense RNA and DNA, and in gene therapy. The  
CC polynucleotide may also be used in preparing PRO polypeptides by  
CC recombinant techniques, and in generating either transgenic animals or  
CC knock-out animals which, in turn, are useful in the development and  
CC screening of therapeutically useful reagents. The PRO polypeptide or the  
CC antibody is used in preparing a medicament for treating a condition  
CC responsive to the polypeptide or antibody, such as tumours, and in  
CC various diagnostic assays. The present sequence represents a PRO  
CC polypeptide  
XX

SQ Sequence 513 AA;

Query Match 99.6%; Score 2752; DB 6; Length 513;  
Best Local Similarity 99.8%; Pred. No. 4.1e-261;  
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MKRLILLCLFFITFSSAPFLVRMTENEENMLQAAVYLNQFYSLIEGNHLVQSKNRLSD 60  
DB 1 MKRLILLCLFFITFSSAPFLVRMTENEENMLQAAVYLNQFYSLIEGNHLVQSKNRLSD 60  
QY 61 DKIREMOAFLVTVGKLDSENTLEIMKTGRCVDPVGVGYTLPGWRKYNLTVAIINYP 120  
DB 61 DKIREMOAFLVTVGKLDSENTLEIMKTGRCVDPVGVGYTLPGWRKYNLTVAIINYP 120  
QY 121 DMARAAVDEALQEGLEWWSKVTPLKFTKISKGTADIMAFRTVRVHGRCPYEDGPIGVLG 180  
DB 121 DMARAAVDEALQEGLEWWSKVTPLKFTKISKGTADIMAFRTVRVHGRCPYEDGPIGVLG 180  
QY 181 HAPPPGGLGGDTHFDEDENTKDGAGFNLFVAHFEFGHALGSHSNDOTALMFPNYS 240  
DB 181 HAPPPGGLGGDTHFDEDENTKDGAGFNLFVAHFEFGHALGSHSNDOTALMFPNYS 240  
QY 241 LDRPKYPLSQDDINGIQSIYGLPKVPAPKEPTIPHACDPDLTTFDAITTRREVMPFKG 300  
DB 241 LDRPKYPLSQDDINGIQSIYGLPKVPAPKEPTIPHACDPDLTTFDAITTRREVMPFKG 300  
QY 301 RHLWRYYDITDVEFEELIASFWPSLPADLQAAAYENPDKILVPEKDNFWMIRGVAVLPDY 360  
DB 301 RHLWRYYDITDVEFEELIASFWPSLPADLQAAAYENPDKILVPEKDNFWMIRGVAVLPDY 360  
QY 361 PKSHTLGFPPGRVKKIDAAVCDKTRTKTYFVGVICWRFDEMTQTMKGFPQRVVKGFP 420  
DB 361 PKSHTLGFPPGRVKKIDAAVCDKTRTKTYFVGVICWRFDEMTQTMKGFPQRVVKGFP 420  
QY 421 ISIRVDAAFQYKGFPPFSRSGSKQFEYNIKTNTIRMTNTWFOCKEPKNSSGFDINKE 480  
DB 421 ISIRVDAAFQYKGFPPFSRSGSKQFEYNIKTNTIRMTNTWFOCKEPKNSSGFDINKE 480  
QY 481 KAHSGGKILYHKLSLIFIGIVHLLKNTSIYQ 513  
DB 481 KAHSGGKILYHKLSLIFIGIVHLLKNTSIYQ 513

RESULT 11

ABU66941

ID ABU66941 standard; protein; 513 AA.

XX AC ABU66941;

XX DT 27-MAY-2003 (first entry)

XX DE Human secreted/transmembrane, PRO, protein SEQ ID 192.

XX KW Human; secreted protein; transmembrane protein; PRO;

KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;

KW infertility; birth defects; premature aging; AIDS; biosensor;  
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;  
 XX bio reactor; tumour.

OS Homo sapiens.

XX US2003032155-A1.

PN

XX 13-FEB-2003.

XX 03-MAY-2002; 2002US-00137865.

XX 31-MAR-1997; 97WO-US005230.

PR 12-JUN-1998; 98WO-US012456.

PR 14-JUL-1998; 98WO-US014552.

PR 28-AUG-1998; 98WO-US017888.

PR 10-SEP-1998; 98WO-US018824.

PR 14-SEP-1998; 98WO-US019093.

PR 14-SEP-1998; 98WO-US019094.

PR 14-SEP-1998; 98WO-US019177.

PR 16-SEP-1998; 98WO-US019330.

PR 17-SEP-1998; 98WO-US019437.

PR 07-OCT-1998; 98WO-US021141.

PR 29-OCT-1998; 98WO-US022991.

PR 29-OCT-1998; 98WO-US022992.

PR 20-NOV-1998; 98WO-US024855.

PR 01-DEC-1998; 98WO-US025108.

PR 05-JAN-1999; 99WO-US000106.

PR 08-MAR-1999; 99WO-US005028.

PR 10-MAR-1999; 99WO-US005190.

PR 20-APR-1999; 99WO-US008615.

PR 14-MAY-1999; 99WO-US010733.

PR 02-JUN-1999; 99WO-US012252.

PR 01-SEP-1999; 99WO-US020111.

PR 08-SEP-1999; 99WO-US020594.

PR 13-SEP-1999; 99WO-US020944.

PR 15-SEP-1999; 99WO-US021090.

PR 05-SEP-1999; 99WO-US021547.

PR 15-OCT-1999; 99WO-US023089.

PR 29-NOV-1999; 99WO-US028214.

PR 30-NOV-1999; 99WO-US028313.

PR 30-NOV-1999; 99WO-US028409.

PR 01-DEC-1999; 99WO-US028301.

PR 01-DEC-1999; 99WO-US028634.

PR 02-DEC-1999; 99WO-US028551.

PR 02-DEC-1999; 99WO-US028564.

PR 02-DEC-1999; 99WO-US028565.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.

PR 20-DEC-1999; 99WO-US030999.

PR 22-DEC-1999; 99WO-US030720.

PR 30-DEC-1999; 99WO-US031243.

PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000277.

PR 11-FEB-2000; 2000WO-US000376.

PR 18-FEB-2000; 2000WO-US0003565.

PR 18-FEB-2000; 2000WO-US004341.

PR 24-FEB-2000; 2000WO-US004342.

PR 24-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US004914.

PR 01-MAR-2000; 2000WO-US005004.

PR 01-MAR-2000; 2000WO-US005604.

PR 02-MAR-2000; 2000WO-US005746.

PR 02-MAR-2000; 2000WO-US005841.

PR 10-MAR-2000; 2000WO-US006319.

PR 15-MAR-2000; 2000WO-US006884.

PR 20-MAR-2000; 2000WO-US007377.

PR 21-MAR-2000; 2000WO-US007532.

PR 30-MAR-2000; 2000WO-US008439.

PR 17-MAY-2000; 2000WO-US013705.

PR 22-MAY-2000; 2000WO-US014042.

PR 30-MAY-2000; 2000WO-US014941.

PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000US-00747259.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PR 28-FEB-2001; 2001US-00796498.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 09-MAR-2001; 2001US-00802706.  
 PR 14-MAR-2001; 2001US-00808689.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 05-APR-2001; 2001US-00828366.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 18-MAY-2001; 2001US-00860216.  
 PR 25-MAY-2001; 2001US-00866028.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 25-MAY-2001; 2001WO-US017092.  
 PR 01-JUN-2001; 2001US-00872035.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 05-JUN-2001; 2001US-00874503.  
 PR 14-JUN-2001; 2001US-00882636.  
 PR 19-JUN-2001; 2001US-00886342.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 21-JUN-2001; 2001US-00887879.  
 PR 22-JUN-2001; 2001WO-US020116.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 18-JUL-2001; 2001US-00908827.  
 PR 06-AUG-2001; 2001US-00924419.  
 PR 09-AUG-2001; 2001US-00927796.  
 PR 16-AUG-2001; 2001US-00931836.  
 PR 19-DEC-2001; 2001US-00028072.  
 XX (GETH ) GENENTECH INC.

PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;

PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

XX WPI; 2003-331925/31.

DR N-PSDB; ACA04119.

XX New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or cancer.

PS Claim 12; Fig 192; 659pp; English.

XX The invention relates to an isolated nucleic acid comprising, or which is at least 80% identical to, or the full-length coding sequence of, any of the 275 nucleotide sequences, encoding the corresponding PRO polypeptide (one of 275 secreted or transmembrane proteins). The nucleic acid further comprises the full-length coding sequence of the DNA deposited under American Type Culture Collection (ATCC) accession number in a list given in the specification. Also included are vectors and host cells for producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO extracellular domains and mature sequences, methods of detecting PRO proteins, methods for stimulating the release of TNF-alpha (tumour necrosis factor alpha) from human blood, (and the proliferation of differentiation of chondrocyte cells, the proliferation of, or gene expression in pericyte cells, the release or proteoglycans from cartilage, proliferation of inner ear utricular supporting cells, the proliferation of T-lymphocyte cells, the release of a cytokine from peripheral blood mononuclear cells (PBMC), or the proliferation of endothelial cells), a method for modulating the uptake of glucose or free fatty acid (FFA) by skeletal muscle cells, a method for inhibiting the

CC binding of A-peptide to factor VIIA, or the differentiation of adipocyte  
CC cells, a method for detecting the presence of a tumour in a mammal and an  
CC oligonucleotide probe derived from any of the nucleotide sequences cited  
CC above. The nucleic acids and polypeptides are useful for treating  
CC inflammatory diseases, organ failure, atherosclerosis, cardiac injury,  
CC infertility, birth defects, premature aging, AIDS (acquired  
CC immunodeficiency syndrome), cancer, or diabetic complications. The  
CC nucleic acids are useful as hybridisation probes, in chromosome and gene  
CC mapping, and in generating antisense RNA or DNA. The polypeptides are  
CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both  
CC are useful in tissue typing. The present sequence represents a PRO  
CC protein of the invention  
XX  
SQ Sequence 513 AA;

Query Match 99.6%; Score 2752; DB 6; Length 513;  
Best Local Similarity 99.8%; Pred. No. 4.1e-261;  
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MKRLLLCLFETESSAPPLVRMTENENMQLAQYLNQFYSLEIEGNHLVQSKNRSIID 60  
Db 1 MKRLLLCLFETESSAPPLVRMTENENMQLAQYLNQFYSLEIEGNHLVQSKNRSIID 60  
Qy 61 DKIREMAFFGLTVTGKLDNSTLIMKTPRCGVDPVQGYGTYLPGWKYMLTYRIINYP 120  
Db 61 DKIREMAFFGLTVTGKLDNSTLIMKTPRCGVDPVQGYGTYLPGWKYMLTYRIINYP 120  
Qy 121 DMARAAVDEAIQEGLEWVSKVTPKTKISKGIADIMAFRTRVHGRCPRYFDGFLGVLG 180  
Db 121 DMARAAVDEAIQEGLEWVSKVTPKTKISKGIADIMAFRTRVHGRCPRYFDGFLGVLG 180  
Qy 181 HAPPPGGLGGDTHFDEENWKDGAGFNPLVAHFEFGALGSHNDQALMFPNYS 240  
Db 181 HAPPPGGLGGDTHFDEENWKDGAGFNPLVAHFEFGALGSHNDQALMFPNYS 240  
Qy 241 LDPRKYPQLSQDDINGISYIGLPGKVPKPKKEPTIPHACDPDLTFTDAITFRREVMPFKG 300  
Db 241 LDPRKYPQLSQDDINGISYIGLPGKVPKPKKEPTIPHACDPDLTFTDAITFRREVMPFKG 300  
Qy 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAYENPRDKILVFXDENFWMIRGVAVLPDY 360  
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAYENPRDKILVFXDENFWMIRGVAVLPDY 360  
Qy 361 PKSHTLGFGRVKKIDAAVCDKTKTRTFYFVGWCRFDEMOTMDKGPQVRVVKFPFG 420  
Db 361 PKSHTLGFGRVKKIDAAVCDKTKTRTFYFVGWCRFDEMOTMDKGPQVRVVKFPFG 420  
Qy 421 ISIRVDAAFQYKGFPPFSRSGSKQFEYNKTKNITRMTNTWFOCKEPKNSSGFGDINKE 480  
Db 421 ISIRVDAAFQYKGFPPFSRSGSKQFEYNKTKNITRMTNTWFOCKEPKNSSGFGDINKE 480  
Qy 481 KAHSGGKILYKHSLSLFIQVHLLKNTSIYQ 513  
Db 481 KAHSGGKILYKHSLSLFIQVHLLKNTSIYQ 513

RESULT 12  
ADA45711  
ID ADA45711 standard; protein; 513 AA.  
XX  
AC ADA45711;  
DT 20-NOV-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PRO5992.  
XX  
KW Human; secreted and transmembrane protein; PRO;  
KW Tumour necrosis factor alpha release; TNF-alpha release;  
KW glucose uptake modulator; FFA uptake modulator;  
KW cell proliferation stimulator; cell differentiation stimulator;  
KW cell differentiation inhibitor; cytokine release stimulator; tumour;  
KW lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;  
KW cervical tumour; liver tumour; chromosome mapping; gene mapping;

KW gene therapy; chromosome identification; chromosome marker.  
XX  
OS Homo sapiens.  
XX US2003022328-A1.  
XX  
PD 30-JAN-2003.  
XX  
PF 16-APR-2002; 2002US-00123904.  
XX  
PR 31-MAR-1997; 97WO-US005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 02-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 03-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.



PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023322.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000US-00747259.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PR 28-FEB-2001; 2001US-00796498.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 09-MAR-2001; 2001US-00802706.  
 PR 14-MAR-2001; 2001US-00808689.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 05-APR-2001; 2001US-00828366.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 18-MAY-2001; 2001US-00860216.  
 PR 25-MAY-2001; 2001US-00866028.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 25-MAY-2001; 2001WO-US017092.  
 PR 01-JUN-2001; 2001US-00872035.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 05-JUN-2001; 2001US-00874503.  
 PR 14-JUN-2001; 2001US-00882636.  
 PR 19-JUN-2001; 2001US-00886342.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 21-JUN-2001; 2001US-00887879.  
 PR 22-JUN-2001; 2001WO-US020116.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 18-JUL-2001; 2001US-00908827.  
 PR 06-AUG-2001; 2001US-00924419.  
 PR 09-AUG-2001; 2001US-00927796.  
 PR 16-AUG-2001; 2001US-00931836.  
 PR 19-DEC-2001; 2001US-00028072.  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tamas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI; 2003-584997/55.  
 DR N-PSDB; ADA45710.  
 XX  
 PT Novel secreted and transmembrane polypeptide for modulating biological  
 PT activity of cell expressing the polypeptide, identifying agonists or  
 PT antagonists of polypeptide, and as molecular weight markers.  
 XX  
 PS Claim 12; Fig 192; 659pp; English.

XX The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (I). (I) is useful for stimulating the release of TNF-alpha from human blood, for modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the release of proteoglycans from cartilage, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the release of a cytokine from PBMC cells, for inhibiting the binding of A-peptide to factor VIIa, for inhibiting the differentiation of adipocyte cells, for stimulating proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligonucleotide probes are useful for isolating genomic and cDNA nucleotide sequences or antisense probes. (I) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding interaction. A polynucleotide (II) encoding (I) is useful in chromosome and gene mapping, in generation of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and

CC screening of therapeutically useful reagents, in gene therapy, for CC chromosome identification, as chromosome marker, and for generating CC probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g. CC detecting its expression in specific cells, tissues or serum, and for CC affinity purification of PRO from recombinant cell culture or natural CC sources. (I) and (II) are useful for tissue typing. This is the amino CC acid sequence of a novel human secreted and transmembrane PRO CC polypeptide.

XX Sequence 513 AA;

SQ Query Match 99.6%; Score 2752; DB 6; Length 513;

Best Local Similarity 99.8%; Pred. No. 4.1e-261;

Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLCLEFFITSSAPPLVRMTENENMOLAAYLNQFYSLEIGHLVQSKNRSLLID 60  
 DB 1 MKRLLLCLEFFITSSAPPLVRMTENENMOLAAYLNQFYSLEIGHLVQSKNRSLLID 60  
 QY 61 DKIREMOAFFGLTVTGKLDNSTLEIMKTPRGVDPVGVGYTLPGWRKXNYLTYRIINYP 120  
 DB 61 DKIREMOAFFGLTVTGKLDNSTLEIMKTPRGVDPVGVGYTLPGWRKXNYLTYRIINYP 120  
 QY 121 DMARAAVDEAIOEGLVMSKVTPKFTKISKIADIATFTRVHGRCPRYFDGGLVIG 180  
 DB 121 DMARAAVDEAIOEGLVMSKVTPKFTKISKIADIATFTRVHGRCPRYFDGGLVIG 180  
 QY 181 HAFPPGGLGGDTHDEDENTKOGAGNLFVAHAHEGHGALGSHSNDQALMFPNYS 240  
 DB 181 HAFPPGGLGGDTHDEDENTKOGAGNLFVAHAHEGHGALGSHSNDQALMFPNYS 240  
 QY 241 LDPRKYPUSQDDINGIQSIYGLPKVPKPKPTIPACDPLDFTDAITTRERVMFFKG 300  
 DB 241 LDPRKYPUSQDDINGIQSIYGLPKVPKPKPTIPACDPLDFTDAITTRERVMFFKG 300  
 QY 301 RHLMRIYYDITDVEFELIASFWPSLPADLQAAYENPRDKILVFKDENFWMIRGVAVLDPY 360  
 DB 301 RHLMRIYYDITDVEFELIASFWPSLPADLQAAYENPRDKILVFKDENFWMIRGVAVLDPY 360  
 QY 361 PKSIIHTLGFGRVKKIDAAVCDKTRTKYFFVGVIGWCFDEMTQMDKGFQVVKVHPFG 420  
 DB 361 PKSIIHTLGFGRVKKIDAAVCDKTRTKYFFVGVIGWCFDEMTQMDKGFQVVKVHPFG 420  
 QY 421 ISIRVDAAFOYKGRFFFSRSGSKQFBNYKTNITRIMTNTWFOCKEPKNSFFGDIINKE 480  
 DB 421 ISIRVDAAFOYKGRFFFSRSGSKQFBNYKTNITRIMTNTWFOCKEPKNSFFGDIINKE 480  
 QY 481 KAHSGGKILYHKLSLFIPIGIVHLLKNTSIYQ 513  
 DB 481 KAHSGGKILYHKLSLFIPIGIVHLLKNTSIYQ 513

RESULT 13

ADA76142  
 ID ADA76142 standard; protein; 513 AA.

XX ADA76142;

AC ADA76142;

XX 20-NOV-2003 (first entry)

XX Human PRO polypeptide #96.

XX Human; PRO; secreted polypeptide; transmembrane polypeptide;  
 KW tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;  
 KW cancer; adrenal; lung; colon; breast; prostate; kidney; cervix;  
 KW liver; microvascular endothelial cell; glucose; FFA;  
 KW skeletal muscle cell; adipocyte cell; pericyte cell;  
 KW inner ear utricular supporting cell; T-lymphocyte cell;  
 KW endothelial cell tube formation; bone disorder; cartilage disorder;  
 KW sports injury; proteoglycan; articular cartilage defect; osteoarthritis;  
 KW rheumatoid arthritis; haemoglobin-associated disorder thalassaemia;  
 KW immune system cell infiltration.

XX



CC various bone and/or cartilage disorders such as sports injuries and  
CC arthritis. PRO polypeptides which stimulate the release of proteoglycans  
CC from cartilage are useful for treating sports-related joint problems, PRO  
CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO  
CC polypeptides are also useful for treating various mammalian haemoglobin-  
CC associated disorders such as various thalassaemias and conditions which  
CC may benefit from enhanced local immune system cell infiltration. This  
CC sequence represents a human PRO polypeptide of the invention. Note: The  
CC sequence data for this patent is also available in electronic format from  
CC USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
SQ Sequence 513 AA;

Query Match 99.6%; Score 2752; DB 6; Length 513;  
Best Local Similarity 99.8%; Pred. No. 4.1e-261;  
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLCLFFITFSSAPPLVMTNEENMQLAQAYLNQFYSLIEGHNHVSQKNSRLID 60  
Db 1 MKRLLLCLFFITFSSAPPLVMTNEENMQLAQAYLNQFYSLIEGHNHVSQKNSRLID 60  
QY 61 DKIREMAFFGLTVGKLDNLTLEIMKTPRCGVPDVGQYVTLPGWRKYNLTIRINVT 120  
Db 61 DKIREMAFFGLTVGKLDNLTLEIMKTPRCGVPDVGQYVTLPGWRKYNLTIRINVT 120  
QY 121 DMARAANDAEIOEGLEVSKVTPLEKTKISKGIADIMIAFRTRVHGRCPRYEDGLGVLG 180  
Db 121 DMARAANDAEIOEGLEVSKVTPLEKTKISKGIADIMIAFRTRVHGRCPRYEDGLGVLG 180  
QY 181 HAPFPGPLGGTHDEDENWTKDAGFNFLVAAHEFGHALGSHNSNDQTALMFPNYS 240  
Db 181 HAPFPGPLGGTHDEDENWTKDAGFNFLVAAHEFGHALGSHNSNDQTALMFPNYS 240  
QY 241 LDPRKYPISQDDINGIQSIYGLPKVPAPKBPPTIPHACDPDLTDAITTFRRVNFVFKG 300  
Db 241 LDPRKYPISQDDINGIQSIYGLPKVPAPKBPPTIPHACDPDLTDAITTFRRVNFVFKG 300  
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLOAYENPRDKILVFKDENFMIRGYAVLPDY 360  
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLOAYENPRDKILVFKDENFMIRGYAVLPDY 360  
QY 361 PKSIHTLPGPRVKKIDAAVCCKTKTYFFVGIWCRFEDMTQTMKGFPPQVVKHFFPG 420  
Db 361 PKSIHTLPGPRVKKIDAAVCCKTKTYFFVGIWCRFEDMTQTMKGFPPQVVKHFFPG 420  
QY 421 ISIRVDAAFQYKGFPPFSSRGSKQFENYIKNTIRMTNTWFOCKBPQNSFFGFDINKE 480  
Db 421 ISIRVDAAFQYKGFPPFSSRGSKQFENYIKNTIRMTNTWFOCKBPQNSFFGFDINKE 480  
QY 481 KAHSGGIKLYHKSLSLFIFGIVHLLKNTSIYQ 513  
Db 481 KAHSGGIKLYHKSLSLFIFGIVHLLKNTSIYQ 513

RESULT 14

ADA18792  
ID ADA18792 standard; protein; 513 AA.  
XX AC  
XX ADA18792;  
DT DT  
DT 20-NOV-2003 (first entry)  
XX DE  
DE Human PRO polypeptide #96.  
XX KW  
KW Human; PRO; secreted polypeptide; transmembrane polypeptide;  
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; lung;  
KW colon; breast; prostate; rectum; cervix; liver; tumour; cancer;  
KW glucose uptake; FFA; adipocyte cell; pericyte cell; proteoglycan;  
KW cartilage; inner ear utricular supporting cell; cytokine; A-peptide;  
KW factor VIIA; endothelial cell.  
XX OS  
OS Homo sapiens.

PN US2003054517-A1.  
XX 20-MAR-2003.  
XX 08-MAY-2002; 2002US-00141755.  
XX 31-MAR-1997; 97WO-US005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 16-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 29-OCT-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 98WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
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PR 30-NOV-1999; 99WO-US028409.  
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PR 01-DEC-1999; 99WO-US028634.  
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PR 02-DEC-1999; 99WO-US028564.  
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PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
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PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.

PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
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PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
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PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 18-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
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PR 09-JUL-2001; 2001WO-US021735.  
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PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC.

XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX WPI; 2003-521854/49.  
XX N-PSDB; ADA18791.

XX New PRO nucleic acid, useful for preparing a composition for treating  
XX e.g., tumors.

XX Claim 12; Fig 192; 660pp; English.

XX The invention relates to isolated human PRO polypeptides (secreted and  
XX transmembrane polypeptides) and the polynucleotides encoding them. The  
XX invention also relates to an antibody which specifically binds to a PRO  
XX polypeptide, a method for stimulating the release of tumour necrosis  
XX factor-alpha (TNF-alpha) from human blood, a method for stimulating the  
XX proliferation or differentiation of chondrocyte cells and a method for  
XX detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,  
XX prostate, rectal, cervical and liver tumours). The polynucleotides are  
XX useful in molecular biology, including uses as hybridisation probes, in  
XX chromosome and gene mapping, in generating antisense RNA and DNA and in  
XX gene therapy. The polynucleotides may also be used in preparing PRO  
XX polypeptides by recombinant techniques and in generating either  
XX transgenic animals or knock-out animals which are useful in the  
XX development and screening of therapeutically useful reagents. The PRO  
XX polypeptides or antibodies are used in preparing a medicament for  
XX treating a condition responsive to the polypeptides or antibodies, such  
XX as tumours, for modulating the uptake of glucose or FFA by adipocyte  
XX cells, for stimulating the proliferation of or gene expression in  
XX pericyte cells, for stimulating the release of proteoglycans from  
XX cartilage, for stimulating the proliferation of inner ear utricular  
XX supporting cells, for stimulating the release of cytokines from PBMC  
XX cells, for inhibiting the binding of A-peptide to factor VIIA, for  
XX inhibiting the differentiation of adipocyte cells and for stimulating the  
XX proliferation of endothelial cells. This sequence represents a human PRO  
XX polypeptide of the invention. Note: The sequence data for this patent is  
XX also available in electronic format from USPTO at

CC seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 513 AA;  
  
Query Match 99.6%; Score 2752; DB 6; Length 513;  
Best Local Similarity 99.8%; Pred. No. 4.le-261;  
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 MKRLLLCLFFITFSSAPPLVRMTENENMQLAQAYLNQFVSLIEGHNHLVQSKNRSIID 60  
Db 1 MKRLLLCLFFITFSSAPPLVRMTENENMQLAQAYLNQFVSLIEGHNHLVQSKNRSIID 60  
  
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Db 61 DKIREMAFFGLTVTGKLDNLTLEIMKTPRCGVPDVGQYTLPGWKNYNTYRIINVT 120  
  
Qy 121 DMARAAVDEAIQEGLEVMSKVTEPKFTKISGKIADIMIAFRTRVHGRCPRYFDGGLGVLG 180  
Db 121 DMARAAVDEAIQEGLEVMSKVTEPKFTKISGKIADIMIAFRTRVHGRCPRYFDGGLGVLG 180  
  
Qy 181 HAPPGGLGGDTHFDEDENWKDGAGFNILVAAHEFGHALGSHSNDQTALMFPNYS 240  
Db 181 HAPPGGLGGDTHFDEDENWKDGAGFNILVAAHEFGHALGSHSNDQTALMFPNYS 240  
  
Qy 241 LDPKPYLSODDINGIQSIYGGLPKVPAPKPEPTIPHACDPDLTFTDAITTFRRVMEFKG 300  
Db 241 LDPKPYLSODDINGIQSIYGGLPKVPAPKPEPTIPHACDPDLTFTDAITTFRRVMEFKG 300  
  
Qy 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFMWIRGAVILPDY 360  
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFMWIRGAVILPDY 360  
  
Qy 361 PKSHTLGFGRVKKIDAAVCDKTRTKTYFVGIVCWRFDEMTQMDKGFQVRVKKFP 420  
Db 361 PKSHTLGFGRVKKIDAAVCDKTRTKTYFVGIVCWRFDEMTQMDKGFQVRVKKFP 420  
  
Qy 421 ISIRVDAAFQYKGFPPFRSGSKOFENYIKTKNTRMTNTWTFCKEKNSSFGFDINKE 480  
Db 421 ISIRVDAAFQYKGFPPFRSGSKOFENYIKTKNTRMTNTWTFCKEKNSSFGFDINKE 480  
  
Qy 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513  
Db 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513

RESULT 15

ADA61415

ID ADA61415 standard; protein; 513 AA.

XX AC ADA61415;

XX DT 20-NOV-2003 (first entry)

XX DE Homo sapiens.

XX Human; secreted and transmembrane protein; PRO;  
XX Tumour necrosis factor alpha release; TNF-alpha release;  
XX glucose uptake modulator; FFA uptake modulator;  
XX cell proliferation stimulator; cell differentiation stimulator;  
XX cell differentiation inhibitor; cytokine release stimulator; tumour;  
XX lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;  
XX cervical tumour; liver tumour; chromosome mapping; gene mapping;  
XX gene therapy; chromosome identification; chromosome marker.

XX OS Novel.

XX human.

XX OS secreted.

XX and.

XX OS transmembrane.

XX OS protein.

XX PROS992.

XX PN US2003049816-A1.

XX PD 13-MAR-2003.  
 XX PF 15-APR-2002; 2002US-00123262.  
 XX 31-MAR-1997; 97WO-US005230.  
 PR 12-JUN-1998; 98WO-US012456.  
 PR 14-JUL-1998; 98WO-US014552.  
 PR 28-AUG-1998; 98WO-US017888.  
 PR 10-SEP-1998; 98WO-US018824.  
 PR 14-SEP-1998; 98WO-US019093.  
 PR 14-SEP-1998; 98WO-US019177.  
 PR 16-SEP-1998; 98WO-US019330.  
 PR 17-SEP-1998; 98WO-US019437.  
 PR 07-OCT-1998; 98WO-US021141.  
 PR 29-OCT-1998; 98WO-US022991.  
 PR 29-OCT-1998; 98WO-US022992.  
 PR 20-NOV-1998; 98WO-US024855.  
 PR 01-DEC-1998; 98WO-US025108.  
 PR 05-JAN-1999; 98WO-US000106.  
 PR 08-MAR-1999; 98WO-US005028.  
 PR 10-MAR-1999; 98WO-US005190.  
 PR 20-APR-1999; 98WO-US008615.  
 PR 14-MAY-1999; 98WO-US010733.  
 PR 02-JUN-1999; 98WO-US012252.  
 PR 01-SEP-1999; 98WO-US020111.  
 PR 08-SEP-1999; 98WO-US020594.  
 PR 13-SEP-1999; 98WO-US020944.  
 PR 15-SEP-1999; 98WO-US021090.  
 PR 15-SEP-1999; 98WO-US021547.  
 PR 05-OCT-1999; 98WO-US023089.  
 PR 29-NOV-1999; 98WO-US028214.  
 PR 30-NOV-1999; 98WO-US028313.  
 PR 30-NOV-1999; 98WO-US028409.  
 PR 01-DEC-1999; 98WO-US028301.  
 PR 01-DEC-1999; 98WO-US028634.  
 PR 02-DEC-1999; 98WO-US028551.  
 PR 02-DEC-1999; 98WO-US028564.  
 PR 02-DEC-1999; 98WO-US028565.  
 PR 16-DEC-1999; 98WO-US030095.  
 PR 20-DEC-1999; 98WO-US030911.  
 PR 20-DEC-1999; 98WO-US030999.  
 PR 22-DEC-1999; 98WO-US030720.  
 PR 30-DEC-1999; 98WO-US031243.  
 PR 30-DEC-1999; 98WO-US031274.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000277.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 18-FEB-2000; 2000WO-US004342.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 01-MAR-2000; 2000WO-US005601.  
 PR 02-MAR-2000; 2000WO-US005745.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 21-MAR-2000; 2000WO-US007532.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000US-00747259.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PR 28-FEB-2001; 2001US-00796498.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006666.  
 PR 09-MAR-2001; 2001US-00802706.  
 PR 14-MAR-2001; 2001US-00808689.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 05-APR-2001; 2001US-00828366.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 18-MAY-2001; 2001US-00854280.  
 PR 18-MAY-2001; 2001US-00860216.  
 PR 25-MAY-2001; 2001US-00866028.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 25-MAY-2001; 2001WO-US017092.  
 PR 01-JUN-2001; 2001US-00872035.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 05-JUN-2001; 2001US-00874503.  
 PR 14-JUN-2001; 2001US-00882636.  
 PR 19-JUN-2001; 2001US-00886342.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 21-JUN-2001; 2001US-00887879.  
 PR 22-JUN-2001; 2001WO-US020116.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 18-JUL-2001; 2001US-00908827.  
 PR 06-AUG-2001; 2001US-00924419.  
 PR 09-AUG-2001; 2001US-00927796.  
 PR 16-AUG-2001; 2001US-00931836.  
 PR 19-DEC-2001; 2001US-00028072.  
 XX (GETH ) GENENTECH INC.  
 PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WT, Zhang Z;  
 XX WPI: 2003-695892/66.  
 DR N-PSDB; ADA61414.  
 XX  
 PT New PRO nucleic acid and encode polypeptides, are useful for  
 PT manufacturing a medicament for diagnosing or treating cancer.  
 PS Claim 12; Fig 192; 660pp; English.  
 XX  
 CC The invention describes 305 nucleic acids encoding PRO (secreted and  
 CC transmembrane) polypeptides (I). (I) is useful for stimulating the  
 CC release of TNF-alpha from human blood, for modulating the uptake of  
 CC glucose or FFA by skeletal muscle cells or adipocyte cells, for  
 CC stimulating the proliferation or differentiation of chondrocyte cells,  
 CC for stimulating the proliferation of or gene expression in pericyte  
 CC cells, for stimulating the release of proteoglycans from cartilage, for  
 CC stimulating the proliferation of inner ear utricular supporting cells,  
 CC for stimulating the proliferation of T-lymphocyte cells, for stimulating  
 CC the release of a cytokine from PMMC cells, for inhibiting the binding of  
 CC A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte  
 CC cells, for stimulating proliferation of endothelial cells, for detecting  
 CC the presence of tumour in a mammal. The tumour is lung, colon, breast,  
 CC prostate, rectal, cervical or liver tumour. The oligonucleotide probes  
 CC are useful for isolating genomic and cDNA nucleotide sequences or  
 CC antisense probes. (I) is also useful as therapeutic agent. PRO is useful  
 CC in assays to identify other proteins or molecules involved in binding  
 CC interaction. A polynucleotide (II) encoding (I) is useful in chromosome  
 CC and gene mapping, in generation of antisense RNA and DNA, in the  
 CC preparation of PRO polypeptide, for generating transgenic animals or  
 CC knockout animals which in turn are useful in the development and  
 CC screening of therapeutically useful reagents, in gene therapy, for  
 CC chromosome identification, as chromosome marker, and for generating  
 CC probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.  
 CC detecting its expression in specific cells, tissues or serum, and for  
 CC affinity purification of PRO from recombinant cell culture or natural  
 CC sources. (I) and (II) are useful for tissue typing. This is the amino

CC acid sequence of a novel human secreted and transmembrane PRO  
CC polypeptide.

XX  
SQ Sequence 513 AA;

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Query Match          99.6%; Score 2752; DB 6; Length 513;
Best Local Similarity 99.8%; Pred. No. 4.1e-261;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 61 DKIREMQAFGLTGTGKLDNTLEIMKTPCGVPDVGQGYTLPGWKYNLTYRIINYP 120

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Db 181 HAPPPGGLGGDTHFDEDENWKDGAGFNFLVAAHEFGHALGLSHSNDQTALMFPNYS 240

QY 241 LDPKPYLSODDINGIOSIYGGLPKPAKPEPTIPHACDPDLTFDAITTFREVMEFKG 300
   |||||
Db 241 LDPKPYLSODDINGIOSIYGGLPKPAKPEPTIPHACDPDLTFDAITTFREVMEFKG 300

QY 301 RHLWRIYYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360
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Db 301 RHLWRIYYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360

QY 361 PKSHTLTGPPGRVKKIDAAVCDKTRKTYFFVGIWCWRPDEMTOTMDKGFPPQVVKHPPG 420
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QY 421 ISIRVDAAFQYKGFPPFSGSKQPEYNIKTNITRMTNTWFOCKEKPKNSSFGFDINKE 480
   |||||
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QY 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513
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Db 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513
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Search completed: November 15, 2004, 20:59:19  
Job time : 92 secs

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5	1254	42.8	477	3	US-09-521-220-20	Sequence 2
6	1250	42.7	477	3	US-08-448-489-15	Sequence 1
7	1250	42.7	477	3	US-09-391-104-21	Sequence 2
8	1234	42.1	476	3	US-08-704-711A-21	Sequence 2
9	1234	42.1	476	3	US-08-448-489-14	Sequence 1
10	1234	42.1	476	3	US-09-521-220-21	Sequence 2
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Qy 24 ATGAAGCGCCTTCTGCTTCTCTGTTTGTCTTTATAACATTTTCTTCTGCAATTTCCCTTA 83

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QY 84 GTCCGATGAGGAAATGAGAAATATGCAATGCTGCTCAGGATATCTCAACAGTTC 143
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Db 41 TyrSerLeuGluLeuGluGluAsnHisLeuValGlnSerLysAsnArgSerLeuLeuAsp 60
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Db 61 AsplysileArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80
QY 264 AACACCTTGATCATGAAGACACACAGGTGGGTGGCTGATGGGCCAGTATGCC 323
Db 81 AsnThrLeuGluLeuMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100
QY 324 TACACCTCTCCCTGGGTGGAGAAATACAACTTACACCTACAGAAATAAATACTACTCCG 383
Db 101 TyrThrLeuProGlyTyrPargLysTyrAsnLeuThrTyrArgIlelleAsnTyrThrPro 120
QY 384 GATATGCCACGAGCTGTGTGATGAGCTATCCAAAGAGTTTGAAGTGTGGAGCAAA 443
Db 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGlyLeuGluValTyrSerLys 140
QY 444 GTCACTCCACTAAATTCACCAAGATTTCAAGGGATTCAGACATCATGATTCCTTT 503
Db 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160
QY 504 AGGACTCGAGTCCATGTCGGTGCCTGCTATTTTGTATGTCCTCTGGAGTCTGGC 563
Db 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
QY 564 CATGCCCTTCTCTCTGTCGGGTCTGGTGGTGCACACTCATTTTGTATGAGGATGAAAC 623
Db 181 HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
QY 624 TGGACCAAGATGAGCAGGATTCACCTGTTTCTGGCTGCTCATGATTTGGTCAT 683
Db 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
QY 684 GCATCGGGCTCTCTCACTCAATGATCAAAAGCTTGTATGTTCCCAAAATATGCTCC 743
Db 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
QY 744 CTGATCCCAAGAAATACCCACTTCTCAGGATGATATCAATGGAATCCAGTCCATCAT 803
Db 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260
QY 804 GGAGTCTGCTAAGTACCTGCTAAGCCAAAGAACCCACTATACCCCATGCTGTGAC 863
Db 261 GlyGlyLeuProLysValProAlaLysProlsGluProThrIleProHisAlaCysAsp 280
QY 864 CCTGACTTGATTTTGGAGCTATCAACATTTCCGACAGAGTAATCTCTTTAAAGGC 923
Db 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
QY 924 AGGCACCTATGAGGATCTATATGATATCAGGATGTTGATTTGAATTAATTCCTTCA 983
Db 301 ArgHisLeuTyrPargIleTyrTyrAspIleThrAspValGluPheGluLeuAlaSer 320
QY 984 TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAGAACCCAGAGATAAGATT 1043
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QY 1044 CTGGTTTTTAAAGATGAAACTCTTGATGATCAGAGGATATGCTGCTTCCAGATAT 1103
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QY 1104 CCCAAATCCATCATATTAGGTTTCCAGACCTGTCAAGAAATAGATGCAGCCCTC 1163
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QY 1284 ATCAGTATCCGTGTGTGATGCTGCTTCCAGTACAAAGGATTCCTTTTTCAGCCGCTGGA 1343
Db 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
QY 1344 TCAAGCAATTTGAATACAAACATTAAGACAAAGAAATATTATCCCGAATCATGAGAACTAAT 1403
Db 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
QY 1404 ACTTGGTTTCAATGCAAAAGAACCAAAAGACTCTCTCATTTGGTTTGTATATCAACAGGAA 1463
Db 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
QY 1464 AAAGCATTTCAGGAGGCATAAAGATATTGTATCATAGAGTTTAAAGCTTGTATTATTTT 1523
Db 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
QY 1524 GGTATTCTTCTATTTGCTGAAAAACACTTCTATTATCAAA 1562
Db 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513

RESULT 2
US-10-140-002-192
; Sequence 192, Application US/10140002
; Patent No. 6725730
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC59
; CURRENT APPLICATION NUMBER: US/10/140,002
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-002-192

Alignment Scores: 3.08e-303 Length: 513
Pred. No.: 2752.00 Matches: 512
Score: 99.81% Conservative: 0
Percent Similarity: 99.81% Mismatches: 1
Best Local Similarity: 99.81% Indels: 0
Query Match: 93.92% Gaps: 0
DB: 4

US-10-729-807-28 (1-1627) x US-10-140-002-192 (1-513)
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QY 786 GGAATCCAGTCCATCTATGGA-----GGTCTGCTAAGGTACCTGCT 827
Db 258 GlyileGlnSerLeuThrGlyProProAspSerProGluThrProLeuValProThr 277
QY 828 AAG-----CCAAAGAACCCCATATACCCCATGCTGTGACCTGACCTTGACTTTTGAC 881
Db 278 GluProValProGluProGlyThrProAlaAsnCysAspProAlaLeuSerPheAsp 297
QY 882 GCTATCACAACATTCGCGAGAGAGTAATGTTCTTTAAAGCGAGGACCTATGAGAGATC 941
Db 298 AlaValSerThrLeuArgGlyGluileLeullePheLysAspArgHisPheTrpArgLys 317
QY 942 TATTATGATATCACGGATGTGAGTTGTAATTAATTCATCTTGGCCATCTCTGCCA 1001
Db 318 SerLeuArgLysLeuGluProGluLeuHisLeulleSerPheTrpProSerLeuPro 337
QY 1002 GCTGATCTCAAGCTGCATACGAG---AACCCCGACAGATAAGATTCTGTTTAAAGAT 1058
Db 338 SerGlyValAspAlaAlaTyrgluValThrSerLysAspLeuValPheillePheLysGly 357
QY 1059 GAAACTTCTGATGATCAGAGATATGCTGTCTTGGCCAGATATCCCAAATCCATCCAT 1118
Db 358 AsnGlnPheTrpAlaileArgGlyAsnGluValArgAlaGlyTyrgProArgGlyileHis 377
QY 1119 ACATTAGGTTTCCAGGAGCTGTGAAGAAAATAGATGCAGCGCTCTGTGATAGACCACA 1178
Db 378 ThrLeuGlyPheProProThrValArgLysileAspAlaileSerAspLysGluLys 397
QY 1179 AGAAAAACCTACTCTTTTGGGCGATTTTGGTGTGGAGTTTTCATGAATGACCCCAAC 1238
Db 398 AsnLysThrTyrgPheValGluAspLysTyrgPheAspGluLysArgAsnSer 417
QY 1239 ATGGCAAAAGGATTCGCGAGAGAGTGTAAACACTTTCCTGGAATCAGTATCCGTGT 1298
Db 418 MetGluProGlyPheProLysGlnileAlaGluAspPheProGlyileAspSerLysile 437
QY 1299 GATGCTGCTTCCAGTACAAAGGATTTCTTTTTCAGCGCGTGGATCAAGCAATTTGAA 1358
Db 438 AspAlaValPheGluGluPheGlyPhePheTyrgPheThrGlySerSerGlnLeuGlu 457
QY 1359 TACAACATTAAACAAAGAAATATTACCCGAAATCATGAGAACTAATCTTGGTTTCAATGC 1418
Db 458 PheAspProAsnAlaLysLysValThrHisThrLeuLysSerAsnSerTrpLeuAsnCys 477

```

## RESULT 6

```

US-08-448-489-15
; Sequence 15, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 15
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-15

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## Alignment Scores:

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Pred. No.: 1,28e-132 Length: 477
Score: 1250.00 Matches: 246
Percent Similarity: 66.04% Conservative: 71
Best Local Similarity: 51.25% Mismatches: 145

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Query Match: 42.66% Indels: 18
DB: 3 Gaps: 9
US-10-729-807-28 (1-1627) x US-08-448-489-15 (1-477)
QY 24 ATGAAGCGCTTCTGCTTCTGCTTCTTATTAACATTTTCTTCTGATTTCCCTTA 83
Db 1 MetLysSerLeuProLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 20
QY 84 GTCGGATGACGGAATAATGAAGAA---AATATGCAACTGGCTCAGGCATATCTCAACCAG 140
Db 21 AspGlyAlaAlaArgGlyGluAspThrSerMetAsnLeuValGlnLysTyrgLysLeu 40
QY 141 TTCTACTCTTCTGAATAGAGGGAATCATCTTTTAAAGCAAGAAATAGGAGTCTCAT 200
Db 41 TyrgLysLeuLysAspValLysGlnPheValArgLysAspSerGlyProVal 60
QY 201 GATGACAAATTCGGGAATCAAGCATTTTGGATTCACAGTGCAGTACGGAACCTGGAC 260
Db 61 ValLysLysileArgGluMetGlnLysPheLeuGlyLeuGluValThrGlyLysLeu 80
QY 261 TCAAACACCTTGTAGATCATGAAGACACCCAGGTGTGGGTGCTGCTGATGTGGCCAGTAT 320
Db 81 SerAspThrLeuGluValMetArgLysProArgCysGlyValProAspValGlyHisPhe 100
QY 321 GGCTACACCTCCCTGGG-----TGGAGAAAATCAACCTACCTACAGATAATA 371
Db 101 ---ArgThrPheProGlyileProLysTrpArgLysThrHisLeuThrTrpArgLysile 119
QY 372 AACTATCTCCGGATATGACGAGCTGCTGGGATGAGGCTATCCAAAGAGTTTAGAA 431
Db 120 AsnTyrgLysLeuProLysAspAlaValAspSerAlaValGluLysAlaLeuLys 139
QY 432 GTGTGAGCAAGTCACTCCACTAAATTTCAACAAGTTTCAAAGGGATTCGACGATC 491
Db 140 ValTrpGluGluValThrProLeuThrPheSerArgLeuTyrgLysGluAlaAsp 159
QY 492 ATGATTGCTTTAGAGTCTGAGTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 548
Db 160 MetLysSerPheAlaValArgGluHisGly-----AspPheTyrgLysProPheAsp 177
QY 549 TTGGGAGTGTGGCCATGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
Db 178 GlyAsnValLeuAlaHisAlaTyrgLysAlaProGlyProGlyileAsnGlyAspAlaHisPhe 197
QY 609 GATGAGGATGAAACTGGCAAGGATGGAGGAGGATTCACACTTGTCTTCTGCTGCTGCT 668
Db 198 AspAspGluGluTrpThrLysAspThrThrGlyThrAsnLeuPheLeuValAlaAla 217
QY 669 CATGAATTTGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 728
Db 218 HisGluileGlyHisSerLeuGlyLeuPheHisSerAlaAsnThrGluAlaLeuMetTyrg 237
QY 729 CCAATATTATGCTCCCTG---GATCCAGAAATAACCCACTTCTCAGGATGATATCAAT 785
Db 238 ProLeuTyrgLysSerLeuThrAspLeuThrArgPheArgLeuSerGlnAspLysLeu 257
QY 786 GGAATCCAGTCCATCTATGGA-----GGTCTGCTAAGGTACCTGCT 827
Db 258 GlyileGlnSerLeuTyrgLysProProAspSerProGluThrProLeuValProThr 277
QY 828 AAG-----CCAAAGAACCCCATATACCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 881
Db 278 GluProValProGluProGlyThrProAlaAsnCysAspProAlaLeuSerPheAsp 297
QY 882 GCTATCACAACATTCGCGAGAGAGTATGTTCTTTAAAGCGAGGACCTATGAGGATC 941
Db 298 AlaValSerThrLeuArgGlyGluileLeullePheLysAspArgHisPheTrpArgLys 317
QY 942 TATTATGATATCACGGATGTGAGTTTGAATTAATTTGCTTCTTCTGCTGCTGCTGCTGCT 1001
Db 318 SerLeuArgLysLeuGluProGluLeuHisLeulleSerPheTrpProSerLeuPro 337

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QY	1074	ATCAGAGGATATGCTGCTGTCGAGATATCCCAATCCATCCATACATAGTTTCCA	1133
Db	362	IleArgGlyAsnGluValGlnAlaGlyTyrProArgGlyLeuHisThrLeuGlyPhePro	381
QY	1134	GGACGCTGTAAGAAATAGATGAGCGCTGCTGTGATAAGACCAAGAAACCTACTTC	1193
Db	382	ProThrIleArgGlyLeuValAlaValSerAspGlyGluLysThrTyrPhe	401
QY	1194	TTTGTGGCATTTGGTGGAGTTTGATGAATGACCAACCAACCTGGACAAAGATTC	1253
Db	402	PheAlaAlaAspLysTyrTrpArgPheAspGluAsnSerGlnSerMetGluGlnGlyPhe	421
QY	1254	CCGACAGAGTGTAAACACTTCTCTGGAATCAGATCCGCTGTCATGCTGCTTCCAG	1313
Db	422	ProArgLeuIleAlaAspPheProGlyValGluProLysValAspAlaValLeuGln	441
QY	1314	TACAAAGGATTCCTTTTTCAGCGCTGGATCAAGCAATTTGAATACAAATTAAGACA	1373
Db	442	AlaPheGlyPhePheTyrPhePheSerGlySerGlnPheGluPheAspProAsnAla	461
QY	1374	AAGAATATTACCGAATCATGAGAACTAATCTTGGTTCAATGC	1418
Db	462	ArgMetValThrHisIleLeuLysSerAsnSerTrpLeuHisCys	476
RESULT 9			
US-08-448-489-14			
; Sequence 14, Application US/08448489			
; Patent No. 6184022			
; GENERAL INFORMATION:			
; APPLICANT: SEIKI, Motoharu			
; APPLICANT: SATO, Hiroshi			
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR			
; FILE REFERENCE: 55-290P			
; CURRENT APPLICATION NUMBER: US/08/448,489			
; CURRENT FILING DATE: 1995-06-07			
; NUMBER OF SEQ ID NOS: 19			
; SOFTWARE: Patentin Ver. 2.0			
; SEQ ID NO 14			
; LENGTH: 476			
; TYPE: PRT			
; ORGANISM: Unknown			
; FEATURE:			
; OTHER INFORMATION: Description of Unknown Organism: Known Member of			
; OTHER INFORMATION: Matrix Metalloproteinase Family			
US-08-448-489-14			
Alignment Scores:			
Pred. No.:	8,4e-131	Length:	476
Score:	1234.00	Matches:	244
Percent Similarity:	67.58%	Conservative:	77
Best Local Similarity:	51.37%	Mismatches:	136
Query Match:	42.12%	Indels:	18
DB:	3	Gaps:	8
US-10-729-807-28 (1-1627) x US-08-448-489-14 (1-476)			
QY	33	CTTCTGCTTCTGTTGTTGTTCTTTTATAACATTTTCTTGTGCAATTCCTTTAGTCGGGATG	92
Db	7	LeuValLeuLeuCysLeu-----ProValCysSerAlaTyrProLeuSerGlyAla	23
QY	93	ACGGAATATGAAGAA---AATATGCACTGGCTCAGGATATCTCAACAGTCTTCTACTCT	149
Db	24	AlaLysGluAluAspSerAspLysAspLeuAlaGlnGlnTyrLeuGluLysTyrAsn	43
QY	150	CTTGAATATGAGGGAATCATCTTCTTCAAGCAAGAAATAGGAGTCTCATAGATGACAAA	209
Db	44	LeuGluLysAspValLysGlnPhe---ArgArgLysAspSerAsnLeuIleValLysLys	62
QY	210	ATTTCGGGAATGCAAGCAATTTTTCGATGACAGTGTGAGTGGAAACCTGACCTCAACACC	269
Db	63	IleGlnGlyMetGlnLysPheLeuGlyLeuGluValThrGlyLysLeuAspThrAspThr	82



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Db      382 ProThrIleArgLysIleAspAlaIaValSerAspLysGluLysIleThrTyrPhe 401
QY      1194 TTTGTGGGCAATTTGGTCTGGAGGTTTGATGAATGACCCAAACCATGGACAAAGGATTC 1253
Db      402 PheAlaalaAspLysTyrTrpArgPheAspGluAsnSerGlnSerMetGluGlnGlyPhe 421
QY      1254 CCGCAGAGAGTGTAACAACATCTTCTCGGAATCAGTATCCGTTGATGCTGCTTCCAG 1313
Db      422 ProArgLeuIleAlaAspAspPheProGlyValGluProLysValAspAlaValLeuGln 441
QY      1314 TACAAGGATCTCTTTTTCAGCCGGGATCAAGCAATTTGAATCAACATTAAGACA 1373
Db      442 AlaPheGlyPhePheTyrPhePheSerGlySerGlnPheGluPheAspProAsnAla 461
QY      1374 AAGAATATTACCCGAATCATGAGAACTAATACTTGGTTTCAATGC 1418
Db      462 ArgMetValThrHisIleLeuLysSerAsnSerTrpLeuHisCys 476

```

## RESULT 11

US-09-391-104-22

; Sequence 22, Application US/09391104

; Patent No. 639371

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Falduto, Michael T.

; APPLICANT: Magnuson, Scott R.

; APPLICANT: Morgan, Douglas W.

; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,

; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS

; TITLE OF INVENTION: OF USING SAME

; FILE REFERENCE: 6073-US.P1

; CURRENT APPLICATION NUMBER: US/09/391,104

; CURRENT FILING DATE: 1999-09-07

; PRIOR APPLICATION NUMBER: US 08/814,394

; PRIOR FILING DATE: 1997-03-11

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 22

; LENGTH: 476

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-391-104-22

## Alignment Scores:

Pred. No.:	8.4e-131	Length:	476
Score:	1234.00	Matches:	244
Percent Similarity:	67.58%	Conservative:	77
Best Local Similarity:	51.37%	Mismatches:	136
Query Match:	42.12%	Indels:	18
DB:	3	Gaps:	8

US-10-729-807-28 (1-1627) x US-09-391-104-22 (1-476)

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QY      33 CTTCGTCTCTGCTGTTCTTTTATAACATTTCTCTGCATTTCCCTTAGTCCGGATG 92
Db      7 LeuValLeuLeuCysLeu-----ProValCysSerAlaTyrProLeuSerGlyAla 23
QY      93 ACGGAATATGAAGAA---AATATGCAACTGGCTCAGGCATATCTCAACACGATTTACTCT 149
Db      24 AlaLysGluGluAspSerAsnLysAspLeuAlaGlnTyrLeuGluLysTyrTrpAsn 43
QY      150 CTTGAATAGAAGGAATCATCTTCTTCAAGCAGATAGAGTCTCATAGATGACAAA 209
Db      44 LeuGluLysAspValLysGlnPhe---ArgArgLysAspSerAsnLeuIleValLysLys 62
QY      210 ATTGGGAAATGCAAGCAATTTTTCGATTGACAGTGCAGTGGAAAACTGCATCTCAACACC 269
Db      63 IleGlnGlyMetGlnLysPheLeuGlyLeuGluValThrGlyLysLeuAspThrAspThr 82
QY      270 CTTGAGATCATGAAGACACCCAGGTGTGGGTGCTGATGGGGCAGCATATGGGTAC--- 326
Db      83 LeuGluValMetArgLysProArgCysGlyValProAspValGlyHisPheSerSerPhe 102

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QY      327 ---ACCTCCCTGGTGGAGAAATACACCTCACCTACAGAAATAATAAACTATACTCCG 383
Db      103 ProGlyMetProLysTyrArgLysThrHisLeuThrTyrArgIleValAsnTyrThrPro 122
QY      384 GATATGGCAGCAGCTGCTGTGGATGAGGCTATCCAAAGAGTTTAGAGTGTGGAGCAAA 443
Db      123 AspLeuProArgAspAlaValAspSerAlaIleGluLysAlaLeuLysValTrpGluGlu 142
QY      444 GTCATCTCCATAAAATTCACCAAGATTTCAAGGGGATTCAGACATCATCATGATTCCTTT 503
Db      143 ValThrProLeuThrPheSerArgLeuTyrGluGlyAlaAlaAspIleMetIleSerPhe 162
QY      504 AGGACTCGACTCCATCGTGGTCTCTCGCTATTTTGTATGCTCCCTGGGAGTGTCTGGC 563
Db      163 AlaValLysGluHisGlyAspPhe---TyrSerPheAspGlyProGlyHisSerLeuAla 181
QY      564 CATGCCCTTTCTCTCGTCCGGGTCTGGGTGGTGCACACTCATTTTGTAGAGGATGAAAC 623
Db      182 HisAlaTyrProGlyProGlyLeuTyrGlyAspIleHisPheAspAspAspGluLys 201
QY      624 TGGACCAAGATGGAGCAGGATTCAGTCTGTTCTTGTGGCTGCTCATGATTTGGTCAT 683
Db      202 TrpThrGluAspAlaSerGlyThrAsnLeuPheLeuValAlaAlaHisGluLeuGlyHis 221
QY      684 GCATCGGGCTCTCTCACTCCATCAATGATCAACAGCCCTTGATGTTCCTCAAAATTTATGTC 743
Db      222 SerLeuGlyLeuPheHisSerAlaAsnThrGluAlaLeuMetTyrProLeuTyrAsnSer 241
QY      744 CTG---GATCCCAAGAAATACCCACTTTCTCAGATGATATCAATGAATCCAGTCCATC 800
Db      242 PheThrGluLeuAlaGlnPheArgLeuSerGlnAspAspValAsnGlyIleGlnSerLeu 261
QY      801 TATGGAGCTGTGCTAAGGTACCTGCTAAGCCAAAGGAAACCCACT----- 845
Db      262 TyrGlyProProAlaSerThrGluGluProLeuValProThrLysSerValProSer 281
QY      846 -----ATACCCCATGCTGTGACCCCTGACCTTTTGACGCTTATCCAGCTATCACAAC 896
Db      282 GlySerGluMetProAlaLysCysAspProAlaLeuSerPheAspAlaIleSerThrLeu 301
QY      897 CGCAGAGAAGTAATGTTCTTTAAAGGAGGAGCCCTATGAGGAGTCTTATGATATATCAG 956
Db      302 ArgGlyGluTyrLeuPhePheLysAspArgTyrPheTrpArgArgSerHisTrpAsnPro 321
QY      957 GATGTTGAGTTGAATTAATTTGCTTCTTCTGCTGCTATCCAGCTATCCAGCTATCAGCT 1016
Db      322 GluProGluPheHisLeuIleSerAlaPheTrpProSerLeuProSerTyrLeuAspAla 341
QY      1017 GCATACGAG---AACCCCGAGAGATAAGATTTCTGTTTAAAGATGAAAACTTCTGGATG 1073
Db      342 AlaTyrGluValAsnSerArgAspThrValPheIlePheLysGlyAsnGluPheTrpAla 361
QY      1074 ATCAGAGATATGCTGCTTCCAGATATTCCTCAATTCCTCCATCCATACATAGTTAGTTTCCA 1133
Db      362 IleArgGlyAsnGluValGlnAlaGlyTyrProArgGlyIleHisThrLeuGlyPhePro 381
QY      1134 GGACGTGTGAAGAAATAGATGACGACGCTGTGTATAGACCAACAAAGAAAACTTACTTC 1193
Db      382 ProThrIleArgLysIleAspAlaValSerAspLysGluLysLysThrTyrPhe 401
QY      1194 TTTGTGGGCAATTTGGTGTGGAGTTTGATCAAAATGATCCCAACCATGGACAAAGGATTC 1253
Db      402 PheAlaAlaAspLysTyrTrpArgPheAspGluAsnSerGlnSerMetGluGlnGlyPhe 421
QY      1254 CCGCAGAGAGTGTGAACACACTTCTCGATCATGATCCGTGTGTGATGCTGCTTCCAG 1313
Db      422 ProArgLeuIleAlaAspAspPheProGlyValGluProLysValAspAlaValLeuGln 441
QY      1314 TACAAGGATCTCTCTTTTTCAGCCGGTCAAGCAATTTGAATCAACATTAAGACA 1373
Db      442 AlaPheGlyPhePheTyrPhePheSerGlySerGlnPheGluPheAspProAsnAla 461

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; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 467  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-178-002-4

## Alignment Scores:

Pred. No.: 1.63e-122 Length: 467  
Score: 1161.00 Matches: 228  
Percent Similarity: 63.35% Conservative: 71  
Best Local Similarity: 48.31% Mismatches: 157  
Query Match: 39.62% Indels: 16  
DB: 1 Gaps: 8

US-10-729-807-28 (1-1627) x US-09-178-002-4 (1-467)

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QY 24 ATCAAGCGCCTCTGCTCTGTGTTTCTTTTATACATTTTCTCTGCATTTCCCTTA 83
Db 4 LeuLysThrLeuProPheLeuLeuLeuLeuHisValGlnIleSerLysAlaPhePro--- 22
QY 84 GTCGGGATGACGAAATATGCAAAATATGCACTGGCTCAGGCATATCTCAACAGTTC 143
Db 23 -----ValSerSerLysGluLysAsnThrLysThrValGlnAspTyrLeuGluLysPhe 40
QY 144 TACTCTCTTCAATAGAGGGAATCATCTGTTCAAAGCAAGATAGGAGTCTCATAGAT 203
Db 41 TyrGlnLeuProSerAsnGlnTyrGlnSerThrArgLysAsnGlyThrAsnValIleVal 60
QY 204 GACAAATTCGGGAAATCGAAGCAATTTTGGATTGACAGTCACTGGAAATCGACTCA 263
Db 61 GluLysLeuLysGluMetGlnArgPheGlyLeuAsnValThrGlyLysProAsnGlu 80
QY 264 AACACCTTCAGATCATGACACACCCAGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 323
Db 81 GluThrLeuAspMetMetLysLysProArgCysGlyValProAspSerGly-----Gly 98
QY 324 TACACCTC-----CCTGGGTGGAGAAATACACCTCACCTACAGATATA 371
Db 99 PheMetLeuThrProGlyAsnProLysTyrGluArgThrAsnLeuThrTyrArgIleArg 118
QY 372 AACTATCTCCGATATGACAGAGCTGCTGTGATGAGGCTATCCAGAGAGGTTTAA 431
Db 119 AsnTyrThrProGlnLeuSerGluAlaGluValGluArgAlaIleLysAspAlaPheGlu 138
QY 432 GTGFGAGCAAAAGTCATCCCACTAAATTCACCAAGATTTCAAAGGGATTCGACATC 491
Db 139 LeuTrpSerValAlaSerProLeuIlePheThrArgIleSerGlnGlyGluAlaAspIle 158
QY 492 ATGATTCCTTAGGACTCGAGTCCATGGT---CGGTGCTCCTCGCTATTTTGTGGTCCC 548
Db 159 AsnIleAlaPheTyrGlnArgAspHisGlyAspAsnSerPro-----PheAspGlyPro 176
QY 549 TTGGAGTGTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
Db 177 AsnGlyIleLeuAlaHisAlaPheGlnProGlyGlnGlyIleGlyGlyAspAlaHisPhe 196
QY 609 GATGAGATGAAATCGACCAAGATGGAGCAGGATTCACCTGTTTCTTGTGGTGGTCT 668
Db 197 AspAlaGluGluThrTrpThrAsnThrSerAlaAsnTyrAsnLeuPheLeuValAlaAla 216
QY 669 CATGAATTTGGTATGATCGGGCTCTCTCACTCCATGATCAACACAGCCTGATGTC 728
Db 217 HisGluPheGlyHisSerLeuGlyLeuAlaHisSerSerAspProGlyAlaLeuMetTyr 236
QY 729 CCAATATTGTCTCCCTGGATCCCAAGAAATACCACTTTCTCAGGATGATATCAATGGA 788
Db 237 ProAsnTyrAlaPheArgGluThrSerAsnTyrSerLeuProGlnAspIleAspGly 256
QY 789 ATCAGTCCATCTATGAGGTCTGCTTAAAGTACTGCTAAGCCAAAGAAACCCACTATA 848
Db 257 IleGlnAlaIleTyr---GlyLeuSerSerAsnProIleGlnProThrGlyProSerThr 275

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QY 849 CCCCATGCTGTGACCTGACTTGACTTTTGAAGCTATCAAACTTTCCGACAGAGATA 908
Db 276 ProLysProCysAspProSerLeuThrPheAspAlaIleThrThrLeuArgGlyGluIle 295
QY 909 ATGTTCTTTAAAGCGACGACCTATGAGGATCTATTATGATATACAGGATGTGAGTTT 968
Db 296 LeuPhePheLysAspArgTyrPheTrpArgHisProGlnLeuGlnArgValGluMet 315
QY 969 GAATTAATTCCTTCATCTGCGCATCTCTGCGAGCTGATCGAAGCTGCATACGAGAAC 1028
Db 316 AsnPheIleSerLeuPheTrpProSerLeuProThrGlyIleGlnAlaIleTyrGluAsp 335
QY 1029 ---CCGACAGATAGATTTCTGTTTAAAGATGAAAACTTCTGGATGATCAGAGGATAT 1085
Db 336 PheAspArgAspLeuIlePheLeuPheLysGlyAsnGlnTyrTrpAlaLeuSerGlyTyr 355
QY 1086 GCTGTCTGTCGACGATATCCAAATCCATCCATACATAGTTTTCAGACGCTGTGAAG 1145
Db 356 AspIleLeuGlnGlyTyrProLysAspIleSerAsnTyrGlyPheProSerSerValGln 375
QY 1146 AAATAGATGACGCGTCTGTGATAGACCAAGCAAAACCTTCTTTTGTGGGCATT 1205
Db 376 AlaIleAspAlaAlaValPheTyrArgSer-----LysThrTyrPhePheValAsnAsp 393
QY 1206 TCGTGTGCGAGGTTTGTATGAATGACCCAAACCATGACAAAGGATTCCCGCAGAGAGTG 1265
Db 394 GlnPheTrpArgTyrAspAsnGlnArgGlnPheMetGluProGlyTyrProLysSerIle 413
QY 1266 GTAACACATTTCTCGAATCAGTATCCGTGTGTGATGCTCTTTCAGTACAAAGGATTC 1325
Db 414 SerGlyAlaPheProGlyIleGluSerLysValAspAlaValPheGlnGlnGluHisPhe 433
QY 1326 TTCTTTTTCAGCGTGGATCAAGCAATTTGAATACAACTTAAGACAAAGAAATATTACC 1385
Db 434 PheHisValPheSerGlyProArgTyrTyrAlaPheAspLeuIleAlaGlnArgValThr 453
QY 1386 CGAATCATGAGAACTAATCTGTTTCAATGCAAA 1421
Db 454 ArgValAlaArgGlyAsnLysTrpLeuAsnCysArg 465

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## RESULT 14

US-09-391-104-24  
; Sequence 24, Application US/09391104  
; Patent No. 6399371  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Falduto, Michael T.  
; APPLICANT: Magnuson, Scott R.  
; APPLICANT: Morgan, Douglas W.  
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE.  
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS  
; TITLE OF INVENTION: OF USING SAME  
; FILE REFERENCE: 6073-US.P1  
; CURRENT APPLICATION NUMBER: US/09/391,104  
; CURRENT FILING DATE: 1999-09-07  
; PRIOR APPLICATION NUMBER: US 08/814,394  
; PRIOR FILING DATE: 1997-03-11  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 24  
; LENGTH: 467  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-391-104-24

Alignment Scores:  
Pred. No.: 1.63e-122 Length: 467  
Score: 1161.00 Matches: 228  
Percent Similarity: 63.35% Conservative: 71  
Best Local Similarity: 48.31% Mismatches: 157  
Query Match: 39.62% Indels: 16  
DB: 1 Gaps: 8



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4 LeuLysThrLeuProPheLeuLeuLeuLeuHisValGlnSerLysAlaPhePro--- 22
QY 84 GTCGGATGACGGAATAAGAAATATATCACTGGCTCAGGCATATCTCAACCAAGTTC 143
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
23 -----ValSerSerLysGluLysAsnThrLysThrValGlnAspTyrLeuGluLysPhe 40
QY 144 TACTCTCTGAATAGAGGAATCACTTGTGTTCAAGCAAGAAATAGGAGTCTCATAGAT 203
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QY 204 GACAAATTCGGAAATGCAAGCATTTTGGATGACAGTCACTGCAAACTGGACTCA 263
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61 GluLysLeuLysGlnMetGlnArgPhePheGlyLeuAsnValThrGlyLysProAsnGlu 80
QY 264 AACACCTTGTAGATCATGAGACACCCAGGTGTGGGGTGCCTGATGTGGGCCAGTATGGC 323
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
81 GluThrLeuAspMetLysLysProArgCysGlyValProAspSerGly-----Gly 98
QY 324 TACACCTC-----CTGGGTGAGAAATACAACTCACTACCTACAGAAATATA 371
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QY 372 AACTATCTCCGATATGACAGCTGCTGCGATGAGCTATCCAGNAGGTATTAGAA 431
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139 LeuTyrSerValAlaSerProLeuIlePheThrArgIleSerGlnGlyGluAlaAspIle 158
QY 492 ATGATTCCTTTAGGACTGAGTCCATGTT---CGGTGCTCCGCTATTTTGTGCTGCT 548
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159 AsnIleAlaPheTyrGlnArgAspHisGlyAspAsnSerPro-----PheAspGlyPro 176
QY 549 TTGGGAGTCTTGGCCATCCTTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
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177 AsnGlyIleLeuAlaHisAlaPheGlnProGlyGlnGlyIleGlyAspAlaHisPhe 196
QY 609 GATGAGTGAATAAAGTGGACCAAGGATGAGCAGGATTCACCTGTTCTTCTGCTGCTGCT 668
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197 AspAlaGluGluThrTrpThrAsnThrSerAlaAsnTyrAsnLeuPheLeuValAlaAla 216
QY 669 CATGATTTGGTATGACATGCGGCTCTCTCACTCCATGATCAACACCGCTGATGTC 728
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
217 HisGluPheGlyHisSerLeuGlyLeuAlaHisSerSerAspProGlyAlaLeuMetTyr 236
QY 729 CCAAAATTATGTCCTCCCTGGATCCAGAAATACCCACTTCTCAGGATGATATCAATGGA 788
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237 ProAsnTyrAlaPheArgGluThrSerAsnTyrSerLeuProGlnAspAspIleAspGly 256
QY 789 ATCCAGTCCATCTATGAGGCTGCTGCTAGGTACCTGCTTAAGCCAAAGCAACCCACTATA 848
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
257 IleGlnAlaIleTyr---GlyLeuSerSerAsnProIleGlnProThrGlyProSerThr 275
QY 849 CCCATGCTGTGACCTGATCTGATCTTTGACGTATCACTCAACACTTTCCGACAGAAAGTA 908
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QY 909 ATGTTCTTTAAAGGACGACCATGAGGAGTCTATTATGATATCAGGATGTTGAGTTT 968
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
296 LeuPhePheLysAspArgTyrPheTrpArgHisProGlnLeuGlnArgValGluMet 315
QY 969 GAATTAATTGCTTCTTGGCCATCTCTGCGAGCTGATCTCAAGCTGCATPACGAGAAC 1028
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
316 AsnPheIleSerLeuPheTrpProSerLeuProThrGlyIleGlnAlaIleTyrGluAsp 335
QY 1029 ---CCAGAGATAAGTCTGTTTTTAAAGATGAAACTTCTGATGATCAGAGATAT 1085
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
336 PheAspArgAspLeuPheLeuPheLysGlyAsnGlnTyrTrpAlaLeuSerGlyTyr 355
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Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
394 GlnPheTrpArgTyrAspAsnGlnArgGlnPheMetGluProGlyTyrProLysSerIle 413
QY 1266 GTAAACACCTTCTCTGGAATCAGTCCGTGTTGATGCTGCTTCCAGTACAAAGATTC 1325
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
414 SerGlyAlaPheProGlyIleGluSerLysValAspAlaValPheGlnGlnHisPhe 433
QY 1326 TTCTTTTTCAGCGCTGATCAAGCAATTGATACAAATTAAGCAAAAGAAATATATACC 1385
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
434 PheHisValPheSerGlyProArgTyrTyrAlaPheAspLeuIleAlaGlnArgValThr 453
QY 1386 CGAATCATGAGAACTAATCTGTTTCAATGCAAA 1421
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
454 ArgValAlaArgGlyAsnLysTrpLeuAsnCysArg 465

RESULT 15
US-08-448-489-13
; Sequence 13, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: X = UNKNOWN
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-13

Alignment Scores:
Pred. No.: 1.63e-122 Length: 468
Score: 1161.00 Matches: 228
Percent Similarity: 63.35% Conservative: 71
Best Local Similarity: 48.31% Mismatches: 157
Query Match: 39.62% Indels: 16
DB: 3 Gaps: 8

US-10-729-807-28 (1-1627) x US-08-448-489-13 (1-468)
QY 24 ATGAGCGCCTTCTGCTTCTGTTGTTTCTTTATAACATTTTCTTCTGCAATTCCTTCA 83
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
4 LeuLysThrLeuProPheLeuLeuLeuLeuHisValGlnSerLysAlaPhePro--- 22
QY 84 GTCGGATGACGGAATAAGAAATATGCAAAATATGCAACTGGCTCAGGCATATCTCAACCAAGTTC 143
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99 PheMetLeuThrProGlyAsnProLysTrpGluArgThrAsnLeuThrTyrArgIleArg 118
QY 372 AACTATCTCCGATATGACAGCTGCTGCGATGAGCTATCCAGNAGGTATTAGAA 431
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139 LeuTyrSerValAlaSerProLeuIlePheThrArgIleSerGlnGlyGluAlaAspIle 158
QY 492 ATGATTCCTTTAGGACTGAGTCCATGTT---CGGTGCTCCGCTATTTTGTGCTGCT 548
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159 AsnIleAlaPheTyrGlnArgAspHisGlyAspAsnSerPro-----PheAspGlyPro 176
QY 549 TTGGGAGTCTTGGCCATCCTTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 608
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177 AsnGlyIleLeuAlaHisAlaPheGlnProGlyGlnGlyIleGlyAspAlaHisPhe 196
QY 609 GATGAGTGAATAAAGTGGACCAAGGATGAGCAGGATTCACCTGTTCTTCTGCTGCTGCT 668
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197 AspAlaGluGluThrTrpThrAsnThrSerAlaAsnTyrAsnLeuPheLeuValAlaAla 216
QY 669 CATGATTTGGTATGACATGCGGCTCTCTCACTCCATGATCAACACCGCTGATGTC 728
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
217 HisGluPheGlyHisSerLeuGlyLeuAlaHisSerSerAspProGlyAlaLeuMetTyr 236
QY 729 CCAAAATTATGTCCTCCCTGGATCCAGAAATACCCACTTCTCAGGATGATATCAATGGA 788
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237 ProAsnTyrAlaPheArgGluThrSerAsnTyrSerLeuProGlnAspAspIleAspGly 256
QY 789 ATCCAGTCCATCTATGAGGCTGCTGCTAGGTACCTGCTTAAGCCAAAGCAACCCACTATA 848
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257 IleGlnAlaIleTyr---GlyLeuSerSerAsnProIleGlnProThrGlyProSerThr 275
QY 849 CCCATGCTGTGACCTGATCTGATCTTTGACGTATCACTCAACACTTTCCGACAGAAAGTA 908
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276 ProLysProCysAspProSerLeuThrPheAspAlaIleThrThrLeuArgGlyGluIle 295
QY 909 ATGTTCTTTAAAGGACGACCATGAGGAGTCTATTATGATATCAGGATGTTGAGTTT 968
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296 LeuPhePheLysAspArgTyrPheTrpArgHisProGlnLeuGlnArgValGluMet 315
QY 969 GAATTAATTGCTTCTTGGCCATCTCTGCGAGCTGATCTCAAGCTGCATPACGAGAAC 1028
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316 AsnPheIleSerLeuPheTrpProSerLeuProThrGlyIleGlnAlaIleTyrGluAsp 335
QY 1029 ---CCAGAGATAAGTCTGTTTTTAAAGATGAAACTTCTGATGATCAGAGATAT 1085
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
336 PheAspArgAspLeuPheLeuPheLysGlyAsnGlnTyrTrpAlaLeuSerGlyTyr 355
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414 SerGlyAlaPheProGlyIleGluSerLysValAspAlaValPheGlnGlnGluHisPhe 433  
1326 TTCTTTTCAGCGTGGATCAAGCAATTTGAATACAACTTAAGACAAAGAAATATTACC 1385  
434 PheHisValPheSerGlyProArgTyrTyrAlaPheAspLeuIleAlaGlnArgValThr 453  
1386 CGAATCATGAGAACTAATACTTGTGTTTCAATGCAAA 1421  
454 ArgValAlaArgGlyAsnLysTyrLeuAsnCysArg 465

Search completed: November 15, 2004, 20:33:26  
Job time : 50 secs

61 GluLysLeuLysGluMetGlnArgPhePheGlyLeuAsnValThrGlyLysProAsnGlu 80  
264 AACACCTTCAGATCATGAAGACACCCAGGTGTGGGTGCTGATGGGCCAGTATGCC 323  
81 GluThrLeuAspMetMetLysLysProArgCysGlyValProAspSerGly-----Gly 98  
324 TACACCTC-----CCTGGGTGGAGAAATACACCTCACCTACAGTATATA 371  
99 PheMetLeuThrProGlyAsnProLysTrpGluArgThrAsnLeuThrTyrArgIleArg 118  
372 AACTATATCCGGATATGGACGAGTCTGTGATCAGGTATCCCAAGAGGTTTGAAG 431  
119 AsnTyrThrProGlnLeuSerGluAlaGluValGluArgAlaIleLysAspAlaPheGlu 138  
432 GTGTGGAGCAAGTCACTCCACTAAATTCACCAAGATTTCAAGGGGATGTCAGATC 491  
139 LeuTrpSerValAlaSerProLeuIlePheThrArgIleSerGlnGlyGluAlaAspIle 158  
492 ATGATTCCTTAGGACTCGAGTCCATGGT---CGGTGCTCTCGCTATTGTGATGTC 548  
159 AsnIleAlaPheTyrGlnArgAspHisGlyAspAsnSerPro-----PheAspGlyPro 176  
549 TTGGAGTGTCTGCCATGCTTCTCTCTGGTCCGGTCTGGGTGGTGCACACTATTT 608  
177 AsnGlyIleLeuAlaHisAlaPheGlnProGlyGlnGlyIleGlyAspAlaHisPhe 196  
609 GATGAGATGAAACCTGGACCAAGGATGAGCAGGATTCACCTTGTGTTCTTGTGGTCT 668  
197 AspAlaGluThrTrpThrAsnThrSerAlaAsnTyrAsnLeuPheLeuValAlaAla 216  
669 CATGAATTTGCTGACTGCTGGGCTCTCTCACTCAATGATCAACAGCCCTTGATGTC 728  
217 HisGluPheGlyHisSerLeuGlyLeuAlaHisSerAspProGlyAlaLeuMetTyr 236  
729 CCAATATTATGCTCCCTGGATCCCAAGAAATACCCACTTCTCAGGATGATATCAATGA 788  
237 ProAsnTyrAlaPheArgGluThrSerAsnTyrSerLeuProGlnAspAspIleAspGly 256  
789 ATCCAGTCCATCTATGGAGTCTGCTTAAGTACTCTGTAAGCCCAAGGAAACCCACTATA 848  
257 IleGlnAlaIleTyr--GlyLeuSerSerAsnProIleGlnProThrGlyProSerThr 275  
849 CCCATGCTGTGACCTGACTTGCCTTTGACGCTATCACAACCTTCCGCGAGAGAGTA 908  
276 ProLysProCysAspProSerLeuThrPheAspAlaIleThrThrLeuArgGlyGluIle 295  
909 ATGTTCTTTAAGGCGAGCAGCTATGGAGGATCTATTATGATATCAGCGATGTTGAGTT 968  
296 LeuPhePheLysAspArgTyrPheTrpArgHisProGlnLeuGlnArgValGluMet 315  
969 GAATTAATTTGCTCATTTGCGCATCTCTGCGAGCTGATTCGCAAGCTGCATCAGAGAAC 1028  
316 AsnPheIleSerLeuPheThrProSerLeuProThrGlyIleGlnAlaAlaTyrGluAsp 335  
1029 ---CCCAGATAGATTTCTGTTTAAAGATGAAACTTCTGATGATCAGAGGATAT 1085  
336 PheAspArgAspLeuIlePheLeuPheLysGlyAsnGlnTyrTrpAlaLeuSerGlyTyr 355  
1086 GCTGCTTCCAGATATCCCAATCCATACATAGGTTTCCAGGAGCTGTGAAG 1145  
356 AspIleLeuGlnGlyTyrProLysAspIleSerAsnTyrGlyPheProSerValGln 375  
1146 AAATAGATGAGCGCTGCTGATAGACCAAGAAACCTACTTCTTTGTGGCAT 1205  
376 AlaIleAspAlaAlaValPheTyrArgSer-----LysThrTyrPhePheValAsnAsp 393  
1206 TGGTCTGGAGTTTGGAAATGACCCAAACCATGGACAAAGGATTCGCCGAGAGATG 1265  
394 GlnPheTrpArgTyrAspAsnGlnArgGlnPheMetGluProGlyTyrProLysSerIle 413  
1266 GTAAACACTTCTCCGGATCAGTATCCGTGTTGATGCTGCTTCCAGTACAAAGATTC 1325

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: November 15, 2004, 16:35:24 ; Search time 128 Seconds

(without alignments)  
9119.571 Million cell updates/sec

Title: US-10-729-807-28

Perfect score: 2930

Sequence: 1 gcttcagctgaagaagaga.....aattcgttcaaaatagaa 1627

Scoring table:

	BLOSUM62	Xgapop 10.0	Xgapext 0.5
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-DB=A_Geneseq 23Sep04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEXT=0			
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15			
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000			
-USER=US10729807 @CGN 1.1.127 @runat 15112004.131150.14678 -NCPU=6 -ICPU=3			
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPHLOCK=100 -LONGLOG			
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6			
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7			

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 4004546

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlh  
-Q/-cgn2.1/USPTO spool/US10729807/runat 15112004.131150.14678/app\_query.fasta\_1.1799  
-DB=A\_Geneseq 23Sep04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPEXT=0  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10729807 @CGN 1.1.127 @runat 15112004.131150.14678 -NCPU=6 -ICPU=3  
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPHLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

	A_Geneseq 23Sep04:*
1:	Geneseqp1980s:*
2:	Geneseqp1990s:*
3:	Geneseqp2000s:*
4:	Geneseqp2001s:*
5:	Geneseqp2002s:*
6:	Geneseqp2003as:*
7:	Geneseqp2003bs:*
8:	Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2763	94.3	513	3	AAE14392 Human mat
3	2752	93.9	513	4	AAU12267 Human PRO
4	2752	93.9	513	4	AAU00469 Human TAN
5	2752	93.9	513	6	ABO17711 Novel hum
6	2752	93.9	513	6	ABU0965 Human PRO
7	2752	93.9	513	6	ABU6665 Human PRO
8	2752	93.9	513	6	ABO32578 Secreted
9	2752	93.9	513	6	ABU59746 Novel sec
10	2752	93.9	513	6	ABO24936 Human sec

11	2752	93.9	513	6	ABU66941	Human sec
12	2752	93.9	513	6	ADA45711	Novel hum
13	2752	93.9	513	6	ADA76142	Human PRO
14	2752	93.9	513	6	ADA18792	Human PRO
15	2752	93.9	513	6	ADA61415	Homo sapi
16	2752	93.9	513	6	ADB19200	Novel hum
17	2752	93.9	513	6	ADB27741	Human PRO
18	2752	93.9	513	6	ADA86220	Novel hum
19	2752	93.9	513	6	ADA15784	Human PRO
20	2752	93.9	513	6	ADA47570	Human PRO
21	2752	93.9	513	6	ADA67365	Human PRO
22	2752	93.9	513	6	ADB30372	Human PRO
23	2752	93.9	513	6	ADA85668	Novel hum
24	2752	93.9	513	6	ADA96880	Human PRO
25	2752	93.9	513	6	ADA79184	Human PRO
26	2752	93.9	513	6	ADA87323	Novel hum
27	2752	93.9	513	6	ADB16525	Human PRO
28	2752	93.9	513	6	ADA91617	Novel hum
29	2752	93.9	513	6	ADB14680	Human PRO
30	2752	93.9	513	6	ADB18641	Novel hum
31	2752	93.9	513	6	ADA93856	Human PRO
32	2752	93.9	513	6	ADB19752	Novel hum
33	2752	93.9	513	6	ADB13064	Human PRO
34	2752	93.9	513	6	ABO43244	Novel hum
35	2752	93.9	513	6	ADA74318	Human PRO
36	2752	93.9	513	6	ADB24551	Human PRO
37	2752	93.9	513	6	ADA82075	Human PRO
38	2752	93.9	513	6	ADA75038	Human PRO
39	2752	93.9	513	6	ADA85116	Novel hum
40	2752	93.9	513	6	ADA84564	Novel hum
41	2752	93.9	513	6	ADB29820	Human PRO
42	2752	93.9	513	6	ADA80348	Human PRO
43	2752	93.9	513	6	ADA75590	Human PRO
44	2752	93.9	513	6	ADA46815	Human PRO
45	2752	93.9	513	6	ADB25111	Human PRO

#### ALIGNMENTS

RESULT 1

AA90293

ID AAY90293 standard; protein; 513 AA.

XX AAY90293;

AC AAY90293;

XX 24-OCT-2000 (first entry)

XX Human peptidase, HPEP-10 protein sequence.

DE Human peptidase, HPEP-10 protein sequence.

XX Human; peptidase; cell proliferative disorder; arteriosclerosis;

KW psoriasis; myelofibrosis; cancer; autoimmune disorder; Crohn's disease;

KW inflammatory disorder; AIDS; anaemia; allergy; asthma; atherosclerosis;

KW Grave's disease; multiple sclerosis; scleroderma; infection; diabetes;

KW metabolic disorder; Addison's disease; cystic fibrosis; diagnosis;

KW glycogen storage disease; obesity; therapy; HPEP-10.

XX Homo sapiens.

OS Homo sapiens.

XX WO200042201-A2.

XX 20-JUL-2000.

XX 11-JAN-2000; 2000WO-US000641.

XX 11-JAN-1999; 99US-0172247P.

PR 03-MAY-1999; 99US-0132253P.

XX 27-MAY-1999; 99US-0136653P.

XX (INCY-) INCYTE PHARM INC.

PA Bandman O, Hillman JL, Tang YT, Azimzai Y, Baughn MR, Lal P;

XX PI Yue H, Lu DM;

XX

WPI: 2000-482832/42.  
N-PSDB; AAA37666.

An isolated polypeptide for diagnosis, prevention and treatment of cell proliferative, autoimmune/ inflammatory and metabolic disorders comprises a sequence encoding a human peptidase.

Claim 2; Page 100-101; 131pp; English.

This sequence represents a human peptidase, designated HPEP-10. The invention relates to 18 human peptidases designated HPEP-1 to HPEP-18, respectively. The peptidases can be used for treating a disease or condition associated with decreased expression or over expression of functional human peptidases. The diseases that can be diagnosed, prevented and treated include cell proliferative disorders (such as arteriosclerosis, psoriasis, myelofibrosis, and cancers), autoimmune/inflammatory disorders (such as AIDS, anaemia, allergies, Crohn's disease, asthma, atherosclerosis, Grave's disease, multiple sclerosis, and scleroderma), infections, and metabolic disorders (such as Addison's disease, diabetes, cystic fibrosis, glycogen storage diseases and obesity)

Sequence 513 AA;

```

Alignment Scores:
Pred. No.:      4.13e-286
Score:          2763.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match:    94.30%
DB:             3
Length:        513
Matches:       513
Conservative:  0
Mismatch:      0
Indels:        0
Gaps:          0
US-10-729-807-28 (1-1627) X AAY90293 (1-513)

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Tue Nov 16 16:10:28 2004

us-10-729-807-28.1ag

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Db      381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400
QY      1224 GAAATGACCAACCAACATGACAAAGGATCCCGCAGAGATGGTAAACACATTTCCTGGA 1283
Db      401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420
QY      1284 ATCAGTATCCGTTGTCATGCTGCTTCCAGTACAAAGGATTCCTTTTCAGCCGTGGA 1343
Db      421 IISerIleArgValAspAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440
QY      1344 TCAAGCAATTTGAATACACATTAACACAAAGATATTAATCCGAAATCATGAGAACTAAT 1403
Db      441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460
QY      1404 ACTTGGTTTCAATGCAAAAGAACCAAAAGAACTCTCATTTGGTTTGTATCAACAGGAA 1463
Db      461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480
QY      1464 AAAGCAATTCAGAGGACATAAGATATTTGATCATAGAGTTTAAGCTTGTATTTT 1523
Db      481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500
QY      1524 GATATCTTTCATTTGCTGAAACACATCTCTATTATCAAA 1562
Db      501 GlyIleValHisLeuLeuLysAsnThrSerIleLysGln 513
RESULT 3
AAU12267
ID AAU12267 standard; protein; 513 AA.
XX
AC AAU12267;
XX
DT 24-OCT-2001 (first entry)
XX
DE Human PRO5992 polypeptide sequence.
XX
KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
KW A-peptide; factor VIIA; gene therapy.
XX
OS Homo sapiens.
PN WO200140466-A2.
XX
PD 07-JUN-2001.
XX
PF 01-DEC-2000; 2000WO-US032678.
XX
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030091.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-018720P.
PR 10-MAR-2000; 2000WO-US006319.
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PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US02328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
XX
PA (GETH ) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2001-408281/43.
DR N-PSDB; AAS21339.
XX
PT Isolated , secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing PRO
PT polypeptides, and detect the presence of mammalian tumors e.g. lung,
PT breast, prostate, cervical.
XX
PS Claim 12; Fig 192; 813pp; English.
XX
CC AAU12172-AAU12446 represent novel human secretory and transmembrane PRO
CC polypeptides. The PRO polypeptides are useful to detect other PRO
CC polypeptides, to link bioactive molecules to cells expressing PRO
CC polypeptides, to modulate biological activities of cells expressing PRO
CC polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample. Some
CC of the 275 sequences are also useful to stimulate the release of tumour
CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or
CC differentiation of chondrocytes, the proliferation or gene expression in
CC pericyte cells, the release of proteoglycans from cartilage, the
CC proliferation of inner ear utricular supporting cells or of T-
CC lymphocytes, the release of a cytokine from peripheral blood monocytes
CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO
CC polypeptides may modulate glucose or free fatty acid uptake by skeletal
CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor
CC VIIA. The PRO polypeptides can be used in assays to identify molecules
CC involved in binding interactions. The polynucleotides encoding PRO
CC polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy
XX
SQ Sequence 513 AA;
XX
Alignment Scores:
Pred. No.: 6,23e-285 Length: 513
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 93.92% Indels: 0
DB: 4 Gaps: 0
XX
US-10-729-807-28 (1-1627) x AAU12267 (1-513)
QY 24 ATGAGCGCCTTCTGCTTCTGTTGTTTATTAACATTTCTTCTGATTTCCCTTA 83
Db 1 MetLysArgLeuLeuLeuPheLeuPheLeuPheLeuPheLeuPheLeuPheLeuPheLeu 20
QY 84 GTCCGATGACGAAATGAGAAATATGCAACTGGCTGGCTATCTCAACAGTTC 143
Db 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
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QY	144	TACTCTTTGAAATAGAGGAATCATCTTGTTCAGAGCAAGAAATAGGAGTCTCATAGAT	203	Db	401	GlutMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly	420
Db	41	TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp	60	QY	1284	ATCAGTATCCGTGTTGATGCTGTTTCCAGTACAAAGAGGATTCTCTTTTTCAGCCGTGGA	1343
QY	204	GACAAATTCGGGAATGCAAGCATTTTGTGGATTCAGAGTACTGGAAAACTGGACTCA	263	Db	421	IleSerIleArgValAspAlaPheGlnTyrLysGlyPhePhePheSerArgGly	440
Db	61	AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer	80	QY	1344	TCAAACCAATTGCAATACAACTAAGACAAAGAATATTACCCGAATCATGAGAATTAAT	1403
QY	264	AACACCTTTGAGATCATGAAGACACCCAGTGTGGGTGCTCATGTGGCCAGTAGTGC	323	Db	441	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
Db	81	AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100	QY	1404	ACTTGTTTCAATGCAAGAACCAAGAACTCTCATTTGGTTTTCATATCAACAGGAA	1463
QY	324	TACACCTCCCTGGGTGGAGAAATACAACCTCACCTACAGATAATAAATACTATCTCG	383	Db	461	ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu	480
Db	101	TyrThrLeuProGlyTrpArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro	120	QY	1464	AAAGCACATTCAGGAGGCATAAAGATATTGTATCATATAAGATTAAAGCTTGTTATTTT	1523
QY	384	GATATGCGCAGGAGCTGCTGTGATGAGGCTATCCAAAGAAGTTTGAAGTGTGGACAAA	443	Db	481	LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPhePhe	500
Db	121	AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys	140	QY	1524	GGTATTGTTCAATTGCTGTAAGAAACATCTTCTATTATCAAA	1562
QY	444	GTCACTCCACTAAATTCACCAAGATTTCAAAGGGATTTCACACATCATGATTCCTTT	503	Db	501	GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln	513
Db	141	ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe	160	RESULT 4			
QY	504	AGGACTCGAGTCCATGTCGTGTCCTCGCTATTTTGTGTCCTTGGAGTGTGCTTGC	563	ID	AAU00469		
Db	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180	XX	AAU00469 standard; protein; 513 AA.		
QY	564	CATGCTTTCCTTCCTGCTCGGTGCTGGGTGTGAGTGTGACACTCATTTTGTGATGAAAC	623	AC	AAU00469;		
Db	181	HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn	200	DT	04-JUL-2001 (first entry)		
QY	624	TGGACCAAGATGGAGCAGGATTCAACTGTTTCTTGTGCTGCTCATGAATTTGGTCA	683	DE	Human TANGO 210 protein.		
Db	201	TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis	220	XX	Human; TANGO 210; clone jthke034a06; TANGO 364; TANGO 366; INTERCEPT 394;		
QY	684	GCATGGGGCTCTCTCACTCCAATGATCAACAGCCTTGATGTTCCCAATTTATGTCCTC	743	KW	INTERCEPT 400; TANGO 405; cellular process regulator; gene therapy;		
Db	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240	KW	MMP-8; matrix metalloproteinase-8; proteinase activity; gene therapy;		
QY	744	CTGGATCCAGAAATACCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT	803	KW	extracellular matrix; kidney disorder; bone marrow disorder;		
Db	241	LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr	260	XX	skin disorder; vascular hypertension; metastatic cancer.		
QY	804	GGAGTCTGCTTAAGTACTCTAAGCCAAAGAACCCACTATACCCCATGCTGTCAC	863	OS	Homo sapiens.		
Db	261	GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp	280	XX	Key	Location/Qualifiers	
QY	864	CCTGACTTGACTTTTGACGCTATCAAACTTTCCGAGAGAGTAAATGTTCTTTAAAGGC	923	FT	Peptide	1..17	
Db	281	ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly	300	FT	/label= Signal peptide	/note= "Specifically claimed"	
QY	924	AGGCACCTATGAGGATCTATTATGATATCAGGATGTGATTTGAATTAATGCTTCA	983	FT	Protein	18..513	
Db	301	ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer	320	FT	/label= Mature TANGO 210 protein	/note= "Specifically claimed"	
QY	984	TTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACGAGAACCCAGAGATAAGATT	1043	FT	Domain	18..498	
Db	321	PheTrpProSerLeuProAlaAspLeuGlnAlaIatyrGluAsnProArgAspLysIle	340	FT	/note= "Optionally in alternative form #1 this domain is extracellular or in alternative form #2 this domain is intracellular. Specifically claimed"		
QY	1044	CTGTTTTTAAAGATGAAACTTCTGGATGATCAGAGATATGCTGCTTCCGAGATTAT	1103	FT	Domain	489..506	
Db	341	LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr	360	FT	/label= Transmembrane domain	/note= "Specifically claimed"	
QY	1104	CCCAATCCATCATATAGTTTTCAGAGCTGTGAAAGAAATAGATGCAAGCCCTC	1163	FT	Domain	507..513	
Db	361	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal	380	FT	/note= "Optionally in alternative form #1 this domain is intracellular or in alternative form #2 this domain is extracellular. Specifically claimed"		
QY	1164	TGTGATAGACACCAAGAAAACCTACTTCTTGTGGCATTTGCTGCTGAGGTTTGTAT	1223	XX	WO200118016-A1.		
Db	381	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp	400	XX	15-MAR-2001.		
QY	1224	GAAATGACCAACCATGGAACAAAGGATTCCCGCAGAGAGTGGTAAACACTTTCTCTGGA	1283	XX	30-JUN-2000; 2000WO-US018174.		
				XX	10-SEP-1999; 99US-00393996.		
				XX	(MILL-) MILLENNIUM PHARM INC.		
				XX	Fraser CC, Sharp JD, Wrighton N, Myers PS, Goodearl ADJ;		
				XX	WPI; 2001-183280/18.		



DR N-PSDB; AAB01367.  
XX Isolated nucleic acid molecules encoding proteins useful as modulating  
PT agents in regulating a variety of cellular processes are used for  
PT treating e.g. cancer and autoimmune disorders.  
XX  
PS Claim 9; Fig 1A-1D; 326pp; English.  
XX  
CC The present sequence representing human TANGO 210 protein is isolated  
CC from cDNA clone jtk034a06 from a human foetal skin cDNA library. It is  
CC 1 of 6 novel human proteins which include TANGO 364 (AAU00471), TANGO 366  
CC (AAU00472), INTERCEPT 394 (AAU00473), INTERCEPT 400 (AAU00476) and TANGO  
CC 405 (AAU00479). Novel sequences for murine TANGO 210 (AAU00470),  
CC INTERCEPT 400 (AAU00477), TANGO 405 (AAU00480) and a rat INTERCEPT 400  
CC (AAU00478) sequence are also described. The nucleic acids encoding these  
CC novel proteins are useful as modulating agents in regulating a variety of  
CC cellular processes and can be used to express the proteins in a host cell  
CC in gene therapy applications. Human TANGO 210 shows sequence homology to  
CC human MMP-8 (matrix metalloproteinase-8). TANGO 210 exhibits proteinase  
CC activity used to degrade one or more proteinaceous components of the  
CC extracellular matrix and can be used to prevent, diagnose or treat  
CC kidney, bone marrow or skin disorders e.g. vascular hypertension, acute  
CC renal failure and metastatic cancers. Note: This sequence has residues  
CC 309-513 missing in the sequence ID listing but the complete sequence is  
CC found in Fig1A-1D  
XX  
SQ Sequence 513 AA;  
  
Alignment Scores:  
Pred. No.: 6,23e-285 Length: 513  
Score: 2752.00 Matches: 512  
Percent Similarity: 99.81% Conservatives: 0  
Best Local Similarity: 99.81% Mismatches: 1  
Query Match: 93.92% Indels: 0  
DB: 4 Gaps: 0  
  
US-10-729-807-28 (1-1627) x AAU00469 (1-513)  
QY 24 ATGAAGCGCTTCTGCTCTGCTGCTGCTTCTTATAACATTTCTTCTGATTCCTTTA 83  
Db 1 MetLysArgLeuLeuLeuLeuPhePhePhePhePhePhePhePhePhePhePhePhe 20  
QY 84 GTCGGGATGCGGAAATGAGAAATATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 143  
Db 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40  
QY 144 TACTCTCTCAATAGAGGGAATCATCTTGTTCAAAGCAAGATAGGAGTCTCATAGAT 203  
Db 41 TyrSerLeuGluLeuGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuLeuLeu 60  
QY 204 GACAAATTCGGAAATGCAAGCATTTTGGATTGACAGTGACTGGAAGAACTGACTCA 263  
Db 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
QY 264 AACACCTTGAGATCATGACACACACCGAGTGTGGGTGCTGATGTGGGCGAGTATGGC 323  
Db 81 AsnThrLeuGluLeuMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
QY 324 TACACCTTCCCTGGGTGAGAAATACAACTTCCACCTACAGAAATAAATACTACTCCG 383  
Db 101 TyrThrLeuProGlyTyrPargLysTyrAsnLeuThrTyrArgIleAsnTyrThrPro 120  
QY 384 GATATGGACGAGTCTGTGGATGAGGCTATCCAGAGGTTGAGAGTGTAGAGTGGAGCAA 443  
Db 121 AspMetAlaArgAlaAlaValAspGluAlaLeuGlnGluGlyLeuGluValTyrSerLys 140  
QY 444 GTCACCTCCACTAAATTCACCAAGATTTCAAAGGGGATTGACAGATCATCATGATGCC 503  
Db 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160  
QY 504 AGGACTCGAGTCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 563  
Db 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180

QY 564 CATGCTCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 623  
Db 181 HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200  
QY 624 TGGACCAAGGATGGAGCAGGATTCAACTTGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 683  
Db 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220  
QY 684 GCACTGGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 743  
Db 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240  
QY 744 CTGGATCCCAAGAAATACCCACTTCTCTGAGGATGATCAATGGAATCCAGTCCATCTAT 803  
Db 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260  
QY 804 GGAGGTCCTCCTAAGTACTGCTAAGCCAAAGAACCCACTATACCCATGCTGCTGCTGCTGCT 863  
Db 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280  
QY 864 CTTGACTTGAATCTTTCAGCTATCAACTTTCCGAGAGAGTAAATGTTCTTTAAAGGC 923  
Db 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300  
QY 924 AGGCACCTATGGAGGATCTATTATGATATCACCGATGTTGAGTTTCAATTAATTGCTTCA 983  
Db 301 ArgHisLeuTrpArgIleTyrIleThrAspValGluPheGluLeuIleAlaSer 320  
QY 984 TTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1043  
Db 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340  
QY 1044 CTGCTTTTAAAGATGAAATCTCTGATGATCAGAGGATATCTGCTGCTGCTGCTGCTGCTGCT 1103  
Db 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360  
QY 1104 CCCAAATCCATCATCATATTAGTGTTCAGGACGCTGTGAAGAAATAGATGACGCGCTC 1163  
Db 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380  
QY 1164 TGTGATAAGACCAACAGAAACCTACTTCTTGTGGGCAATTTGGTCTGAGGCTTTGAT 1223  
Db 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400  
QY 1224 GAAATGACCCCAACCAATGGAAGGATTCCTGAGAGAGTGGTAAACACATTTCTCTGGA 1283  
Db 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420  
QY 1284 ATCAGTATCCGTGTGTGCTGCTTCTCCAGTACAAAGGATTCCTTCTTCTGAGCGGTGGA 1343  
Db 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePhePheSerArgGly 440  
QY 1344 TCAAGCAATTTGAATACCAATTAACAGAAATATTATCCCAATCATGAGAACTAAT 1403  
Db 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460  
QY 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCTCTTCTTGTGTTTGTATATCAACAGAA 1463  
Db 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480  
QY 1464 AAAGCACAATTCAGGAGGCATAAAGATATTGTATCATAGAGTTTAAGCTTGTATTATTTT 1523  
Db 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500  
QY 1524 GGTATTGTTCTGCTGAAACACCTCTTATTTATCAA 1562  
Db 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513  
RESULT 5  
AB017711 standard; protein; 513 AA.  
ID AB017711  
XX



AC ABO17711;  
 XX  
 DT  
 XX 26-AUG-2003 (first entry)  
 DE  
 XX Novel human secreted and transmembrane protein PRO5992.  
 XX  
 KW Human; secreted and transmembrane protein; PRO; anti-inflammatory;  
 KW antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic;  
 KW antidiabetic; gene therapy; tumour necrosis factor (TNF)-alpha release;  
 KW TNF-alpha release; cell proliferation; cell differentiation;  
 KW gene expression modulator; proteoglycan release; cytokine release;  
 KW tumour; inflammatory disease; organ failure; atherosclerosis;  
 KW cardiac injury; infertility; birth defect; premature aging; AIDS;  
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;  
 KW chromosome mapping; gene mapping; pharmaceutical; diagnostic; biosensor;  
 KW bio-reactor; tissue typing.  
 XX  
 XX Homo sapiens.  
 OS  
 XX US2003032156-A1.  
 PN  
 XX 13-FEB-2003.  
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 XX  
 XX 06-MAY-2002; 2002US-00140474.  
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 XX 31-MAR-1997; 97WO-US005230.  
 PR 12-JUN-1998; 98WO-US012456.  
 PR 14-JUL-1998; 98WO-US014552.  
 PR 28-AUG-1998; 98WO-US017888.  
 PR 10-SEP-1998; 98WO-US018824.  
 PR 14-SEP-1998; 98WO-US019093.  
 PR 14-SEP-1998; 98WO-US019177.  
 PR 16-SEP-1998; 98WO-US019330.  
 PR 17-SEP-1998; 98WO-US019437.  
 PR 07-OCT-1998; 98WO-US021141.  
 PR 29-OCT-1998; 98WO-US022991.  
 PR 29-OCT-1998; 98WO-US022992.  
 PR 20-NOV-1998; 98WO-US024855.  
 PR 01-DEC-1998; 98WO-US025108.  
 PR 05-JAN-1999; 98WO-US000106.  
 PR 08-MAR-1999; 98WO-US005028.  
 PR 10-MAR-1999; 98WO-US005190.  
 PR 20-APR-1999; 98WO-US008615.  
 PR 14-MAY-1999; 98WO-US010733.  
 PR 02-JUN-1999; 98WO-US012252.  
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 PR 08-SEP-1999; 98WO-US020594.  
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 PR 30-NOV-1999; 98WO-US028409.  
 PR 01-DEC-1999; 98WO-US028301.  
 PR 01-DEC-1999; 98WO-US028634.  
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 PR 16-DEC-1999; 98WO-US030095.  
 PR 20-DEC-1999; 98WO-US030911.  
 PR 20-DEC-1999; 98WO-US030999.  
 PR 22-DEC-1999; 98WO-US030720.  
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 PR 30-DEC-1999; 98WO-US031274.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000277.  
 PR 06-JAN-2000; 2000WO-US003376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 18-FEB-2000; 2000WO-US004342.  
 PR 22-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US004914.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 01-MAR-2000; 2000WO-US005601.  
 PR 02-MAR-2000; 2000WO-US005746.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 21-MAR-2000; 2000WO-US007532.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US020331.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000US-00747259.  
 PR 20-DEC-2000; 2000WO-US034956.  
 PR 28-FEB-2001; 2001US-00796498.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US006656.  
 PR 14-MAR-2001; 2001US-00802706.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 05-APR-2001; 2001US-00828366.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 18-MAY-2001; 2001US-00860216.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 25-MAY-2001; 2001WO-US017092.  
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 PR 01-JUN-2001; 2001WO-US017800.  
 PR 05-JUN-2001; 2001US-00874503.  
 PR 14-JUN-2001; 2001US-00882636.  
 PR 19-JUN-2001; 2001US-00886342.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 21-JUN-2001; 2001US-00887879.  
 PR 22-JUN-2001; 2001WO-US020116.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 18-JUL-2001; 2001US-00908827.  
 PR 06-AUG-2001; 2001US-00924419.  
 PR 09-AUG-2001; 2001US-00927796.  
 PR 16-AUG-2001; 2001US-00931836.  
 PR 19-DEC-2001; 2001US-00028072.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerisken ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX  
 DR WPI; 2003-341980/32.  
 DR N-PSDB; ACD23948.  
 XX  
 PT New secreted and transmembrane PRO nucleic acids, for treating  
 PT inflammation, organ failure, atherosclerosis, cardiac injury,  
 PT infertility, birth defects, premature aging, acquired immunodeficiency  
 PT syndrome (AIDS), or cancer.  
 XX  
 PS Claim 12; Fig 192; 660pp; English.  
 XX  
 CC The invention describes an isolated nucleic acid (I) comprising, or which  
 CC has 80 % sequence identity to, or the full-length coding sequence of, one  
 CC of 275 nucleotide sequences, and which encodes a corresponding  
 CC polypeptide selected from 275 amino acid sequences, where all sequences  
 CC are given in the specification. The polypeptide encoded by (I) is used to

CC detect PRO polypeptides, link a bioactive molecule to a cell expressing a  
 CC PRO polypeptide, modulate a biological activity of a cell, stimulate the  
 CC release of tumour necrosis factor (TNF)-alpha from human blood, modulate  
 CC the uptake of glucose or free fatty acid by cells, stimulate or inhibit  
 CC the proliferation or differentiation of cells or gene expression,  
 CC stimulate the release of proteoglycans, stimulate the release of cytokine  
 CC from peripheral blood mononuclear cells, inhibit the binding of A-peptide  
 CC to factor VIIA, or detect the presence of tumour in a mammal. The nucleic  
 CC acid and polypeptide encoded by it, are useful for treating inflammatory  
 CC diseases, organ failure, atherosclerosis, cardiac injury, infertility,  
 CC birth defects, premature aging, acquired immunodeficiency syndrome  
 CC (AIDS), cancer, or diabetic complications. The nucleic acid is useful as  
 CC hybridisation probes, in chromosome and gene mapping, and in generating  
 CC antisense RNA or DNA. The polypeptides are useful as pharmaceuticals,  
 CC diagnostics, biosensors or bioreactors. Both are useful in tissue typing.  
 CC This is the amino acid sequence of a novel human secreted and  
 CC transmembrane PRO polypeptide  
 CC  
 XX Sequence 513 AA;

SQ

Alignment Scores:  
 Pred. No.: 6,23e-285 Length: 513  
 Score: 2752.00 Matches: 512  
 Percent Similarity: 99.81% Conservative: 0  
 Best Local Similarity: 99.81% Mismatches: 1  
 Query Match: 93.92% Indels: 0  
 DB: 6 Gaps: 0

US-10-729-807-28 (1-1627) x AB017711 (1-513)

QY	24	ATGAAGCGCTCTGCTCTGCTGCTGCTCTTATACATTTCTCTGCTGCTTCCCTTA	83
DB	1	MetLysArgLeuLeuLeuLeuPheLeuPhePheLeuPheSerAlaPheProLeu	20
QY	84	GTCGGATGACGAAATGAAGAAATATGCAATGGCTCAGGCATATCTCAACAGTTC	143
DB	21	ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe	40
QY	144	TACTCTCTGAAATAGAGGAATCATCTGTTTCAAGCAAGAAATAGAGTCTCATAGAT	203
DB	41	TyrSerLeuGluLeuGluGluAsnHisLeuValGlnSerLysAsnArgSerLeuLeuAsp	60
QY	204	GACAAATTCGGGAATGCAAGCATTTTGGATTGACAGTGCAGTGGAAACTCGACTCA	263
DB	61	AspLysileArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer	80
QY	264	AACACCTCTGAGATCATGAACACACCCAGGTGTGGGTGCTGATGTGGCCAGTATGCC	323
DB	81	AsnThrLeuGluLeuMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100
QY	324	TACACCTCTCGGTGGAGAAATATACACCTCCTACAGAAATATTAAGTCTACTCCG	383
DB	101	TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgLysLeuAsnTyrThrPro	120
QY	384	GATATGCAAGCATGCTGTGGATGAGGCTATCCAAAGAGTGTAGAGTGTGGAGCAA	443
DB	121	AspMetAlaArgAlaAlaValAspGluAlaGlnGlnGluGlyLeuGluValTrpSerLys	140
QY	444	GTCACCTCACATAAATTCACCAAGATTTCAAGGGGATTCAGACATCATGATTCCTTT	503
DB	141	ValThrProLeuLysPheThrLysileSerLysGlyLeuAlaAspMetLeuAlaPhe	160
QY	504	AGGACTGAGTCCATGTCGGTGTGCTGCTATTTGATGTCCTGGGAGTGTGCTGGC	563
DB	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180
QY	564	CATGCTTTCTCTGTCGGGTCTGGTGTGACACTCATTTTGTGAGGATGAAAC	623
DB	181	HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn	200
QY	624	TGGACCAAGATGGACGAGGATTCACCTGTTCTGCTGCTCATGAATTTGGTCAAT	683
DB	201	TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis	220

QY	684	GCACCTGGGCTCTCTCACCTCAATGATCAAAAGCCTTGATGTTCCCAATATGCTCC	743
DB	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
QY	744	CTGGATCCCAAGAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT	803
DB	241	LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr	260
QY	804	GGAGGTCTGCCTAAGTACTGCTAAGCAACCAAGAACCCACTATACCCATGCTGAC	863
DB	261	GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp	280
QY	864	CCTGACTTCGCTTTTTCAGCGCTATCACAACTTTCCGACAGAGAAGTATGTTCTTTAAAGGC	923
DB	281	ProAspLeuThrPheAspAlaIleThrPheArgArgGluValMetPhePheLysGly	300
QY	924	AGGCACCTATGGAGGATCTATTATGATATACACGATGTTGAGTTGAATTAATGCTTCA	983
DB	301	ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer	320
QY	984	TTCTGGCCATCTCTGCGCAGCTGATCTGCAAGTGCATACGAGAACCCAGAGATAAGATT	1043
DB	321	PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle	340
QY	1044	CTGGTTTAAAGATGAAACTTCTCGATGATCAGAGGATATGCTGTTCTTCCAGATTAT	1103
DB	341	LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr	360
QY	1104	CCCAATCCATCCATCATATTAGTGTTCAGGACGCTGGAAGAAATAGATGCGCCGCTC	1163
DB	361	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal	380
QY	1164	TGTGATAGACCAAGAAAACCTACTCTTGTGGGCATTTGGTCTCGAGGTTTGAT	1223
DB	381	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp	400
QY	1224	GAATGACCCCAACCCATGGACAAAGGATTCGCCAGAGAGTGGTAAACACTTTCTCTGGA	1283
DB	401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly	420
QY	1284	ATCAGTATCCGTGTGATGCTGCTTCCAGTACAAAGGATTTCTTTTTCAGCCGTGGA	1343
DB	421	IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly	440
QY	1344	TCAAAGCAATTTGATACACATTTAAGCAAGAAATATTACCCGAATCATGAGAACTAAT	1403
DB	441	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
QY	1404	ACTTGGTTTCAATGCAAGAACCAAGAACTCTCTCATTTGGTTTGTATATCAACAAGAA	1463
DB	461	ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu	480
QY	1464	AAAGCAATTCAGAGGAGCATTAAGATATTGTATCATAGAGTTTAAGCTGTTTATTTT	1523
DB	481	LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe	500
QY	1524	GGTATTGTTCTGCTGAAACACACTTCTATTATCAA	1562
DB	501	GlyIleValHisLeuLeuLysAsnThrSerIleIleTyrGln	513

RESULT 6

ABU80965  
 ID ABU80965 standard; protein; 513 AA.

AC ABU80965;

DT 23-JUN-2003 (first entry)

XX Human PRO polypeptide #96.

XX Human; PRO polypeptide; secreted and transmembrane protein;  
 KW anti-PRO antibody; diagnostic assay; gene expression; diabetes;



QY	24	ATGAGAGCGCTTCTCTGCTCTCTGTTGTTCTTTATAACATATTTCTTCTGCAATTCCTCCCTTA	83
Db	1	MetLysArgLeuLeuLeuPheLeuPhePheIleThrPheSerSerAlaPheProLeu	20
QY	84	GTCGCGATGACGGAAAATGAAGAAAATATGCAACTGGCTCAGGCGATATCTCAACAGATTC	143
Db	21	ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe	40
QY	144	TACTCTCTTGAATATAGAAGGGAATCATCTTGTTCAAAGCAGAAATAGGAGTCTCATAGAT	203
Db	41	TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuLeuLeuLeu	60
QY	204	GACAAAATTCGGGAAATCGACAGCATTTTTCGATTGACAGTCAGTCAGTGGAAAACTGACATCA	263
Db	61	AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer	80
QY	264	AACACCTTGAAGATCATGAAGACACCCAGGTGTGGGTGCCCTGATGTGGGCGAGATGGC	323
Db	81	AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100
QY	324	TACACCTTCCCTGGGTGGAGAAAATACAACTCAGTCACAGATAATAAACTATACTCCG	383
Db	101	TyrThrLeuProGlyTyrPargLysTyrAsnLeuThrTyrArgIleAsnTyrThrPro	120
QY	384	GATATGGACAGAGCTGCTCGATCAGAGCTATCCAAAGAGGTTTAGAAGTGGAGCAAA	443
Db	121	AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys	140
QY	444	GTCACTCCACTAAAATTCCACAAAGATTTCAAAGGGGATTGCACAGCATCATGATCCCTTT	503
Db	141	ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe	160
QY	504	AGGACTCGAGTCCATGTCGGTGTCTCTCGCTATTTTGTATGGTCCCTTGGGAGTGCTTGGC	563
Db	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180
QY	564	CATGCTTTCTCTCTGTCGGGTCTGGGTGTGACACTCATTTTGTAGCAGCATGAAAC	623
Db	181	HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn	200
QY	624	TGGACCAAGATGGAGCAGGATTCAACTTGTTCCTGTGGCTGCTCATGAATTTGGTCAAT	683
Db	201	TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis	220
QY	684	GCACCTGGGGCTCTCTCACTCCAATCATCAAACAGCCTTCATGCTTCCCAATATATCTCTCC	743
Db	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
QY	744	CTGGATCCGACAAAATACCCACTTTCTCAGGATGATATCAATGGGAATCCAGTCCATCTAT	803
Db	241	LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr	260
QY	804	GGAGTGTCCCTTAAGGTACCTGCTAAGCAAGGAACCCACTATATCCCCCATGCTGTGAC	863
Db	261	GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp	280
QY	864	CCTGACTTGACTTTTGAGCTATCAACACTTTCCGACAGAGAGTATGTTCTTTAAAGGC	923
Db	281	ProAspLeuThrPheAspAlaIleThrThrPheArgGluValMetPhePheLysGly	300
QY	924	AGGCGACTATGGAGGATCTATTATGATATCACCGGATGTTGAGTTTCAATTAATTTGCTTCA	983

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PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
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PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
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PR 13-SEP-1999; 98WO-US020944.
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PR 02-DEC-1999; 98WO-US028551.
PR 02-DEC-1999; 98WO-US028564.
PR 16-DEC-1999; 98WO-US028565.
PR 16-DEC-1999; 98WO-US030095.
PR 20-DEC-1999; 98WO-US030911.
PR 20-DEC-1999; 98WO-US030999.
PR 22-DEC-1999; 98WO-US030720.
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PR 30-DEC-1999; 98WO-US031274.
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PR 18-FEB-2000; 2000WO-US004341.
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PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
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PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US0074259.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-008660216.
PR 25-MAY-2001; 2001US-00866028.

PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PU, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-332040/31.
XX N-PSDB; ACA03698.
XX
XX New secreted and transmembrane PRO nucleic acids, useful for gene
PT therapy, in chromosome and gene mapping, as chromosome markers, in tissue
PT typing, and in chromosome identification.
XX
XX Claim 12; Fig 192; 660pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides are useful for detecting other PRO polypeptides, for linking
CC bioactive molecules to cells expressing PRO polypeptides, for modulating
CC biological activities of cells expressing PRO polypeptides, and for
CC identifying agonists or antagonists. The PRO polypeptides are useful for
CC for stimulating the release of tumour necrosis factor (TNF)-alpha from
CC human blood, for stimulating the proliferation or differentiation of
CC chondrocytes, and detecting the presence of tumours. The polynucleotide
CC sequences encoding PRO polypeptides are useful as hybridisation probes,
CC in chromosome and gene mapping, in the generation of antisense RNA and
CC DNA, in the preparation of PRO polypeptides, for generating transgenic
CC animals or knockout animals, for the genetic analysis of individuals with
CC genetic disorders, and in gene therapy. ABU66570-ABU66844 represent the
CC human PRO polypeptides of the invention. Note: The sequence data for this
CC patent was obtained in electronic format directly from the USPTO web site
XX at seqdata.uspto.gov/psipspIDEntry.html
XX
XX Sequence 513 AA;
SQ
Alignment Scores:
Pred. No.: 6 23e-285 Length: 513
Score: 2752.00 Matches: 512
Percent Similarity: 99.81% Conservative: 0
Best Local Similarity: 99.81% Mismatches: 1
Query Match: 93.92% Indels: 0
DB: 6 Gaps: 0
US-10-729-807-28 (1-1627) x ABU66665 (1-513)
QY 24 ATGAAGCGCTTCTGCTTCTGTTTGTCTTTATACATTTTCTGCAATTCCTTCA 83
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QY 84 GTCCGGATCAGGAAATGAAGAAATATGCAATGGCTGCTAGGCATATCTCAACAGTTC 143
Db 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40
QY 144 TACTCTCTTGAATAGAAGGAATCATCTTGTTCAAAGCAGAGATAGGAGTCTCATAGAT 203

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Db	401	GlumMetThrGlnThrMetAspLysGlyPheProGlnArgValVallLysHisPheProGly	420
Qy	1284	ATCAGTATCCGTTGATGCTGCTTTCCAGTACAAAGGATCTCTCTTTTCAGCCGFGGA	1343
Db	421	IleSerIleArgValAspAlaIlePheGlnTyrLysGlyPhePhePheSerArgGly	440
Qy	1344	TCAAGCAATTTGAATACACATATAGACAAAGAATATTACCCGAATCATGAGAACTAAT	1403
Db	441	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
Qy	1404	ACTTGGTTTCAATGCAAGAACCAAGAACTCTCATTTTGGTTTGTATATCAACAAGGAA	1463
Db	461	ThrTrpPheGlnCysLysGluProLysAsnSerPheGlyPheAspIleAsnLysGlu	480
Qy	1464	AAAGCACATTTCAGGAGGCATAAAGATATTGTATCATAGAAGTTTAAAGCTTTGTTATTTT	1523
Db	481	LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe	500
Qy	1524	GGTATTGTTCAATTGCTGTAATAAACACTTCTATTATCAA	1562
Db	501	GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln	513
RESULT 8			
ABO32578	standard; protein; 513 AA.		
ID	ABO32578		
XX	ABO32578;		
AC	(first entry)		
XX	17-SEP-2003		
DT	Secreted polypeptide-related protein #40.		
DE	Human; TANGO; INTERCEPT; secreted polypeptide; immune disorder;		
XX	hormonal disorder; proliferative disorder; cancer; thyroid disorder;		
KW	diabetes; multiple sclerosis; lupus; neurological disorder; anaemia;		
KW	Alzheimer's disease; Parkinson's disease; cardiovascular disorder;		
KW	myocardial infarction; congestive heart disease; blood platelet disorder;		
KW	thrombocytopenia; blood vessel; atherosclerosis; vasculitis.		
XX	Homo sapiens.		
OS	US2003022279-A1.		
XX	30-JAN-2003.		
PF	12-JAN-2001; 2001US-00759130.		
XX	14-JUN-1999; 99US-00333159.		
PR	29-JUN-1999; 99US-00342364.		
PR	10-SEP-1999; 99US-00393996.		
PR	19-OCT-1999; 99US-00420707.		
PR	07-JAN-2000; 2000US-00479249.		
PR	27-APR-2000; 2000US-00559497.		
PR	24-MAY-2000; 2000US-00578063.		
PR	16-JUN-2000; 2000US-00596194.		
PR	23-JUN-2000; 2000US-00602871.		
XX	30-JUN-2000; 2000US-00608452.		
XX	(FRAS/) FRASER C C.		
PA	(BARN/) BARNES T M.		
PA	(SHAR/) SHARP J D.		
PA	(KIRS/) KIRST S J.		
PA	(MYER/) MYERS P S.		
PA	(LEIB/) LEIBY K R.		
PA	(HOLT/) HOLTZMAN D A.		
PA	(MCCA/) MCCARTHY S A.		
PA	(WRIG/) WRIGHTON N.		
PA	(MACK/) MACKAY C R.		
PA	(GOOD/) GOODEARL A D J.		
XX	Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;		
PI	Holtzman DA, Mccarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;		
XX			

DR WPI: 2003-456230/43.  
 XX N-PSDB; ACD66739, ACD66740.  
 PT New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,  
 PT TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or  
 PT treating disorders such as cancer, diabetes or atherosclerosis, and in  
 PT forensic biology.  
 XX  
 PS Claim 9; Fig 15A-15D; 482pp; English.  
 XX  
 CC The invention relates to secreted polypeptide-related proteins and  
 CC nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The  
 CC nucleic acids, proteins and antibodies specific to the proteins are  
 CC useful in screening assays, predictive medicine (e.g. diagnostic assays,  
 CC prognostic assays, monitoring clinical trials and pharmacogenetics) and  
 CC prophylactic and therapeutic methods. The sequences are used in  
 CC diagnosing, preventing or treating proliferative disorders (e.g.  
 CC cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune  
 CC disorders (e.g. multiple sclerosis or lupus), neurological disorders  
 CC (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular  
 CC disorders (e.g. myocardial infarction or congestive heart disease), blood  
 CC platelet disorders (e.g. thrombocytopenia or anaemia) and disorders  
 CC involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic  
 CC acids may also be used in chromosome mapping, tissue typing and forensic  
 CC biology, and as surrogate markers. This sequence represents a secreted  
 CC polypeptide-related protein of the invention. Note: The sequence data for  
 CC this patent was obtained in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html  
 XX  
 SQ Sequence 513 AA;

Alignment Scores:  
 Pred. No.: 6,23e-285 Length: 513  
 Score: 2752.00 Matches: 512  
 Percent Similarity: 99.81% Conservative: 0  
 Best Local Similarity: 99.81% Mismatches: 1  
 Query Match: 93.92% Indels: 0  
 DB: 6 Gaps: 0

US-10-729-807-28 (1-1627) x ABO32578 (1-513)

QY 24 ATGAAGCGCTTCTGCTCTGTTTGTGTTTATTAACATTTTCTTCTGCAATTTCCCTTA 83  
 DB 1 MetLysArgLeuLeuLeuLeuPheLeuPhePheLeuThrPheSerSerAlaPheProLeu 20  
 QY 84 GTCGGGATGACGGAATCAAGAAATATGCACTGGCTCAGGCATATCTCAACAGTTC 143  
 DB 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40  
 QY 144 TACTCTCTGAAATAGAAGGAATCATCTTGTTCAAAGCAAGATAGGAGTCTCATAGAT 203  
 DB 41 TyrSerLeuGluLeuGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuLeuLeu 60  
 QY 204 GACAAATTCGGAAATGCAACATTTTGTGATTGACAGTCACTGGAAATCTGACATCA 263  
 DB 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
 QY 264 AACACCTTGAGATCATGNAGACACCCAGGTGTGGGTCCCTGATGTGGCCAGATGGC 323  
 DB 81 AsnThrLeuGluLeuMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
 QY 324 TACACCTCTCCCTGGGTGGGAAATACAACTCACCCTACAGATAATTAACATATACTCCG 383  
 DB 101 TyrThrLeuProGlyTyrPheArgLysTyrAsnLeuThrTyrArgIleLeuAsnTyrThrPro 120  
 QY 384 GATATGGCAGCGCTGCTGTGATGAGGCTATCCAAAGAGGTTTGAAGTGTGGAGCAAA 443  
 DB 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140  
 QY 444 GTCACCTCCACATAAATTCACCAAGATTTCAAGGGGATGGAGACATCATGATTCGCTTT 503  
 DB 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160

QY 504 AGGACTCGAGTCCATGGTGGTGTCTCGCTATTTTGTAGTGTCCCTTGGAGTGGCTTGGC 563  
 DB 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180  
 QY 564 CATGCCCTTCTCTCGTCCGGGTCTGGGTGTGGTGTGACACTCATTTTGTAGTGGATGAAAC 623  
 DB 181 HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200  
 QY 624 TGGACCAAGATGGAGCAGGATCAACTTGTCTTGTGGCTCTCATGAATTTGTGTCAT 683  
 DB 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaHisGluPheGlyHis 220  
 QY 684 GCACTGGGCTCTCTCACTCCCAATGATCAACAGCCTGTGATGTTCCCAATATGTCCTCC 743  
 DB 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240  
 QY 744 CTGGATCCCAAGAAATACCCACTTTCTCAGGATGATATCAATGGAAATCCAGTCCATCTAT 803  
 DB 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260  
 QY 804 GGAGTCTGCTTAAGTACTCTGTAAGCCAAAGAACCCACTATATCCCATGCTGTGAC 863  
 DB 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280  
 QY 864 CTGACTTGACTTTTGACGCTATCACACTTTCCGAGAGAGTATGTTCTTTAAAGGC 923  
 DB 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPheLysGly 300  
 QY 924 AGGCACCTATGGAGGATCTATTATGATATCAGGATGTTGAGTTTGAATTAATTTGTTCA 983  
 DB 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320  
 QY 984 TTCTGGCATCTCTGCCAGCTGATCTGAGCTGATGACAGAACCCAGAGATTAAGATT 1043  
 DB 321 PheTrpProSerLeuProAlaAspLeuGlnAlaTyrGluAsnProArgAspLysIle 340  
 QY 1044 CTGGTTTTAAAGATGAAACTTCTGGATGATCAGAGGATATGCTGCTTGGCCAGATTAT 1103  
 DB 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360  
 QY 1104 CCCAAATCCATCATACATTTAGTGTTCAGGACCTGTGAAGAAATAGATGACGCGTC 1163  
 DB 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380  
 QY 1164 TGTGATAGACACAAAGAAACCTACTTCTTTGTGGGCAATTTGTGCTGGAGGTTGAT 1223  
 DB 381 CysAspLysThrThrArgLysThrTyrPheValGlyIleTrpCysTrpArgPheAsp 400  
 QY 1224 GAAATGACCCAAACCATGGACAAAGATTCCCGCAGAGAGTGTAAACACATTTCTCTGA 1283  
 DB 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420  
 QY 1284 ATCAGTATCCGTGTTGATGCTTTCAGTACAAAGGATTCCTCTTTTTCAGCCGTGGA 1343  
 DB 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440  
 QY 1344 TCAAGCAATTTGAATACAACTTAAGCAAGAATATATCCCGAATCATGAGAACTAAT 1403  
 DB 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460  
 QY 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCTCATTTGTTTGTATATCAACAGGAA 1463  
 DB 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480  
 QY 1464 AAAGCACATTCAGGAGGCATAAAGATTTGTATCATAGAGTTTAAAGCTTGTATTATTTT 1523  
 DB 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500  
 QY 1524 GGTATTTGTTCTGCTGAAACCACTTCTCTATTATCAA 1562  
 DB 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513

RESULT 9



ABU59746  
ID ABU59746 standard; protein; 513 AA.  
XX  
AC ABU59746;  
XX  
DT 13-MAY-2003 (first entry)  
XX  
DE Novel secreted and transmembrane protein PRO5992.  
XX  
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
KW cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disease;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis.  
XX  
OS Homo sapiens.  
XX  
XX US2003017563-A1.  
XX  
PD 23-JAN-2003.  
XX  
XX 07-MAY-2002; 2002US-00140808.  
XX  
PR 31-MAR-1997; 97WO-US0005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 98WO-US000106.  
PR 08-MAR-1999; 99WO-US0005028.  
PR 10-MAR-1999; 99WO-US0005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 29-NOV-1999; 99WO-US023089.  
PR 30-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030999.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 18-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00860208.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
PR 22-JUN-2001; 2001WO-US020116.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.  
PR 09-AUG-2001; 2001US-00927796.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX WPI; 2003-148238/14.  
XX N-PSDB; ABX89236.  
XX  
XX Two hundred and seventy five nucleic acids encoding PRO polypeptides,  
XX useful for treating pericyte-associated tumors, diabetes and various bone  
XX and/or cartilage disorders, e.g. arthritis.  
XX  
XX Claim 12; Fig 192; 659pp; English.  
XX  
XX The invention describes an isolated human PRO polypeptide. The PRO  
XX polypeptides are useful in detecting PRO polypeptides in a sample, in  
XX linking a bioactive molecule to a cell expressing a PRO polypeptide, and

in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO536, PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126, PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of retinal neurons cells (PRO1132 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813 and PRO1066 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpeticiformis or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein

SQ Sequence 513 AA;

#### Alignment Scores:

Pred. No.: 6.23e-285 Length: 513  
Score: 2752.00 Matches: 512  
Percent Similarity: 99.81% Conservative: 0  
Best Local Similarity: 99.81% Mismatches: 1  
Query Match: 93.92% Indels: 0  
DB: 6 Gaps: 0

US-10-729-807-28 (1-1627) x ABUS9746 (1-513)

QY 24 ATGAAGCGCTCTCTGCTTCTGTTGTTCTTTATTAACATTTTCTCTCATTTCCCTTA 83  
DB 1 MetLysArgLeuLeuLeuLeuPheLeuPhePheIleThrPheSerSerAlaPheProLeu 20  
QY 84 GTCCGGATCAGCGAAATACAGAAATATGCACTGGCTCAGGCATATCTCAACAGTTC 143  
DB 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40  
QY 144 TACTCTTTGAATAGAGGGAATCATCTTTGTTCAAGCAAGATAGGAGTCTCATAGAT 203  
DB 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60  
QY 204 GCAAAATTCGGGAATGCAAGCATTTTGTGATTGACAGTGCAGTGGAAAACTGGACTCA 263  
DB 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
QY 264 AACACCTTTGACATCATGAAGACACCCAGTGTGGGTGCTGATGTCGGCCAGTATGSC 323  
DB 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
QY 324 TACACCTCTCCCTGGGTGGGAAATACAACTCACCCTACAGATAATAAATATACTCCG 383  
DB 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120  
QY 384 GATATGGCAGAGCTGCTGTGATGAGGTATTCAGAAAGGTTTACAGTGGAGCAAA 443  
DB 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys 140  
QY 444 GTCACTCCCAATAATTCACCAAGATTTCAAGGGGATTCGACATCATGATTCGCTTT 503  
DB 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160  
QY 504 AGGACTCGAGTCCATGCTCGGTGCTCGTCTATTTGATGTCCTTGGGAGTCTTGCC 563

DB 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180  
QY 564 CATGCTTTCCTCTCTGGTCCGGTCTGGGTGGTGACACACTCATTTTGTATGAGGATGAAC 623  
DB 181 HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200  
QY 624 TGGACCAAGGATGAGCAGAGATTCACACTTGTCTTCTGTGGCTGCTCATGATTTGGTCAT 683  
DB 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220  
QY 684 GCACTGGGGTCTCTCTCACTCCCAATGATCAACAGCCTTGATGTTCCCAATATTGTCTCC 743  
DB 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240  
QY 744 CTGGATCCCGAAAAATPACCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803  
DB 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260  
QY 804 GGAGTCTCCCTAAGGTACTCTGTAAGCCAAAGAACCCACTATACCCCATGCTCTGTGAC 863  
DB 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280  
QY 864 CTGACTTCTGACTTTTCACTGCTATCAACTTTCCGAGAGAGTAACTATGTTCTTAAAGC 923  
DB 281 ProAspLeuThrPheAspAlaIleThrThrPheArgGluValMetPhePheLysGly 300  
QY 924 AGSCACTATGAGGAGTCTATTATGATATCACGGATGTTGAGTTTGAATTAATTTGTTCA 983  
DB 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320  
QY 984 TTCTGGCCTCTCTGCGACTGATCTGCAAGCTGCATAGAGAACCCAGAGATAGATT 1043  
DB 321 PheTrpProSerLeuProAlaAspLeuGlnAlaTyrGluAsnProArgAspLysIle 340  
QY 1044 CTGGTTTTTAAAGATGAAAACTTCTGGATGATCAGAGGATATGCTCTTCCAGATTAT 1103  
DB 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360  
QY 1104 CCAAAATCCATACATATAGTGTTCAGGACCTGTGAGAAAGAAATAGATGACGCGTC 1163  
DB 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal 380  
QY 1164 TGTGATAGACACACAAAGAAACCTACTCTTTTGGGGCATTTGGTCTGGAGTTTGTAT 1223  
DB 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400  
QY 1224 GAAATGACCAACCACTGACAAAGATTCCTCCGAGAGAGTGTAAACACTTTCTCTGGA 1283  
DB 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420  
QY 1284 ATCAGTATCCGTGTTGATGCTCTTTCAGTACAAAGGATTCCTTTTTCAGCCGTGA 1343  
DB 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440  
QY 1344 TCAAGACATTTGATACAAACATTAAGCAAGATATTTACCGAATCATGAGAACTAAT 1403  
DB 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460  
QY 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCTCATTTGTTGTTGATATCAACAGGAA 1463  
DB 461 ThrTrpPheGlnCysLysGluProLysAsnSerPheGlyPheAspIleAsnLysGlu 480  
QY 1464 AAAGCACATTCAGGAGGCATAAAGATATTGTTATCAATAAGAGTTTAAAGCTTGTATTATTT 1523  
DB 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500  
QY 1524 GGTATTGTTCACTTCTGCTGAAAAACCTCTCATATTATCAA 1562  
DB 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513  
RESULT 10  
ABO24936  
ID ABO24936 standard; protein; 513 AA.

XX	ABO24936;	01-MAR-2000;	2000WO-US005601.	PR
AC		02-MAR-2000;	2000WO-US005746.	PR
XX		02-MAR-2000;	2000WO-US005841.	PR
DT		10-MAR-2000;	2000WO-US006319.	PR
XX		15-MAR-2000;	2000WO-US006884.	PR
XX		20-MAR-2000;	2000WO-US007377.	PR
XX		21-MAR-2000;	2000WO-US007532.	PR
XX	Human secreted/transmembrane protein (PRO) #96.	30-MAR-2000;	2000WO-US008439.	PR
XX		17-MAY-2000;	2000WO-US013705.	PR
KW	Human; PRO; secreted protein; transmembrane protein; tumour; cytostatic;	22-MAY-2000;	2000WO-US014042.	PR
KW	gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood;	30-MAY-2000;	2000WO-US014941.	PR
KW	proteoglycan; cartilage; cytokine; peripheral blood mononuclear cell;	28-JUN-2000;	2000WO-US015264.	PR
KW	PMBC; glucose uptake; FFA; skeletal muscle cell; adipocyte cell;	28-JUL-2000;	2000WO-US020710.	PR
KW	chondrocyte cell proliferation; chondrocyte cell differentiation;	11-AUG-2000;	2000WO-US022031.	PR
KW	pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell;	23-AUG-2000;	2000WO-US023522.	PR
KW	endothelial cell; A-peptide; factor VIIa.	24-AUG-2000;	2000WO-US023328.	PR
XX		08-NOV-2000;	2000WO-US030952.	PR
OS	Homo sapiens.	10-NOV-2000;	2000WO-US030873.	PR
XX		01-DEC-2000;	2000WO-US032678.	PR
XX		20-DEC-2000;	2000US-00747259.	PR
PD		20-DEC-2000;	2000WO-US034956.	PR
XX		28-FEB-2001;	2001US-00796498.	PR
XX		28-FEB-2001;	2001WO-US006520.	PR
XX		01-MAR-2001;	2001WO-US006566.	PR
XX		09-MAR-2001;	2001US-00802706.	PR
XX		14-MAR-2001;	2001US-00808689.	PR
PR		22-MAR-2001;	2001US-00816744.	PR
PR		05-APR-2001;	2001US-00828366.	PR
PR		10-MAY-2001;	2001US-00854208.	PR
PR		18-MAY-2001;	2001US-00860216.	PR
PR		25-MAY-2001;	2001US-00866028.	PR
PR		25-MAY-2001;	2001US-00866034.	PR
PR		25-MAY-2001;	2001WO-US017092.	PR
PR		01-JUN-2001;	2001US-00872035.	PR
PR		01-JUN-2001;	2001WO-US017800.	PR
PR		05-JUN-2001;	2001US-00874503.	PR
PR		14-JUN-2001;	2001US-00882636.	PR
PR		19-JUN-2001;	2001US-00886342.	PR
PR		20-JUN-2001;	2001WO-US019692.	PR
PR		21-JUN-2001;	2001US-00887879.	PR
PR		22-JUN-2001;	2001WO-US020116.	PR
PR		29-JUN-2001;	2001WO-US021066.	PR
PR		09-JUL-2001;	2001WO-US021735.	PR
PR		18-JUL-2001;	2001US-00908827.	PR
PR		06-AUG-2001;	2001US-00924419.	PR
PR		09-AUG-2001;	2001US-00927796.	PR
PR		16-AUG-2001;	2001US-00931836.	PR
PR		19-DEC-2001;	2001US-00028072.	PR
XX		(GETH ) GENENTECH INC.		PA
XX		Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;		XX
PI		Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;		PI
PI		Smith V, Stewart TA, Tumas D, Watanabe CX, Wood WL, Zhang Z;		PI
XX		WPI; 2003-466355/44.		XX
DR		N-FSDB; ACD41890.		DR
XX				XX
PT	New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or			PT
PT	PRO4978, useful in molecular biology, chromosome and gene mapping, in			PT
PT	generating antisense RNA and DNA, and in gene therapy.			PT
XX	Claim 12; Fig 192; 659pp; English.			XX
PS				PS
CC	The invention relates to an isolated nucleic acid comprising at least 80%			CC
CC	sequence identity to a PRO (secreted and transmembrane protein) cDNA			CC
CC	comprising a nucleic acid (a) encoding a PRO polypeptide, or its			CC
CC	extracellular domain (with or without its associated signal peptide),			CC
CC	which comprises any of the 275 120-850 residue amino acid sequences,			CC
CC	given in the specification; (b) comprising any of the 275 300-3500			CC
CC	nucleotide sequences, given in the specification; or (c) comprising the			CC
CC	full-length coding sequence of the nucleotide sequences given in the			CC

specification, or of the DNA deposited under any of the American Type Culture Collection (ATCC) Accession Numbers listed in the specification. Also included are a vector comprising the novel nucleic acid, a host cell comprising the vector, producing a PRO polypeptide, the isolated PRO polypeptides detailed above, a chimaeric molecule comprising the PRO polypeptide of fused to a heterologous amino acid sequence, an anti-PRO antibody, detecting a PRO polypeptide in a sample suspected of containing the PRO polypeptide, linking a bioactive molecule to a cell expressing a PRO polypeptide, modulating at least one biological activity of a cell expressing a PRO polypeptide, stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, (or proteoglycans from cartilage or cytokine from peripheral blood mononuclear cells (PBMC)), modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, stimulating the proliferation or differentiation of chondrocyte cells (or proliferation of or gene expression in pericyte cells), stimulating the proliferation of inner ear utricular supporting cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the binding of A-peptide to factor VIIA, or differentiation of adipocyte cells, detecting the presence of a tumour in a mammal and an oligonucleotide probe derived from any of the nucleotide sequences given in the specification. The polynucleotide is useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA, and in gene therapy. The polynucleotide may also be used in preparing PRO polypeptides by recombinant techniques, and in generating either transgenic animals or knock-out animals which, in turn, are useful in the development and screening of therapeutically useful reagents. The PRO polypeptide or the antibody is used in preparing a medicament for treating a condition responsive to the polypeptide or antibody, such as tumours, and in various diagnostic assays. The present sequence represents a PRO polypeptide

XX  
SQ

Sequence 513 AA;  
Alignment Scores:  
Pred. No.: 6,23e-285 Length: 513  
Score: 2752.00 Matches: 512  
Percent Similarity: 99.81% Conservative: 0  
Best Local Similarity: 99.81% Mismatches: 1  
Query Match: 93.92% Indels: 0  
DB: 6 Gaps: 0

US-10-729-807-28 (1-1627) x ABO24936 (1-513)

QY 24 ATGAAGCGCTCTGCTTCTGTTGTTGTTTATACATTTTCTTCTGCTTCCCTTA 83  
DB 1 MetLysArgLeuLeuLeuLeuPheLeuPhePheLeuPheSerSerAlaPheProLeu 20  
QY 84 GTCCGGATGACGGAAAATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACAGTTC 143  
DB 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40  
QY 144 TACTCTCTTGAATAGAGGGAATCATCTTGTTCAAAGCAAGATAGAGTCTATAGAT 203  
DB 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60  
QY 204 GACAAAATTCGGGAATGCAAGCATTTTGTGATTGACAGTCACTGGAAAACCTGACTCA 263  
DB 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
QY 264 AACACCTTGAGATCATGAAGACACCCAGGTGTGGGGTGCCTGATGTGGGCGAGTATGGC 323  
DB 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
QY 324 TACACCTCCCTGGGTGAGAAAATACAACTCACCCTACAGATTAATAACTACTCCG 383  
DB 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleAsnTyrThrPro 120  
QY 384 GATATGGCAGCAGCTGCTGTGATCAGGCTATCCAAAGAGGTTTAGAAGTGTGGAGCAA 443  
DB 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140  
QY 444 GTCACCTCCACTAAATTCACCAAGATTTCAAAGGGGATTGCAGACATCATGATTGCCTTT 503

DB 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160  
QY 504 AGGACTCGAGTCCATGGTCGGTGTCTCGCTATTTTGTGCTGCTCCCTTGGAGTGTGGC 563  
DB 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180  
QY 564 CATGCTTTCCCTCCGCTCGGCTCGGCTCGGCTGAGCAGTCTTGTGATGAGGATGAAAC 623  
DB 181 HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200  
QY 624 TGGACCAAGATGGAGCAGGATTCACCTTGTGCTGCTGCTCATGAATTTGTGCTAT 683  
DB 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220  
QY 684 GCATGGGGCTCTCTCACCCTCAATGATCAACAGAGCTTGTGCTCCCAATATATGTCTCC 743  
DB 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240  
QY 744 CTGGATCCAGAAAATACCACTTTCTCAGGATGATATCAATGGAAATCCAGTCCATCTAT 803  
DB 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260  
QY 804 GGAGTCTGCTTAAGGTACTCTTAAGCCAAAGGAACCCACTATATACCCCATCGCTGTGAC 863  
DB 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280  
QY 864 CTGACTTGACTTTTGGAGCTATCAACTTCCGAGAGAAAGTAAATGTTCTTTAAAGC 923  
DB 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300  
QY 924 AGGCACCTATGGAGGATCTATATGATATACGGATGTTGAGTTTGAATTAATTCCTTCA 983  
DB 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAspSer 320  
QY 984 TTCTGCGCATCTCTCCAGCTGATCTGCAAGCTGCATACGAGAACCCAGAGATTAAGATT 1043  
DB 321 PheTrpProSerLeuProAlaAspLeuGlnAlaTyrGluAsnProArgAspLysIle 340  
QY 1044 CTGGTTTTTAAAGATGAAAACCTTCTGGATGATCAGAGGATATGCTGTCTGCGAGATTAT 1103  
DB 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360  
QY 1104 CCCAAATCCATCCATACATTAAGTTTCCAGACCTGTGAAGAAATAGATGACGCCGTC 1163  
DB 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380  
QY 1164 TGTGATAAGACCAAGAAAAACCTACTTCTTTGTGGGCATTTGGTGTGGAGGTTTGAT 1223  
DB 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTrpArgPheAsp 400  
QY 1224 GAATGACCCAAACCATGGAACAAAGGATTCGCGAGAGAGTGGTAAACACTTTCTCTGGA 1283  
DB 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420  
QY 1284 ATCAGTATCCGTGTGATGCTGCTTCCAGTACAAAGATTTCTTCTTTTTCAGCGGTGA 1343  
DB 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePhePheSerArgGly 440  
QY 1344 TCAAGCAATTTGAATCAACATTAAGCAAAAGAAATATTACCCGAATCATCAGAACTAAT 1403  
DB 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetCargThrAsn 460  
QY 1404 ACTTGGTTTCAATCAAGAACCAAGAACTCTCATTTGGTTTTTGTATATCAACAAGAA 1463  
DB 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480  
QY 1464 AAAGCAGATTCAGAGGCGATTAAGATATTGATCATAGAGTTTAAAGTTCTGTTTATTTT 1523  
DB 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500  
QY 1524 GGTATTGTTTCAATTTGCTGAAAACACTTCTATTATCAAA 1562

Db 501 GlylleValHisLeuLeuLysAnThrSerIleTyGln 513

RESULT 11

ABU66941

ID ABU66941 standard; protein; 513 AA.

XX AC ABU66941;

XX DT 27-MAY-2003 (first entry)

XX DE Human secreted/transmembrane, PRO, protein SEQ ID 192.

XX KW Human; secreted protein; transmembrane protein; PRO;

XX KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;

XX KW infertility; birth defects; premature aging; AIDS; biosensor;

XX KW acquired immunodeficiency syndrome; cancer; diabetic complication;

XX KW bioreactor; tumour.

XX OS Homo sapiens.

XX PN US2003032155-A1.

XX PD 13-FEB-2003.

XX PF 03-MAY-2002; 2002US-00137865.

XX 31-MAR-1997; 97WO-US005230.

XX 12-JUN-1998; 98WO-US012456.

XX 14-JUL-1998; 98WO-US014552.

XX 28-AUG-1998; 98WO-US017888.

XX 10-SEP-1998; 98WO-US018824.

XX 14-SEP-1998; 98WO-US019093.

XX 14-SEP-1998; 98WO-US019094.

XX 14-SEP-1998; 98WO-US019177.

XX 16-SEP-1998; 98WO-US019330.

XX 17-SEP-1998; 98WO-US019437.

XX 07-OCT-1998; 98WO-US021141.

XX 23-OCT-1998; 98WO-US022991.

XX 23-OCT-1998; 98WO-US022992.

XX 20-NOV-1998; 98WO-US024855.

XX 01-DEC-1998; 98WO-US025108.

XX 05-JAN-1999; 99WO-US000106.

XX 08-MAR-1999; 99WO-US005028.

XX 10-MAR-1999; 99WO-US005190.

XX 20-APR-1999; 99WO-US008615.

XX 14-MAY-1999; 99WO-US010733.

XX 02-JUN-1999; 99WO-US012252.

XX 01-SEP-1999; 99WO-US020111.

XX 08-SEP-1999; 99WO-US020594.

XX 13-SEP-1999; 99WO-US020944.

XX 15-SEP-1999; 99WO-US021090.

XX 15-SEP-1999; 99WO-US021547.

XX 05-OCT-1999; 99WO-US023089.

XX 29-NOV-1999; 99WO-US028214.

XX 30-NOV-1999; 99WO-US028313.

XX 30-NOV-1999; 99WO-US028409.

XX 01-DEC-1999; 99WO-US028301.

XX 01-DEC-1999; 99WO-US028634.

XX 02-DEC-1999; 99WO-US028551.

XX 02-DEC-1999; 99WO-US028564.

XX 02-DEC-1999; 99WO-US028565.

XX 16-DEC-1999; 99WO-US030095.

XX 20-DEC-1999; 99WO-US030911.

XX 20-DEC-1999; 99WO-US030999.

XX 22-DEC-1999; 99WO-US030720.

XX 30-DEC-1999; 99WO-US031243.

XX 30-DEC-1999; 99WO-US031274.

XX 05-JAN-2000; 2000WO-US000219.

XX 06-JAN-2000; 2000WO-US000277.

XX 06-JAN-2000; 2000WO-US000376.

XX 11-FEB-2000; 2000WO-US003565.

XX 18-FEB-2000; 2000WO-US004341.

XX 18-FEB-2000; 2000WO-US004342.

22-FEB-2000; 2000WO-US004414.

24-FEB-2000; 2000WO-US004914.

24-FEB-2000; 2000WO-US005004.

01-MAR-2000; 2000WO-US005601.

02-MAR-2000; 2000WO-US005746.

02-MAR-2000; 2000WO-US005841.

10-MAR-2000; 2000WO-US006319.

15-MAR-2000; 2000WO-US006884.

20-MAR-2000; 2000WO-US007377.

21-MAR-2000; 2000WO-US007532.

30-MAR-2000; 2000WO-US008439.

17-MAY-2000; 2000WO-US013705.

22-MAY-2000; 2000WO-US014042.

30-MAY-2000; 2000WO-US014941.

02-JUN-2000; 2000WO-US015264.

28-JUL-2000; 2000WO-US020710.

11-AUG-2000; 2000WO-US022031.

23-AUG-2000; 2000WO-US023522.

24-AUG-2000; 2000WO-US023328.

08-NOV-2000; 2000WO-US030952.

10-NOV-2000; 2000WO-US030873.

01-DEC-2000; 2000WO-US032678.

20-DEC-2000; 2000US-00747259.

28-FEB-2001; 2000WO-US034956.

28-FEB-2001; 2001US-00796498.

01-MAR-2001; 2001WO-US006520.

09-MAR-2001; 2001US-00802706.

14-MAR-2001; 2001US-00808689.

22-MAR-2001; 2001US-00816744.

05-APR-2001; 2001US-00828366.

10-MAY-2001; 2001US-00854208.

10-MAY-2001; 2001US-00854280.

18-MAY-2001; 2001US-00860216.

25-MAY-2001; 2001US-00866028.

25-MAY-2001; 2001WO-US017092.

01-JUN-2001; 2001US-00872035.

01-JUN-2001; 2001WO-US017800.

05-JUN-2001; 2001US-00874503.

14-JUN-2001; 2001US-00882636.

19-JUN-2001; 2001US-00886342.

20-JUN-2001; 2001WO-US019692.

21-JUN-2001; 2001US-00887879.

22-JUN-2001; 2001WO-US020116.

29-JUN-2001; 2001WO-US021066.

09-JUL-2001; 2001WO-US021735.

18-JUL-2001; 2001US-00908827.

06-AUG-2001; 2001US-00924419.

09-AUG-2001; 2001US-00927796.

16-AUG-2001; 2001US-00931836.

19-DEC-2001; 2001US-00028072.

(GETH ) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;

Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;

Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-331925/31.

N-PSDB; ACA04119.

New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or cancer.

Claim 12; Fig 192; 659pp; English.

The invention relates to an isolated nucleic acid comprising, or which is at least 80% identical to, or the full-length coding sequence of, any of the 275 nucleotide sequences, encoding the corresponding PRO polypeptide (one of 275 secreted or transmembrane proteins). the nucleic acid further

comprises the full-length coding sequence of the DNA deposited under American Type Culture Collection (ATCC) accession number in a list given in the specification. Also included are vectors and host cells for producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO extracellular domains and mature sequences, methods of detecting PRO proteins, methods for stimulating the release of TNF-alpha (tumour necrosis factor alpha) from human blood, (and the proliferation of differentiation of chondrocyte cells, the proliferation of, or gene expression in pericyte cells, the release or proteoglycans from cartilage, proliferation of inner ear articular supporting cells, the proliferation of T-lymphocyte cells, the release of a cytokine from peripheral blood mononuclear cells (PBMC), or the proliferation of endothelial cells), a method for modulating the uptake of glucose or free fatty acid (FFA) by skeletal muscle cells, a method for inhibiting the binding of A-peptide to factor VIIA, or the differentiation of adipocyte cells, a method for detecting the presence of a tumour in a mammal and an oligonucleotide probe derived from any of the nucleotide sequences cited above. The nucleic acids and polypeptides are useful for treating CC inflammatory diseases, organ failure, atherosclerosis, cardiac injury, CC infertility, birth defects, premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or diabetic complications. The CC nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are CC useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both CC are useful in tissue typing. The present sequence represents a PRO protein of the invention

XX  
SQ Sequence 513 AA;

#### Alignment Scores:

Pred. No.: 6,23e-285 Length: 513  
Score: 2752.00 Matches: 512  
Percent Similarity: 99.81% Conservative: 0  
Best Local Similarity: 99.81% Mismatches: 1  
Query Match: 93.92% Indels: 0  
DB: 6 Gaps: 0

US-10-729-807-28 (1-1627) x ABU66941 (1-513)

QY	24	ATGACGCGCTCTGCTTCTGCTTCTGCTTTTATTAACATTTCTTCTGCTTCCCTTA	83
Db	1	MetLysArgLeuLeuLeuLeuPheLeuPhePheIleThrPheSerSerAlaPheProLeu	20
QY	84	GTCGGATCACGGAATAATGCAAGAAATATGCAACTGCTCAGGCATATCTCAACAGTTC	143
Db	21	ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaIleLeuAsnGlnPhe	40
QY	144	TACTCTCTTGAATAGAGGGAATCATCTGTTCCTCAAGCAAGATAGGAGTCTCATAGAT	203
Db	41	TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp	60
QY	204	GACAAATTCGGGAATGCAAGCATTTTGGATTGACAGTCACTGGAAAACTGGACTCA	263
Db	61	AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer	80
QY	264	AACACCTTTGAGATCATGAAGACACCCAGGTGGGGTGCCTGATGTGGCCAGATATGC	323
Db	81	AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnIleGly	100
QY	324	TACACCTCCCTGGGTGGAGAAATACAACTCCTACAGATATAATAACTATATCTCG	383
Db	101	TyrThrLeuProGlyIleMetLysThrProArgCysGlyValProAspValGlyGlnIleGly	120
QY	384	GATATGGCAGAGCTGCTGTGATGAGCTATCCAGAGGTTAGAGTGGAGCAMA	443
Db	121	AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys	140
QY	444	GTCACCTCCACTAAAATTCACCAAGATTCACAAAGGGATTGCAGACATCATGATGCTTT	503
Db	141	ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe	160
QY	504	AGGACTCGAGTCCATGGTGGTGTCTCGCTATTTTGATGGTCCCTTGGGAGTGTGGC	563

Db	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180
QY	564	CATGCCCTTCTCTGCTCCGGGTCTGGGTGGTGGACACTCATTTTGATGAGGATGAAAC	623
Db	181	HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn	200
QY	624	TGCACCAAGGATGAGCAGAGATTCAACTTGTCTTCTGCTGCTCATGATTTGGTCAT	683
Db	201	TrpThrLysAspGlyAlaGlyPheAsnLeuPheValAlaAlaHisGluPheGlyHis	220
QY	684	GCACTGGGGTCTCTCACTCCAATGATCAACAGCCTTGATGTTCCCAATATATGCTCC	743
Db	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
QY	744	CTGGATCCCAAAAAATACCCACTTCTCAGGATCATATCAATGGAATCCAGTCCATCAT	803
Db	241	LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr	260
QY	804	GGAGGTCTGCTAAGCTACTGCTAAGCCCAAGCAACCCACTATACCCCTGCTGTGAC	863
Db	261	GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp	280
QY	864	CCTGACTTCACTTTTCACTGCTATCAACAACCTTCCGAGAGAGTAATGTTCTTTAAAGGC	923
Db	281	ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly	300
QY	924	AGGCACCTATGGAGGATCTATTATGATATCACCGATGTTGAGTTGAATTAATTTGCTTCA	983
Db	301	ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer	320
QY	984	TTCTGCCCATCTCTGCTCAGCTGATCTGCAAGCTGCTACAGAACCCAGAGATAGATT	1043
Db	321	PheTrpProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnProArgAspLysIle	340
QY	1044	CTGGTTTTTAAAGATGAAAACTTCTGGATGATCAGAGGATATGCTCTCTTCCAGATTAT	1103
Db	341	LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr	360
QY	1104	CCCAATTCATCATATACATTAGGTTTTCCAGGACGTGTGAAGAAAAATAGATGCAGCGTC	1163
Db	361	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaIleVal	380
QY	1164	TCTGATAACACCAACCAAAACCTACTTCTTGTGGGATTTGGTCTGGAGTTTGTAT	1223
Db	381	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp	400
QY	1224	GAAATGACCAACCAATGACAAAGATTCCCGCAGAGAGTGTAAACACATTTCTCTGGA	1283
Db	401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly	420
QY	1284	ATCAGTATCCGTGTGATGCTCTTCCAGTACAAAGGATTCCTCTTTTTCAGCCGTGA	1343
Db	421	IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePhePheSerArgGly	440
QY	1344	TCAAGCAATTTGAATACACATTAAGCAAAAGATTTACCCGATCATGAGAACTAT	1403
Db	441	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
QY	1404	ACTTGTTTCAATGCAAGAACCAAGAACTCTCATTTGGTTTTGATATCAACAGGAA	1463
Db	461	ThrTrpPheGlnCysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu	480
QY	1464	AAAGCACATTCAGGAGGCATAAAGATATGTATCATATAAGAGTTAAGCTTGTATTTT	1523
Db	481	LysAlaHisSerGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe	500
QY	1524	GCTATGTTCTATTCCTGAAACAACTCTCTATTTATCAA	1562
Db	501	GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln	513

RESULT 12  
ADA45711  
ID ADA45711 standard; protein; 513 AA.

XX AC ADA45711;  
XX DT 20-NOV-2003 (first entry)  
XX DE Novel human secreted and transmembrane protein PRO5992.  
XX KW Human; secreted and transmembrane protein; PRO;  
KW Tumour necrosis factor alpha release; TNF-alpha release;  
KW Glucose uptake modulator; FFA uptake modulator;  
KW Cell proliferation stimulator; cell differentiation stimulator;  
KW Cell differentiation inhibitor; cytokine release stimulator; tumour;  
KW lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;  
KW cervical tumour; liver tumour; chromosome mapping; gene mapping;  
KW gene therapy; chromosome identification; chromosome marker.  
XX OS Homo sapiens.  
XX PN US2003022328-A1.  
XX PD 30-JAN-2003.  
XX PF 16-APR-2002; 2002US-00123904.  
XX PR 31-MAR-1997; 97WO-US005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022992.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012252.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 20-DEC-1999; 99WO-US030939.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US000356.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 18-MAY-2001; 2001US-00854280.  
PR 25-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
PR 22-JUN-2001; 2001WO-US020116.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.  
PR 09-AUG-2001; 2001US-00927796.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.  
XX (GETH ) GENENTECH INC.  
PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX WPI; 2003-584997/55.  
DR N-PSDB; ADA45710.  
XX Novel secreted and transmembrane polypeptide for modulating biological  
PT activity of cell expressing the polypeptide, identifying agonists or  
PT antagonists of polypeptide, and as molecular weight markers.  
XX Claim 12; Fig 192; 659pp; English.  
XX The invention describes 305 nucleic acids encoding PRO (secreted and  
CC transmembrane) polypeptides (I). (I) is useful for stimulating the  
CC release of TNF-alpha from human blood, for modulating the uptake of  
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for  
CC stimulating the proliferation or differentiation of chondrocyte cells,  
CC for stimulating the proliferation of or gene expression in paricycle  
CC cells, for stimulating the release of proteoglycans from cartilage, for



stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the release of a cytokine from PBMC cells, for inhibiting the binding of A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte cells, for stimulating proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast, prostate, rectal, cervical or liver tumour. The oligonucleotide probes are useful for isolating genomic and cDNA nucleotide sequences or antisense probes. (I) is also useful as therapeutic agent. PRO is useful in assays to identify other proteins or molecules involved in binding interaction. A polynucleotide (II) encoding (I) is useful in chromosome and gene mapping, in generation of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, in gene therapy, for chromosome identification, as chromosome marker, and for generating probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g. detecting its expression in specific cells, tissues or serum, and for affinity purification of PRO from recombinant cell culture or natural sources. (I) and (II) are useful for tissue typing. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide.

Sequence 513 AA;

Alignment Scores:

Pred. No.:	6,238-285	Length:	513
Score:	2752.00	Matches:	512
Percent Similarity:	99.81%	Conservative:	0
Best Local Similarity:	99.81%	Mismatches:	1
Query Match:	93.92%	Indels:	0
DB:	6	Gaps:	0

US-10-729-807-28 (1-1627) x ADA45711 (1-513)

QY	24	ATGAAGCGCTCTGCTTCTGTGTGTTTATTAACATTTCTTCGCATTTCCTTA	83
Db	1	MetLysArgLeuLeuLeuPheLeuPhePheIleThrPheSerSerAlaPheProLeu	20
QY	84	GTCCGGATCAGCGAAATGAAGAAAATATGCACTGGCTCAGGCATATCTCAACCAAGTTC	143
Db	21	ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe	40
QY	144	TACTCTTTGAATAGAAGGAATCATCTCTTCAACAGACATAGAGTCTCATAGAT	203
Db	41	TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp	60
QY	204	GACAAAATTCCGGAAATCAAGCATTTTTCGATTGACAGTGACTGCAAACTGGACTCA	263
Db	61	AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer	80
QY	264	AACACCTTGTAGATCATGAAGACACCCAGGTGTGGGGTGCTGATGTGGGCCAGTAGTC	323
Db	81	AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100
QY	324	TACACCTCCCTGGGTGGAGAAATACAACTCCACCTACAGATAATAACTATCTCCG	383
Db	101	TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro	120
QY	384	GATATGGCAGCAGCTGTGTGGATCAGGCTATCCAAGAGGTTTAGAAGTGTGCAGCAA	443
Db	121	AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys	140
QY	444	GTCATCTCCACTAAAATTCAACAAGATTTCAAAGGGGATTCAGACATCATGATTGCCTTT	503
Db	141	ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe	160
QY	504	AGGACTCGAGTCCATGGTCGGTGTCTCGCTATTATTTGATGGTCCCTTGGGAGTGCTTGG	563
Db	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180
QY	564	CATGCCTTTCTCTCGTTCGGGTGGTGGCTGACACTCATTTTGATGAGTAGTGAAC	623





XX DT 20-NOV-2003 (first entry)  
XX DE Human PRO polypeptide #96.  
XX KW Human; PRO; secreted polypeptide; transmembrane polypeptide;  
KW tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; lung;  
KW colon; breast; prostate; rectum; cervix; liver; tumour; cancer;  
KW Glucose uptake; FFA; adipocyte cell; pericyte cell; proteoglycan;  
KW cartilage; inner ear utricular supporting cell; cytokine; A-peptide;  
KW factor VIIA; endothelial cell.  
XX OS Homo sapiens.  
XX PN US2003054517-A1.  
XX PD 20-MAR-2003.  
XX PF 08-MAY-2002; 2002US-00141755.  
XX PR 31-MAR-1997; 97WO-US005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 98WO-US000106.  
PR 08-MAR-1999; 98WO-US005028.  
PR 10-MAR-1999; 98WO-US005190.  
PR 20-APR-1999; 98WO-US008615.  
PR 14-MAY-1999; 98WO-US010733.  
PR 02-JUN-1999; 98WO-US012252.  
PR 08-SEP-1999; 98WO-US020111.  
PR 13-SEP-1999; 98WO-US020944.  
PR 15-SEP-1999; 98WO-US021090.  
PR 15-SEP-1999; 98WO-US021547.  
PR 05-OCT-1999; 98WO-US023089.  
PR 29-NOV-1999; 98WO-US028214.  
PR 30-NOV-1999; 98WO-US028313.  
PR 30-NOV-1999; 98WO-US028409.  
PR 01-DEC-1999; 98WO-US028301.  
PR 01-DEC-1999; 98WO-US028634.  
PR 02-DEC-1999; 98WO-US028551.  
PR 02-DEC-1999; 98WO-US028564.  
PR 02-DEC-1999; 98WO-US028565.  
PR 16-DEC-1999; 98WO-US030095.  
PR 20-DEC-1999; 98WO-US030911.  
PR 20-DEC-1999; 98WO-US030999.  
PR 22-DEC-1999; 98WO-US030720.  
PR 30-DEC-1999; 98WO-US031243.  
PR 30-DEC-1999; 98WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032878.  
PR 20-DEC-2000; 2000US-00747259.  
PR 20-DEC-2000; 2000WO-US034956.  
PR 28-FEB-2001; 2001US-00796498.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 10-MAY-2001; 2001US-00854280.  
PR 18-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
PR 22-JUN-2001; 2001WO-US020116.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.  
PR 09-AUG-2001; 2001US-00927796.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.  
XX (GETH ) GENENTECH INC.  
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WT, Zhang Z;  
XX WPI; 2003-521854/49.  
XX N-PSDB; ADA18791.  
XX New PRO nucleic acid, useful for preparing a composition for treating  
XX e.g., tumors.  
XX Claim 12; Fig 192; 660pp; English.  
XX The invention relates to isolated human PRO polypeptides (secreted and  
CC transmembrane polypeptides) and the polynucleotides encoding them. The  
CC invention also relates to an antibody which specifically binds to a PRO  
CC polypeptide, a method for stimulating the release of tumour necrosis  
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the  
CC proliferation or differentiation of chondrocyte cells and a method for  
CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,  
CC prostate, rectal, cervical and liver tumours). The polynucleotides are  
CC useful in molecular biology, including uses as hybridisation probes, in  
CC chromosome and gene mapping, in generating antisense RNA and DNA and in  
CC gene therapy. The polynucleotides may also be used in preparing PRO  
CC polypeptides by recombinant techniques and in generating either

transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for modulating the uptake of glucose or FFA by adipocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the release of proteoglycans from cartilage, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the release of cytokines from PBMC cells, for inhibiting the binding of A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte cells and for stimulating the proliferation of endothelial cells. This sequence represents a human PRO polypeptide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

XX  
SQ Sequence 513 AA;

Alignment Scores:  
Pred. No.: 6,23e-285 Length: 513  
Score: 2752.00 Matches: 512  
Percent Similarity: 99.81% Conservatives: 0  
Best Local Similarity: 99.81% Mismatches: 1  
Query Match: 93.92% Indels: 0  
DB: Gaps: 0

US-10-729-807-28 (1-1627) x ADA18792 (1-513)

QY 24 ATCAAGCGCTTCGCTTCGCTTCTTTTATTAACATTTCTCTGCAATTCCTCTA 83  
DB 1 MetLysArgLeuLeuLeuPheLeuPhePheLeuThrPheSerSerAlaPheProLeu 20  
QY 84 GTCGGCATGACGGAATAAGAGAAATATGCAACTGCGCTCAGGCATATCTCACCGATTC 143  
DB 21 ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40  
QY 144 TACTCTTTGAAATAGAGGGAATCATCTTTGTTCAAAGCAAGAAATAGGAGTCTCATAGAT 203  
DB 41 TyrSerLeuGluIleGluGlnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60  
QY 204 GACAAATTCGGGAATGCAAGCATTTTGTGGATTGACAGTGCAGAAACTGGACTCA 263  
DB 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
QY 264 AACACCTTGAGATCATGAGACACCGAGTCGGGTGCGCTCATGTGGCCAGTATGCG 323  
DB 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
QY 324 TACACCTCCCTGGGTGGAGAAATACAACTCACCTACAGATAATAAACTATATCTCCG 383  
DB 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleAsnTyrThrPro 120  
QY 384 GATATGGACGAGCTGCTGTGATGAGGTATCCAAAGAGGTTTAGAAGTGGAGCAAA 443  
DB 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140  
QY 444 GTCACCTCCACTAAATTCACCAAGATTTCAAAGGGGATTGCACATCATGATGCTTTT 503  
DB 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160  
QY 504 AGGACTCGAGTCCATGGTCGGTGTCTCGCTATTTTGTAGTGGTCCCTTGGGAGTCTGGC 563  
DB 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180  
QY 564 CATGCTTTCTCTGGTCCGGGTCTGGGTGGTGACACTCATTTGATGAGGATGAAAC 623  
DB 181 HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200  
QY 624 TGGACCAAGGAGGACGAGTTCACCTGTTCTTGTGGCTGCTCATGATTTGGTCTAT 683  
DB 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheValAlaAlaHisGluPheGlyHis 220  
QY 684 GCACTGGGCTCTCTCACTCCAATGATCAACAGCGCTTGATGTTCCCAATATGTCTCC 743

DB 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240  
QY 744 CTGGATCCCAAAAAATACCCACATTTCTCAGGATGATATCAATGAATCCAGTCCATCAT 803  
DB 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260  
QY 804 GAGGCTCTGCTAAGTACTGCTAGCCAAAGCAAGCACTATACCCCATGCTGTGAC 863  
DB 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280  
QY 864 CTTGACTTCTACTTTTCCAGCTATCAACACTTCCGAGAGAGTAAATGTTCTTAAAGGC 923  
DB 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300  
QY 924 AGGCACCTATGGAGGATCTATTATGATATCACGGATGTTGAGTTTGAATTAATTTGCTTCA 983  
DB 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320  
QY 984 TTCTGGCCATCTCTGCCAGTGTATCTGCAAGCTGCATACAGAACCCCGAGAGATAAGATT 1043  
DB 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340  
QY 1044 CTGGTTTTTAAAGATGAAAACTTCTGGATGATCAGAGGATATCTGCTTTCAGAGATTAT 1103  
DB 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360  
QY 1104 CCCAAATCCATCATACATTAGGTTTCCAGGACGTGTGAAGAAAATAGATGCAGCGTC 1163  
DB 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380  
QY 1164 TGTGATAAGACCAACAGAAAACTTCTTGTGGGATTTGCTGCTGGAGTTTGAT 1223  
DB 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPheAsp 400  
QY 1224 GAAATGACCCAAACCAATGACAAAGATTCCCGCAGAGAGTGTGTAACACACTTTCCTGGA 1283  
DB 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly 420  
QY 1284 ATCAGTATCCGTTGTGATGCTCTTCCAGTACAAAGGATTTCTTTTTCAGCCCTGGA 1343  
DB 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440  
QY 1344 TCAAGCAATTTGAATACAACTTAAGCAAAAGATATTACCGAATCATGAGAACTAAT 1403  
DB 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460  
QY 1404 ACTTGTGTTTCAATGCAAGAACCAAGAACTCTCATTTGTTGTTGATATCAACAGGAA 1463  
DB 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480  
QY 1464 AAAGCACATTCAGGAGGCATAAGATATTGTATCATAGAGTTTAAGCTTGTATTATTTT 1523  
DB 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500  
QY 1524 GGTATGTTTCATTCTGTAAGAAACACTTCTATTATCAA 1562  
DB 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513  
RESULT 15  
ADA61415  
ID ADA61415 standard; protein; 513 AA.  
XX  
AC ADA61415;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Homo sapiens.  
XX  
KW Human; secreted and transmembrane protein; PRO;  
KW Tumour necrosis factor alpha release; TNF-alpha release;  
KW glucose uptake modulator; FFA uptake modulator;  
KW cell proliferation stimulator; cell differentiation stimulator;

cell differentiation inhibitor; cytokine release stimulator; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour; chromosome mapping; gene mapping; gene therapy; chromosome identification; chromosome marker

Novel.  
human.  
secreted.  
and.  
transmembrane.  
protein.  
PRO5992.

US2003049816-A1.

13-MAR-2003.

15-APR-2002: 2002US-00123262.

31-MAR-1997: 97WO-US005230.

12-JUN-1998; 98WO-03012430;  
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[illegible]

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31-MAY-2001;	2001WO-US017092;
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01-JUN-2001;	2001US-US0717800;
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(GETH ) GENENTECH INC.

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WPT: 2003-695892/66

N-PSDB: ADA61414.

New PRO nucleic acid and encode polypeptides, are useful for manufacturing a medicament for diagnosing or treating cancer.

Claim 12: Fig 192: 660pp: English.

The invention describes 305 nucleic acids encoding PRO (secreted and transmembrane) polypeptides (1). (II) is useful for stimulating the release of TNF- $\alpha$  from human blood, for modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of or gene expression in pericyte cells, for stimulating the release of proteoglycans from cartilage, for stimulating the proliferation of inner ear utricular supporting cells, for stimulating the proliferation of T-lymphocyte cells, for stimulating the release of a cytokine from BMMC cells, for inhibiting the binding of A-peptide to factor VIIa, for inhibiting the differentiation of adipocyte cells, for stimulating proliferation of endothelial cells, for detecting the presence of tumour in a mammal. The tumour is lung, colon, breast,



Qy	684	GC	ACTGGGGCTCTCTCACTCTCCAAATGATCAAAACAGCCTTGATGTGTCCAAATATGATGTCC	743
Db	221	Ala	LeuGlyIeuSerHisSerAsnAspGlnThrAlaIeuMetPheProAsnTyrValSer	240
Qy	744	CT	GATCCCGAGAAATACCCACTTTCTCAGGATGATATCAATGAATCCAGCTCCATCTAT	803
Db	241	Leu	aspProArgIysTyrProLeuSerGlnAspAspIleuGlnSerIleTyr	260
Qy	804	GG	AGGTCGTGCTAAGGTACCTGCTTAAGCGAAAGAACCCATATACCCCATGCTGTGTAC	863
Db	261	Gly	GlyLeuProIlysValProAlaIysProIysGluProThrIleProHisAlaCysAsp	280
Qy	864	CCT	GACTTGACTTTTGTACGGCTATCACAACTTTTCGCGACAGAGAAGTAATGTTCTTTAAAGGC	923
Db	281	Pro	AspLeuThrPheAspAlaIleThrPheArgargGluValMetPhePheLysGly	300

924 AGGCACCTATGGAGGATCTATTATGATATCACGGATGTTGAGTTTGAATTAATTGCTTCA 983

Db 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320

Qy	984	TTCTGGCCATCTCTGCCAGCTGATCTCCAAGTCGATACGAGAACCCGAGAGATAAGATT	1043
Db	321	PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle	340
Qy	1044	CTGGTTTTAAAGATGAAACTTCTCGATGATCAGAGGATATGCTGCTTGCACGATTAT	1103

Db 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360

QY 1104 CCCAAATCCATCCATACATTAGGTTTCCAGGACGTGTGAAGAAAATAGATGCAGCCGTC 1163

Db 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380

QY 1164 TGATAGACCACAAGAAAACCTACTTCTTTGTGGGCATTGTGCTGGAGGTTTGAT 1223

DD 381 CYSASP LYS LNR LNR ARG LYS LNR L YR PHE PHE VAL GLY I L E TRP CYS TRP ARG PHE ASP 400

1224 GAAATGACCCAAACCATGGACAAAGGATTCCCGCAGAGAGTGGTAAACACTTTCCTGGA 1283

Db 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420

QY 1284 A T C A G T A T C C G T G T T G A T G C T G C T T T C C A G T A C A A G G A T T C T T C T T T T C A G C C G T G G A 1343

Db 421 I I e s e r I l e a r g v a l a s p a l a a l a p h e g l n t y r l y s g l y p h e p h e p h e s e r a r g g l y 440

QY 1344 TCAAGCAATTTGAAATCAACAATTAAAGACAAAGAATATTACCGAATCATGAGAACTAAT 1403

441 SerLYSGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460

QY I404 ACTTGGTTCAAATGCAAAAGAACCCCTCATTTGGTTTGTATATCAACAAGGAA 1463

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QY 1404 AAAGCACATTCAGGAGGCATAAAGAATATGTAACATAGAGTTTAAGCTTGTTTATTTT 1523

DD LYSATANTSERGLTYTTELTYSTLEUITYRHHISLYSSERLEUSERLEUPHEILEPHE 500

QY 1324 GGATGGTTCATTGCTGAAATACACTTCTATTTATCAA 1562

DS 301 GlyLeuValHisLeuLeuLysAsnThrSerIleLeuArgin 513

Search completed: November 15, 2004 20:25:04

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Search completed: November 15, 2004, 20:25:04  
Job time : 156 secs



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GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: November 15, 2004, 20:03:11 ; Search time 35.5 Seconds

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Title: US-10-729-807-28

Perfect score: 2930

Sequence: 1 gcttcagctgaagaagaga.....aattctgcttcaaatagaa 1627

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_n2p.model -DEV=xlh  
-Q=/cgn2\_1/USPTO\_spool/US10729807/runat\_15112004\_131151\_14700/app\_query.fasta\_1.1799  
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-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFWT=ptp -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10729807@cgn\_1\_1\_43 @runat\_15112004\_131151\_14700 -NCPU=6 -ICPU=3  
-NO\_WMAP -LARGQUERY -NEG SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR\_79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	1271.5	43.4	478	1 KCRBS1	stromelysin 1 (EC
2	1250	42.7	477	1 KCHUS1	stromelysin 1 (EC
3	1243.5	42.4	476	1 JCG505	stromelysin 2 (EC
4	1237.5	42.2	477	1 KCHSS1	stromelysin 1 (EC
5	1234	42.1	476	1 KCHS2	stromelysin 2 (EC
6	1205	41.1	469	1 KCPGI	interstitial colla
7	1198.5	40.9	476	1 KRTS2	stromelysin 2 (EC
8	1177.5	40.2	469	1 KCHOI	interstitial colla
9	1173.5	40.1	475	1 KCTIH	stromelysin 1 (EC
10	1170.5	39.9	468	1 KCRBI	interstitial colla
11	1161.5	39.6	467	1 KCHUI	interstitial colla
12	1161	39.6	469	1 KCHUI	neutrophil colla
13	1141	38.9	471	2 A53711	collagenase 3 (EC
14	1133	38.7	470	2 A49499	metalloelastase HM

# SUMMARIES

15 1126 38.4 466 2 A23685 interstitial colla  
16 1119.5 38.2 472 2 S29243 interstitial colla  
17 1020.5 34.8 462 2 A42401 macrophage elastat  
18 1002.5 34.2 483 2 JCS743 matrix metalloprot  
19 798 27.2 384 2 I51267 collagenase (EC 3.  
20 797 27.2 660 1 A28153 gelatinase A (EC 3  
21 790 27.0 662 2 A42496 gelatinase A (EC 3  
22 790 27.0 662 2 S34780 gelatinase A (EC 3  
23 783 26.7 662 2 S70365 gelatinase A (EC 3  
24 769.5 26.3 663 1 S46492 matrix metalloprot  
25 715.5 24.4 669 2 I38029 matrix metalloprot  
26 713 24.3 582 2 I38028 matrix metalloprot  
27 698 23.8 582 2 I84471 matrix metalloprot  
28 667 22.8 582 2 I48673 matrix metalloprot  
29 626.5 21.4 712 1 I46031 gelatinase B (EC 3  
30 603.5 20.6 491 2 JCG197 stromelysin 3 (EC  
31 594.5 20.3 267 1 KCHUM matrilysin (EC 3.4  
32 593 20.2 707 1 A34458 gelatinase B (EC 3  
33 590 20.1 492 2 A44399 stromelysin 3 (EC  
34 590 20.1 707 1 A53796 gelatinase B (EC 3  
35 586 20.0 730 2 JCL456 gelatinase B (EC 3  
36 585 20.0 730 1 I52580 gelatinase B (EC 3  
37 577 19.7 508 2 JCS082 matrix metalloprot  
38 574 19.6 488 2 S13423 stromelysin 3 (EC  
39 559.5 19.1 708 2 JCG364 gelatinase B (EC 3  
40 556 19.0 477 1 I51645 stromelysin 3 (EC  
41 551.5 18.8 708 2 S29077 gelatinase B (EC 3  
42 550.5 18.8 267 2 A57490 matrilysin (EC 3.4  
43 413 14.1 579 2 T37248 probable matrix me  
44 413 14.1 598 2 T32166 hypothetical prote  
45 400.5 13.7 587 2 S12805 envlysin (EC 3.4.

## ALIGNMENTS

### RESULT 1

#### KCRBS1

stromelysin 1 (EC 3.4.24.17) precursor - rabbit

N/Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); pr

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004

C/Accession: A37306; A29157

R/Finl, M.E.; Karmilowicz, M.J.; Ruby, P.L.; Beeman, A.M.; Borges, K.A.; Brinckerhoff, C

A/Title: Cloning of a complementary DNA for rabbit proactivator. A metalloproteinase tha

ed with collagenase.

A/Reference number: A37306; MUID:88077214; PMID:2825726

A/Accession: A37306

A/Molecule type: mRNA

A/Residues: 1-478 <FIN>

A/Cross-references: UNIPROT:P28863; GB:M25664; NID:G165709; PIDN:AAA1467.1; PID:G165710

R/Whitham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris,

Biochem. J. 240, 913-916, 1986

A/Title: Comparison of human stromelysin and collagenase by cloning and sequence analysi

A/Reference number: A90336; MUID:87156645; PMID:3030290

A/Accession: A29157

A/Status: nucleic acid sequence not shown; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-82,'D',84-127,'K',129-167,'GNS', <WHI>

C/Comment: This enzyme degrades various extracellular matrix proteins, including fibron

C/Comment: Stromelysin 1 hydrolyzes peptide bonds in plasminogen to yield a fragment wit

C/Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation

C/Comment: Stromelysin is found in glycosylated and unglycosylated forms, both of whi

C/Function:

A/Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl si

C/Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei

C/Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo

F/1-17/Domain: signal sequence #status predicted <SIG>

F/18-478/Product: prostromelysin 1 #status predicted <PRO>

F/18-100/Domain: activation peptide #status predicted <ACT>

F/61-265/Domain: matrix metalloproteinase homology <MMP>

F/91-98/Region: autoinhibitory

F/101-478/Product: stromelysin 1 #status predicted <MAT>

US-10-729-807-28 (1-1627) x KCRBS1 (1-478)

178	ProGlyAsnValLeuAlaHisAlaTyraProGlyProGlyLeuAsnGlyAspAlaHis	665
Qy	606 TTTGATGAGGATGAACCTGGACCAAGGATGAGCAGCAGGATTCAACTTTGTTCTTCTGTGGCT	665
Db	198 PheAspAspAspGluGlnTrpThrLysAspThrThrGlyThrAsnLeuPheLeuValAla	217
Qy	666 GCTCATGAATTGGTCATGCACCTGGGGCTCTCTCACTCCAATGATCAACACGACCTTGATG	725
Db	218 AlaHisGluLeuGlyHisSerLeuGlyLeuPheHisSerAlaAsnProGluAlaLeuMet	237
Qy	726 TTCCCAAAATTATGTCCTCCCTG---GATCCACAGAAAATCCCACTTTCTCAGGATGATATC	782
Db	238 TyrProValTyrAsnAlaPheThrAspLeuAlaArgPheArgLeuSerGlnAspAspVal	257
Qy	783 AATGAATCCAGTCATCTATGGA-----GGTCTGGCT	815
Db	258 AspGlyLeuGlnSerLeuTyrGlyProAlaProAlaSerProAspAsnSerGlyValPro	277

A:Accession: A28399

A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-49, 'G', 51-419, 'L', 421-477 <WIL>  
A:Cross-references: GB:U78045; NID:gi1688257; PIDN:AAB36942.1; PID:gi1688259  
A:Note: part of the sequence, including the amino end of the proenzyme, was confirmed by  
R:Lark, M.W.; Walakowits, L.A.; Shah, T.K.; Vammiddlesworth, J.; Cameron, P.M.; Lin, T.Y.  
Connect. Tissue Res. 25, 49-65, 1990  
A:Title: Production and purification of prostromelysin and procollagenase from IL-1 beta  
A:Reference number: A60964; MUID:91059606; PMID:2173990  
A:Accession: A60964  
A:Molecule type: protein  
A:Residues: 18-29;100-108 <LAR>  
R:Koklitis, P.A.; Murphy, G.; Sutton, C.; Angal, S.  
Biochem. J. 276, 217-221, 1991  
A:Title: Purification of recombinant human prostromelysin. Studies on heat activation to  
A:Reference number: S15427; MUID:91248150; PMID:2039471  
A:Accession: S15427  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 18-23 <BIO>  
R:Lijnen, H.R.; Ugwu, F.; Bini, A.; Collen, D.  
Biochemistry 37, 4699-4702, 1998  
A:Title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1 (M  
A:Reference number: A58812; MUID:9548733; PMID:9548733  
A:Contents: annotation  
R:Becker, J.W.  
submitted to the Brookhaven Protein Data Bank, February 1997  
A:Reference number: A68466; PDB:1HFS  
A:Contents: annotation; X-ray crystallography, 1.70 angstroms, residues 105-160  
R:Becker, J.W.; Marcy, A.I.; Rokosz, L.L.; Axel, M.G.; Burbaum, J.J.; Fitzgeraid, P.M.D.  
Protein Sci. 4, 1966-1976, 1995  
A:Title: Stromelysin-1: three-dimensional structure of the inhibited catalytic domain an  
A:Reference number: A58814; MUID:96117647; PMID:8535233  
A:Contents: annotation; X-ray crystallography, 1.70 angstroms  
R:Marcy, A.I.; Eiberger, L.L.; Harrison, R.; Chan, H.K.; Hutchinson, N.I.; Hagmann, W.K.  
Biochemistry 30, 5476-5483, 1991  
A:Title: Human fibroblast stromelysin catalytic domain: expression, purification, and ch  
A:Reference number: A39589; MUID:91274238; PMID:1647201  
A:Contents: annotation  
R:Becker, J.W.  
submitted to the Brookhaven Protein Data Bank, August 1995  
A:Reference number: A66637; PDB:1SLM  
A:Contents: annotation; X-ray crystallography, 1.90 angstroms, residues 33-47;57-267  
R:Gooley, P.R.; O'Connell, J.F.  
submitted to the Brookhaven Protein Data Bank, March 1995  
A:Reference number: A67284; PDB:2SRT  
A:Contents: annotation; conformation by (1)H-NMR, residues 100-272  
R:Gooley, P.R.; Johnson, B.A.; Marcy, A.I.; Cuca, G.C.; Salowe, S.P.; Hagmann, W.K.; Ess  
Biochemistry 32, 13098-14008, 1993  
A:Title: Secondary structure and zinc ligation of human recombinant short-form stromelys  
A:Reference number: A58815; MUID:94059987; PMID:8241164  
A:Contents: annotation; conformation by (1)H-NMR  
C:Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation  
C:Comment: Prostromelysin is found in glycosylated and unglycosylated forms, both of whi  
C:Genetics:  
A:Gene: GDB:MMP3; STMY; STMY1  
A:Cross-references: GDB:120727; OMIM:185250  
A:Map position: 11q23-11q23  
C:Function:  
A:Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl si  
A:Note: degrades various extracellular matrix proteins, including fibronectin, plasminog  
plasminogen to yield a fragment with angiotensin activity  
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei  
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo  
E:1-17/Domain: signal sequence #status predicted <SIG>  
F:18-477/Product: prostromelysin 1 #status experimental <PRO>  
F:18-99/Domain: activation peptide #status experimental <ACT>  
F:60-264/Domain: matrix metalloproteinase homology <MMP>  
F:100-477/Product: stromelysin 1 #status experimental <MAT>  
E:284-477/Domain: hemopexin repeat homology <PXN>  
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited)  
F:120/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;218,222,228/Binding site: zinc, catalytic (His) (active) #status experimental  
F;219/Active site: Glu #status predicted  
F;290-477/Disulfide bonds: #status predicted

Alignment Scores:  
Pred. No.: 9,29e-99 Length: 477  
Score: 1250.00 Matches: 246  
Percent Similarity: 66.04% Conservative: 71  
Best Local Similarity: 51.25% Mismatches: 145  
Query Match: 42.66% Indels: 18  
DB: 1 Gaps: 9

US-10-729-807-28 (1-1627) x KCHU51 (1-477)

Qy	24	ATGAAGCGCTTCTGCTCTGTGGTTTCCTTTATAACATTTTCTTCTGCATTTCCCTTA	83
Db	1	MetLysSerLeuProIleLeuLeuLeuCysValAlaValCysSerAlaTyrProLeu	20
Qy	84	GTCGGATGACGGAAATAGAAGAA---AATATGCAACTGGCTCAGGCATATCTCAACCAG	140
Db	21	AspGlyAlaAlaArgGlyGluAspThrSerMetAsnLeuValGlnTyrTyrLeuGluAsn	40
Qy	141	TTCTACTCTTGAAATAGAGGAATCATCTGTTCAAAGCAGATATGAGTGTCTCATTA	200
Db	41	TyrTyrAspLeuLysAspValLysGlnPheValArgLysValProVal	60
Qy	201	GATCACAAAATTCGGAAATGCAAGCATTTTTGGATTGACAGTAGCTGAAAACTGCAC	260
Db	61	VallysLysIleArgGluMetGlnLysPheLeuGlyLeuGluValThrGlyLysLeuAsp	80
Qy	261	TCAAACACCTTGAGATCATGAAGACACCAGGTGTGGGTGCTGATGGGCCAGTAT	320
Db	81	SerAspThrLeuGluValMetArgLysProArgCysGlyValProAspValGlyHisPhe	100
Qy	321	GGGTACACCTCCCTCGG-----TGAGAAATACAACCTCACCTACAGATAATA	371
Db	101	--ArgThrPheProGlyIleProLysTrpArgLysThrHisLeuThrTyrArgIleVal	119
Qy	372	AACATACTCCGATATGGCAGCAGCTGTGTGATGAGGCTATCCAAGAGGTTTAGAA	431
Db	120	AsnTyrThrProAspLeuProLysAspAlaValAspSerAlaValGluLysAlaLeuLys	139
Qy	432	GTGTGGAGCAAGTCACTCCACTAAAATTCACCAAGATTTCAAAGGGATTCGACAGATC	491
Db	140	ValTrpGluGluValThrProLeuThrPheSerArgLeuTyrGluGlyGluAlaAspile	159
Qy	492	ATGATTCCTTTAGGACTCGAGTCCATGTGTCGGTGTCTCGCTAT----TTTGATGGTCCC	548
Db	160	MetIleSerPheAlaValArgGluHisGly-----AspPheTyrProPheAspGlyPro	177
Qy	549	TTGGAGTGTGTGGCCATGCTTTCTCCTCGGTCCGGTCTGGGTGTGACACTCATTTT	608
Db	178	GlyAsnValLeuAlaHisAlaTyrAlaProGlyProGlyIleAsnGlyAspAlaHisPhe	197
Qy	609	GATGAGGATGAAACTGGACCAAGGATGGAGCAGGATTCAACTTGTTTCTGTGGCTGCT	668
Db	198	AspAspAspGluGlnTrpThrLysAspThrThrGlyThrAsnLeuPheLeuValAlaAla	217
Qy	669	CATGAATTTGGTCATGCACNCGGGCTCTCTCACTCCATCATCAACAGCGCTTGATGTT	728
Db	218	HisGluIleGlyHisSerLeuGlyLeuPheHisSerAlaAsnThrGluAlaLeuMetTyr	237
Qy	729	CCAAATATGCTCCCTCG--GATCCAGAAAAATACCACCTTTCTCAGGATGATATCAAT	785
Db	238	ProLeuTyrHisSerLeuThrAspLeuThrArgPheArgLeuSerGlnAspIleAsn	257
Qy	786	GGATCCAGTCCATCATATGGA-----GGTCTGCTCAGGTACCTGCT	827
Db	258	GlyIleGlnSerLeuTyrGlyProProAspSerProGluThrProLeuValProThr	277
Qy	828	AAG-----CCAAAGGAACCCATATACCCCATGCTGTGACCTGACTTGACTTTTGAC	881
Db	278	ValProValProProGluProGlyThrProAlaAsnCysAspProAlaLeuSerPheAsp	297



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Db      317 SerHisTspAsnProGluProGluPheHisLeuIleSerAlaPheTyrProThrLeuPro 336
QY      1002 GCTGATCTGCAAGCTGCATACAG--AACCCAGAGATAGATTCTGGTTTAAAGAT 1058
Db      337 SerAspLeuAspAlaAlaTyrGluAlaHisAnThrAspSerValLeuIlePheIysGly 356
QY      1059 GAAAACTTCTGATCATCAGAGGATATGCTGCTTTCGCCAGATTATCCAAATCCATCCAT 1118
Db      357 SerGlnPheTyrPalaValArgGlyAsnGluValGlnAlaGlyTyrProIysGlyIleHis 376
QY      1119 ACATTAGGTTTCCAGGACGTGTGAAGAAATAGATGACGCCGTCTGTGATAGACACACA 1178
Db      377 ThrLeuGlyPheProProThrValIysIleAspAlaAlaValPheGluIysGluLys 396
QY      1179 AGAAAACTTACTTCTTGTGGGCATTTGGTCTCGAGGTTTGTATGAAATGACCCAAACC 1238
Db      397 LysLysThrTyrPhePheValGlyAspLysTyrTyrPheAspGluThrArgHisVal 416
QY      1239 ATGGCAAAAGGATCCCGCAGAGATGGTAAACACTTTCCTCGAATCAGTATCCGTGTT 1298
Db      417 MetAspLysGlyPheProArgGlnIleThrAspAspPheProGlyIleGluProGlnVal 436
QY      1299 GATGCTGCTTTCCAGTACAAAGATTCTTCTTTTCAGCCGTGATCAAGCAATTTGAA 1358
Db      437 AspAlaValLeuHisGluPheGlyPhePheTyrPhePheArgGlySerSerGlnPheGlu 456
QY      1359 TACAACATTAGACAAAGAAATATACCGAATCATGAGAACTAATACTTGGTTTCAATGC 1418
Db      457 PheAspProAsnAlaArgThrValThrHisIleLeuLysSerAsnSerTrpLeuLeuCys 476

RESULT 4
KMSS1
stromelysin 1 (EC 3.4.24.17) precursor - mouse
A:Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); pr
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1992 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: J01476; S18867; S32963; S33139
R:Hammani, K.; Henriot, P.; Beckhout, Y.
Gene 120, 321-322, 1992
A:Title: Cloning and sequencing of a cDNA encoding mouse stromelysin 1.
A:Reference number: J01476; MUID:93013057; PMID:1398148
A:Accession: J01476
A:Molecule type: mRNA
A:Residues: 1-477 <LIF>
A:Cross-references: UNIPROT:P28862; EMBL:X66402; NID:G296167; PIDN:CAA47029.1; PID:G2961
A:Note: it is uncertain whether Met-1 is the initiator or whether translation is initiat
R:Li, F.; Strange, R.; Saurer, S.; Niemann, H.; Friis, R.R.
Genes Dev. 3, 848-859, 1989
A:Title: Genes for extracellular matrix-degrading metalloproteinases and their inhibitor
A:Reference number: A32963; MUID:89306621; PMID:2744464
A:Accession: B32963
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 415-467, 'T', 469 <BRE>
A:Experimental source: clone EMS-2
C:Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation
C:Comment: This enzyme degrades various extracellular matrix proteins, including fibron
C:Comment: Stromelysin 1 hydrolyzes peptide bonds in plasminogen to yield a fragment wit
C:Comment: Prostromelysin is found in glycosylated and unglycosylated forms, both of whi
C:Function:
A:Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl si
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
F:17-17/Domain: signal sequence #status predicted <SIG>
F:18-477/Product: prostromelysin 1 #status predicted <PRO>
F:18-99/Domain: activation peptide #status predicted <ACT>

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F:60-264/Domain: matrix metalloproteinase homology <MMP>
F:90-97/Region: autoinhibitory
F:100-477/Product: hemopexin repeat homology <HMP>
F:284-477/Domain: hemopexin repeat homology <HPN>
F:218,218,222,228/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F:219/Active site: Glu #status predicted
F:290-477/Disulfide bonds: #status predicted

Alignment Scores:
Pred. No.: 1,09e-97 Length: 477
Score: 1237.50 Matches: 246
Percent Similarity: 66.18% Conservative: 73
Best Local Similarity: 51.04% Mismatches: 142
Query Match: 42.24% Indels: 21
DB: 1 Gaps: 10

US-10-729-807-28 (1-1627) x KMSS1 (1-477)
QY      18 AGAGCAATGAACGCGCTTCTGCTCTGTTGTTGTTTATTAACATTTTCTTCTGCAATT 77
Db      2 LysGlyLeuProValLeuLeuTrpLeuCys-----ValValValCysSerSerTyr 18
QY      78 CCTTAGTCCGATGACGGAATAATGAAGAA---AATATGCAACTGGCTCAGGCATATCTC 134
Db      19 ProLeuHisAspSerAlaArgAspAspAlaGlyMetGluLeuLeuGlnLysTyrLeu 38
QY      135 AACCAAGTTCTACTCTCTTAAATAGAAAGGAATCATCTTGTTCAAAGCAAGAAATAGGAGT 194
Db      39 GluAsnTyrTyrGlyLeuAlaLysAspValLysGlnPheIleLysLysLysAspSerSer 58
QY      195 CTCATAGATGACAAATTCGGGAATTCGAAGCATTTTGGATTCACATTCACATTCGGAATA 254
Db      59 LeuIleValLysLysIleGlnGluMetGlnLysPheLeuGlyLeuGluMetThrGlyLys 78
QY      255 CTGCACTCAACACACCTTTCAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGGC 314
Db      79 LeuAspSerAsnThrMetGluLeuMetHisLysProArgCysGlyValProAspValGly 98
QY      315 CAGTATGGCTACACCTCCCTGGG-----TGGAGAAATAACAACCTACCTACAGA 365
Db      99 GlyPheSer--ThrPheProGlySerProLysTyrPheLysSerHisIleThrTyrArg 117
QY      366 ATAATAACTATCTCCGGATATGCGACGAGCTGCTGTGGATGAGCTATCCAAAGAGT 425
Db      118 IleValAsnTyrThrProAspLeuProArgGlnSerValAspSerAlaIleGlnLysAla 137
QY      426 TTAGAAGTGTGGAGCAAAAGTCACTCCATTAATAATTCACCAAGATTTCAAGGGGATTGCA 485
Db      138 LeuLysValTyrGluGluValThrProLeuThrPheSerArgIleSerGluGlyGluAla 157
QY      486 GACATCATGATGCTTTTAGGACTCGAGTCGATCGATGTCGG-----TGTCCTCGCTATTGTTGAT 542
Db      158 AspileMetIleSerPheAlaValGlyGluHisGlyAspPheValPro-----PheAsp 175
QY      543 GGTCCCTTGGGAGTCTTGGCCATCCCTTCTCTGCTCCGGCTCGGTGGTGGTGCACACT 602
Db      176 GlyProGlyThrValLeuAlaHisAlaTyrAlaProGlyProGlyIleAsnGlyAspAla 195
QY      603 CATTTTGTAGAGGATGAAAACTGGACCAAGGATGGAGCAGGATTCACATGTTGTTCTTGTG 662
Db      196 HisPheAspAspAspGluArgTyrThrGluAspValThrGlyThrAsnLeuPheLeuVal 215
QY      663 GCTGCTCATGAATTTGGTCATGCACTGGGGTCTCTCTCACTCAATGATCAACACAGCCTTG 722
Db      216 AlaAlaHisGluLeuGlyHisSerLeuGlyLeuTyrHisSerAlaLysAlaGluAlaLeu 235
QY      723 ATGTTCCCAATTAT---GTCTCCCTGATCCGAAATAATACCCATTTTCTCAGGATCAT 779
Db      236 MetTyrProValTyrLysSerSerThrAspLeuSerArgPheHisLeuSerGlnAspAsp 255
QY      780 ATCAATGGAATCCAGTCCATCTATGGA-----GGTCTCGCTAAGGTA 821

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Db 256 ValAspGlyIleGlnSerLeuTyrGlyThrProThrAlaSerProAspValLeuValVal 275  
Qy 822 CTGTGTAAGCAAG-----GAACCCATATACCCCATGCTGTGACCTGACTGACT 875  
Db 276 ProThrLysSerAsnSerLeuGluProGluThrSerProMetCysSerSerThrLeuPhe 295  
Qy 876 TTTGACGCTATCAACTTCCGACAGAGAGTAACTGTTTAAAGCAGCAGCCTATGG 935  
Db 296 PheAspAlaValSerThrLeuArgGlyGluValLeuPhePheLysAspArgHisPheTrp 315  
Qy 936 AGGATCTATTATGATATACACGAGTGTGAGTTGAATTAATGCTTCAATCTGCGCATCT 995  
Db 316 ArgLysSerLeuArgThrProGluProGluPheThrLeuLeuSerSerPheTrpProSer 335  
Qy 996 CTCCGAGCTGATCTGCAAGTGTGATACGAG-----AACCACAGAGATAGATCTGGTTTT 1052  
Db 336 LeuProSerAsnMetAspAlaAlaTyrGluValThrAsnArgAspThrValPheIlePhe 355  
Qy 1053 AAGATGCAAACTTCTGGATGATCAGAGGATATGCTCTTGGCAGATTATCCAAATCC 1112  
Db 356 LysGlyAsnGlnPheTrpAlaIleArgGlyHisGluLeuAlaGlyTyrProLysSer 375  
Qy 1113 ATCATATACATAGCTTTTCCAGGACGCTGCAAGAAATAGATGACGCGCTGTGATAAG 1172  
Db 376 IleHisThrLeuGlyLeuProAlaThrValLysLysIleAspAlaIleSerAsnLys 395  
Qy 1173 ACCACAGAAAACTTCTTTGTTGGGATTTGTTGGTGCTGGAGGTTTGATGAAATGACC 1232  
Db 396 GluLysArgLysThrTyrPhePheValGluAspLysTyrTrpArgPheAspGluLysLys 415  
Qy 1233 CAACACATGACAAAGGATTCGCGCAGAGAGTGTAAACACTTTCCTGCGAATCAGTATC 1292  
Db 416 GlnSerMetGluProGlyPheProArgLysIleAlaGluAspPheProGlyValAspSer 435  
Qy 1293 CGTGTGATGCTGTTTCCAGTACAAAGGATTTCTTTTTCAGCCGTGGATCAAGCAA 1352  
Db 436 ArgValAspAlaValPheGluAlaPheGlyPheLeuTyrPhePheSerGlySerSerGln 455  
Qy 1353 TTTGATATCAACATTAAAGACAGATATATACCGAATCATGAGAACTATATCTGTTTT 1412  
Db 456 LeuGluPheAspProAsnAlaLysLysValHisIleLeuLysSerAsnSerTrpPhe 475  
Qy 1413 CAATGC 1418  
Db 476 AsnCys 477

RESULT 5  
KCHUS2  
stromelysin 2 (EC 3.4.24.22) precursor [validated] - human  
N;Alternate names: matrix metalloproteinase 10 (MMP10); transin-2  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 09-Jul-2004  
C;Accession: A28816; A47496  
R;Muller, D.; Quantin, B.; Gesnel, M.C.; Millon-Collard, R.; Abecassis, J.; Breathnach, Biochem. J. 253, 187-192, 1988  
A;Title: The collagenase gene family in humans consists of at least four members.  
A;Reference number: A90339; MUID:88339885; PMID:2844164  
A;Accession: A28816  
A;Molecule type: mRNA  
A;Residues: 1-476 <MUL>  
A;Cross-references: UNIPROT:P09238; EMBL:X07820; NID:g36628; PIDN:CAA30679.1; PID:g36629  
A;Note: mRNA for this protein was detected in several human tumors  
R;Windsor, L.J.; Grenett, H.; Birkedal-Hansen, B.; Borden, M.K.; Engler, J.A.; Birkedal-J. Biol. Chem. 268, 17341-17347, 1993  
A;Title: Cell type-specific regulation of SL-1 and SL-2 genes. Induction of the SL-2 gene  
A;Reference number: A47496; MUID:93352520; PMID:8349617  
A;Accession: A47496  
A;Molecule type: protein  
A;Residues: 17-33 <WIN>  
C;Comment: This enzyme degrades various extracellular matrix proteins, including fibronectin  
A;Gene: GDB:MMP10; STMY2  
A;Cross-references: GDB:120392; OMIM:185260

A;Map position: 11q22.3-11q23  
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotease  
F;1-16/Domain: signal sequence #status predicted <SIG>  
F;17-476/Product: prostromelysin 2 #status experimental <PRO>  
F;17-98/Domain: activation peptide #status predicted <ACT>  
F;59-263/Domain: matrix metalloproteinase homology <MMP>  
F;89-96/Region: autoinhibitory  
F;99-476/Product: stromelysin 2 #status predicted <MAT>  
F;93-476/Domain: hemopexin repeat homology <PN>  
F;91,217,221,227/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status  
F;119/Binding site: carboxylate (Asn) (covalent) #status predicted  
F;217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted  
F;218/Active site: Glu #status predicted  
F;289-476/Disulfide bonds: #status predicted

Alignment Scores: 2.18e-97 Length: 476  
Pred. No.: 1234.00 Matches: 244  
Score: 67.58% Conservative: 77  
Percent Similarity: 51.37% Mismatches: 136  
Best Local Similarity: 42.12% Indels: 18  
Query Match: 1 Gaps: 8  
DB: 1

US-10-729-807-28 (1-1627) x KCHUS2 (1-476)

Qy 33 CTTCGCTTCTGTTGTTGTTTCTTTTAAACATTTCTTCGCAATTCCTTAGTCCGGATG 92  
Db 7 LeuValLeuLeuCysLeu-----ProValCysSerAlaTyrProLeuSerGlyAla 23  
Qy 93 ACGGAAATCAAGAA--AATATGCAACTGGCTCAGCATATCTCAACCAAGTTCTACTCT 149  
Db 24 AlaLysGluGlnAspSerAsnLysAspLeuAlaGlnGlnTyrLeuGluLysTyrTyrAsn 43  
Qy 150 CTTGAAATAGAGGGAATCATCTTGTTCAAAGCAAGAAATAGAGTCTCATAGATGACAA 209  
Db 44 LeuGluLysAspValLysGlnPhe--ArgArgLysAspSerAsnLeuIleValLysLys 62  
Qy 210 ATTGGGAATGCAAGCATTTTGGATTGACAGTGCATGGAAGTCTGGAAGTCTCAACACC 269  
Db 63 IleGlnGlyMetGlnLysPheLeuGlyLeuGluValThrGlyLysLeuAspThrAspThr 82  
Qy 270 CTTGAGATCATGAAGCACCCAGCTGGGGTGGCTGCTGTCGTCAGTGGCCATATGGCTAC-- 326  
Db 83 LeuGluValMetArgLysProArgCysGlyValProAspValGlyHisPheSerSerPhe 102  
Qy 327 ---ACCTCCCTGGTGAGAAAATAACACCTCACCTACAGAATAATAAATACTATACCTCG 383  
Db 103 ProGlyMetProLysTrpArgLysThrHisLeuThrTyrArgIleValAsnTyrThrPro 122  
Qy 384 GATATGCGACGAGCTGCTGTTGGATGAGGCTATCCAGAAGTTTAGAAGTGTGGAGCAA 443  
Db 123 AspLeuProArgAspAlaValAspSerAlaIleGluLysAlaLeuLysValTrpGluGlu 142  
Qy 444 GTCACTCCACTAAATTCACCAAGATTCAAGAGGATTCAAGAGGATTCAGACATCATGATTCCTTT 503  
Db 143 ValThrProLeuThrPheSerArgLeuTyrGluGlyGluAlaAspIleMetIleSerPhe 162  
Qy 504 AGGACTCGAGTCCATGCTCGGTGCTCTGCTATTTTGTATGCTGCTGCGAGTGTGGC 563  
Db 163 AlaValLysGluHisGlyAspPhe--TyrSerPheAspGlyProGlyHisSerLeuAla 181  
Qy 564 CATGCTTTCTGCTGCTGGTCCGGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 623  
Db 182 HisAlaTyrProGlyProGlyProGlyLeuTyrGlyAspIleHisPheAspAspGluLys 201  
Qy 624 TGGACCAAGATGAGCAGGATTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 683  
Db 202 TrpThrGluAspAlaSerGlyThrAsnLeuPheLeuValAlaAlaHisGluLeuGlyHis 221  
Qy 684 GCATGGGGCTCTCTCATCTCAATGATCAACAGCCTTGATGTGCCAAATATGCTCC 743  
Db 222 SerLeuGlyLeuPheHisSerAlaAsnThrGluAlaLeuMetTyrProLeuTyrAsnSer 241





Db 184 AlaPheGlnProGlyProGlyIleGlyAspAlaHisPheAspGluAspGluArgTyr 203  
 QY 627 ACCAAGATGAGCAGGAGTCAACTGTTTCTTGTGGCTGCTCATGAATTTGGTCATGCA 686  
 Db 204 ThrLysAsnPheArgAspTyrAsnLeuTyrArgValAlaAlaHisGluLeuGlyHisSer 223  
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 Db 224 LeuGlyLeuSerHisSerThrAspIleGlyAlaLeuMetTyrProAsnTyrIleTyrThr 243  
 QY 747 GATCCAGAAAATACCCACTTCTCAGGATGATCAATGAATCCAGTCCATCTATGGA 806  
 Db 244 Gly-----AspValGlnLeuSerGlnAspAspIleAspGlyIleGlnAlaIleTyrGly 261  
 QY 807 GGTCTGCTTAAGTACTGTCTAAGCCAAAGAACCCACTATACCCCATGCTGTGACCT 866  
 Db 262 Pro---SerGluAsnProValGlnProSerGlyProGlnThrProGlnValCysAspSer 280  
 QY 867 GACTGTGACTTTCAGCGTATCACAACTTTCGGCAGAGAAGTAAATGTTCTTTAAAGGCAGG 926  
 Db 281 LysLeuThrPheAspAlaIleThrThrLeuArgGlyGluLeuMetPhePheLysAspArg 300  
 QY 927 CACTATGAGGAGTATTATGATATCACGGATGTTCAGTTTGAATTAATTCCTCATTC 986  
 Db 301 PheTyrMetArgThrAsnSerPheTyrProGluValGluLeuAsnPheIleSerValPhe 320  
 QY 987 TGGCCATCTCTGCCAGTGTGTCGAAGCTGCATACGAG---AACCCAGCAGATAGATT 1043  
 Db 321 TrpProGlnValProAsnGlyLeuGlnAlaAlaTyrGluIleAlaAspArgAspGluVal 340  
 QY 1044 CTGGTGTAAAGATGAAACTCTGATGATCAGAGGATATGCTGCTTGGCCAGATTAT 1103  
 Db 341 ArgPhePheLysGlyAsnLysTyrTrpAlaValArgGlyGlnAspValLeuTyrGlyTyr 360  
 QY 1104 CCCAAATCCATCCAT---ACATTAGTGTTCACGAGCTGTGAAGAAAATAGATGCAGCC 1160  
 Db 361 ProllysAspIleHisArgSerPheGlyPheProSerThrValLysAsnIleAspAlaAla 380  
 QY 1161 GTCTGTGATTAAGACCAAGAAAACCTACTTCTTGTGGCATTTGGTGTGAGGTTT 1220  
 Db 381 ValPheGluGluAspThrGlyLysThrTyrPhePheValAlaHisGluCysTrpArgTyr 400  
 QY 1221 GATGAATACCCAAACCATGGACAAAGGATTCCTCCGACAGAGTGGTAAACACTTTCCT 1280  
 Db 401 AspGluTyrLysGlnSerMetAspThrGlyTyrProllysMetIleAlaGluGluPhePro 420  
 QY 1281 GGAATCAGTATCCGTGTGTGCTGCTTTCAGTACAAAGGATTCCTTTTTCAGCCGT 1340  
 Db 421 GlyIleGlyAsnLysValAspAlaValPheGlnLysAspGlyPheLeuTyrPhePheHis 440  
 QY 1341 GGATCAAGCAATTTGAATACACATTAAGCAAAAGATATTATCCCGAATCATGAGACT 1400  
 Db 441 GlyThrArgGlnTyrGlnPheAspPheLysThrLysArgIleLeuThrLeuGlnLysAla 460  
 QY 1401 AATACTTGGTTTCAATGCAAGAA 1424  
 Db 461 AsnSerTrpPheAsnCysArgLys 468

## RESULT 7

KCRTS2  
 N:Alternative names: matrix metalloproteinase 10 (MMP10); transin-2  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text\_change 09-Jul-2004  
 C:Accession: B26403; A41775; S26498  
 R:Breatnach, R.; Matrisian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P.  
 Nucleic Acids Res. 15, 1139-1151, 1987  
 A:Title: Sequences coding for part of oncogene-induced transin are highly conserved in a  
 A:Reference number: A26403; MUID:87146421; PMID:3547333  
 A:Accession: B26403  
 A:Molecule type: mRNA  
 A:Residues: 1-476 <BRE>  
 A:Cross-references: UNIPROT:P07152; EMBL:X05083; NID:g57388; PIDN:CAA28739.1; PID:g57389

A:Note: intron positions were determined by comparison of the cDNA sequence to genomic  
 A:Note: mRNA for this protein was expressed in several transformed rat embryo fibroblasts  
 R:Chan, J.C.; Scanlon, M.; Zhang, H.Z.; Jia, L.B.; Yu, D.H.; Hung, M.C.; French, M.; Eas  
 J. Biol. Chem. 267, 1099-1103, 1992  
 A:Title: Molecular cloning and characterization of v-mos-activated transformation-associ  
 A:Reference number: A41775; MUID:92112748; PMID:1370458  
 A:Accession: A41775  
 A:Molecule type: mRNA  
 A:Residues: 1-476 <CHA>  
 A:Cross-references: GB:M65253; NID:g207150; PIDN:AAA42202.1; PID:g207151  
 A:Note: sequence extracted from NCBI backbone (NCBIP:76184)  
 R:de Vouge, M.W.; Mukherjee, B.B.  
 Oncogene 7, 109-119, 1992  
 A:Title: Transformation of normal rat kidney cells by v-K-ras enhances expression of tra  
 A:Reference number: S26496; MUID:92158347; PMID:1741158  
 A:Accession: S26498  
 A:Status: preliminary; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 31-103,'L',241-242,'TQMEBKPH',251,'L',253-254,'CE',293-294,'L',296 <DEV>  
 A:Cross-references: EMBL:X64020  
 C:Genetics:  
 A:Introns: 35/3; 117/2; 167/1; 209/1; 264/1; 311/2; 356/1; 409/2; 444/1  
 C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote  
 C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo  
 F:1-17/Domain: signal sequence #status predicted <SIG>  
 F:18-476/Product: prostomelysin 2 #status predicted <PRO>  
 F:18-99/Domain: activation peptide #status predicted <ACT>  
 F:60-264/Domain: matrix metalloproteinase homology <MMP>  
 F:90-97/Region: autoinhibitory  
 F:100-476/Product: stromelysin 2 #status predicted <MAT>  
 F:283-476/Domain: hemopexin repeat homology <PXN>  
 F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status  
 F:120/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted  
 F:219/Active site: Glu #status predicted  
 F:289-476/Disulfide bonds: #status predicted  
 Alignment Scores:  
 Pred. No.: 2,4e-94 Length: 476  
 Score: 1198.50 Matches: 243  
 Percent Similarity: 64.24% Conservative: 66  
 Best Local Similarity: 50.52% Mismatches: 151  
 Query Match: 40.90% Indels: 21  
 DB: 1 Gaps: 9  
 US-10-729-807-28 (1-1627) x KCRTS2 (1-476)  
 QY 24 ATGAAGCGCTCTGCTCTCTGTTCTTTTATAACATTTCTTCTGATTTCCCTTA 83  
 Db 1 MetGluProLeuAlaIleLeuValLeuLeuCysPheProIleCysSerAlaTyrProLeu 20  
 QY 84 -----GTCCGATGACGGAATAATGAAGAAATATGCAACCTGCTCAGGCATATCTC 134  
 Db 21 HisGlyAlaValArg-----GlnAspHisSerThrMetAspLeuAlaGlnGlnTyrLeu 38  
 QY 135 AACCAAGTCTACTCTCTTGAATAATAGAAGGAATCATCTTGTTCAAAGCAAGATAGGAGT 194  
 Db 39 GluLysTyrTyrAsnPheArgLysAsnGluLysGlnPhePheLysArgLysAspSerSer 58  
 QY 195 CTCATGATGACAAAATTCGGGAAATGCAAGCATTTTTCGATTCAGTCAGTCTGGAAGA 254  
 Db 59 ProValValLysLysIleGluGluMetGlnLysPheLeuGlyLeuGluMetThrGlyLys 78  
 QY 255 CTGACCTCAACACCTTCGATCATCAAGACACCCAGGTGTGGGTGCTGATGTGGGC 314  
 Db 79 LeuAspSerAsnThrValGluMetMetHisLysProArgCysGlyValProAspValGly 98  
 QY 315 CAGTATGGCTACACCTCCCTCTGGG-----TGGAGAAATAACAACTCACCTACAGA 365  
 Db 99 GlyPheSer---ThrPheProGlySerProLysTrpArgLysAsnHisIleSerTyrArg 117  
 QY 366 ATAATAACTATATCTCCGGATATGGCAGCACTCTGTGGATGAGGCTATCCAGAGGT 425



QY 321 GGCTACACCTCCTCTGGG-----TGAGAAAATACAACTCCCTACAGAAATAA 371  
 Db 101 ValLeuThr-----ProGlyLysSerCysTrpGluAsnThrAsnLeuThrTyraArgileGlu 119  
 QY 372 AACTATCTCCGATATGGCAGCAGCTCTGTGGATGAGGCTATCCAAAGAGTGTAGAA 431  
 Db 120 AsnTyrrThrProAspLeuSerArgAlaAspValAspGlnAlaIleGluLysAlaPheGln 139  
 QY 432 GTGTGGAGCAAGTCACTCCCAATAATTCACCAAGATTTCAAGGGAGTTGAGACATC 491  
 Db 140 LeuTrpSerAsnValThrProLeuThrPheThrLysValSerGluGlyGlnAlaAspIle 159  
 QY 492 ATGATTCCTTTAGGACTCCAGTCCAGTCGGTGTCTCGCTATTTTGTATGTCCTCG 551  
 Db 160 MetIleSerPhe---ValArgGlyAspHisArgAspAsnSerProPheAspGlyProGly 178  
 QY 552 GGAAGTGTCTGGCATGCTTCTCTCTCTGGTCCGGGCTCTGGGTGGTGCACACTCAATTTGAT 611  
 Db 179 GlyAsnLeuAlaHisAlaPheGlnProGlyAlaGlyIleGlyAspAlaHisPheAsp 198  
 QY 612 GAGGATGAACCTGGACCAAGGATGGAGAGGATTCACCTGTTTCTTGGCTGCTCAT 671  
 Db 199 AspAspGluTrpTrpThrSerAsnPheGlnAspTyrrAsnLeuTyraArgValAlaAlaHis 218  
 QY 672 GAATTTGGTATGCACCTGGGCTCTCTCACTCCCAATGATCAACAGCCTTGATGTTCCCA 731  
 Db 219 GluPheGlyHisSerLeuGlyLeuAlaHisSerThrAspIleGlyAlaLeuMetTyrrPro 238  
 QY 732 AATTATGTC---TCCCTGGATCCCAAGAAATACCCACTTCTCAGGATGATATCAATGGA 788  
 Db 239 SerTyrrThrPheSerGlyAspValGln-----LeuSerGlnAspAspIleAspGly 255  
 QY 789 ATCCAGTCCATCTATGAGGCTCTCCCTAAGTACTCTGTAAGCCAAAGGAAACCCACTATA 848  
 Db 256 IleGlnAlaIleTyrrGlyPro---SerGlnAsnProThrGlnProValGlyProGlnThr 274  
 QY 849 CCCATGCTGTGACCTGACTTTCACCTTTCACCTATCACTTCCGAGAGAGTA 908  
 Db 275 ProGluValCysAspSerLysLeuThrPheAspAlaIleThrIleArgGlyGluVal 294  
 QY 909 ATGTCTCTTAAAGCCAGCCTATGAGGATCTATTATGATATCAACGGATGTTGAGTTT 968  
 Db 295 MetPheLysAspArgPheTyrrMetArgThrAsnProLeuTyrrProGluValGluLeu 314  
 QY 969 GAATTAATGCTTCATCTGCGCATCTCTGCGAGCTGATCTGCAAGCTGATAGAG--- 1025  
 Db 315 AsnPheIleSerValPheTrpProGlnLeuProAsnGlyLeuGlnAlaAlaTyrrGluVal 334  
 QY 1026 AACCCAGAGATAAGATTCTGGTTTAAAGATGAAACTTCTCGATGATCAGAGGATAT 1085  
 Db 335 AlaAspArgAspGluValArgPhePheLysGlyAsnLysTyrrTrpAlaValLysGlyGln 354  
 QY 1086 GCTGCTTGGCAGATATCCCAATCCATCCAT---ACATTAGGTTTCCAGGACGTGTG 1142  
 Db 355 AspValLeuArgGlyTyrrProArgAspIleTyrrArgSerPheGlyPheProArgThrVal 374  
 QY 1143 AAGAAAATAGATGACGCGCTGTGTATGATGACCAAGAACCAAGAAACCTACTCTTTGTGGGC 1202  
 Db 375 LysSerIleAspAlaAlaValSerGluGluAspThrGlyLysThrTyrrPhePheValAla 394  
 QY 1203 ATTTGGTCTGAGGTTTGATGAATGATGACCAACCAAGGATTCCTCCGAGAGA 1262  
 Db 395 AsnLysCysTrpArgTyrrAspGluTyrrLysGlnSerMetAspAlaGlyTyrrProLysMet 414  
 QY 1263 GTGGTAAACACTTCTCTGGAAATCAGTATCCGTGTGATGCTGCTTCCAGTACAAAGGA 1322  
 Db 415 IleAlaGluAspPheProGlyIleGlyAsnLysValAspAlaValPheGlnLysGlyGly 434  
 QY 1323 TTCTCTTTTTCAGCGGTGATCAAGCAATTTGAATACACATTAAGACAAAGATATT 1382  
 Db 435 PhePheTyrrPhePheHisGlyArgArgGlnTyrrLysPheAspProGlnThrLysArgile 454  
 QY 1383 ACCCGAATCATGAGAACTAATACTTGTGTTTCAATGCAAGAA 1424

Db 455 LeuThrLeuLysAlaAsnSerTrpPheAsnCysArgLys 468

## RESULT 9

KCRTLH  
 Stromelysin 1 (EC 3.4.24.17) precursor - rat  
 N;Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3);  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 13-Aug-1986 #sequence revision 13-Aug-1986 #text\_change 09-Jul-2004  
 R;Accession: A00997; PS0150; S22767  
 R;Matrisian, L.M.; Glatchenhause, N.; Gesnel, M.C.; Breathnach, R.  
 EMBO J. 4, 1435-1440, 1985  
 A;Title: Epidermal growth factor and oncogenes induce transcription of the same cellular  
 A;Reference number: A00997; MUID:85284930; PMID:3875482  
 A;Accession: A00997  
 A;Molecule type: mRNA  
 A;Residues: 1-475 <NAL>  
 A;Cross-references: UNIPROT:P03957; GB:X02601; NID:G57460; PIDN:CA26448.1; PID:G57461  
 R;Umenishi, F.; Yasumitsu, H.; Ashida, Y.; Yamauti, J.; Umeda, M.; Miyazaki, K.  
 J. Biochem. 108, 537-543, 1990  
 A;Title: Purification and properties of extracellular matrix-degrading metallo-proteinase  
 A;Reference number: PS0150; MUID:91154156; PMID:1963430  
 A;Accession: PS0150  
 A;Molecule type: protein  
 A;Residues: 19-20,'X',22-28;110-112,'X',114-115,'X',117,'X',119;309-325 <UME>  
 R;Breathnach, R.; Matrisian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P.  
 Nucleic Acids Res. 15, 1139-1151, 1987  
 A;Title: Sequences coding for part of oncogene-induced transin are highly conserved in  
 A;Reference number: A26403; MUID:87146421; PMID:3547333  
 A;Contents: annotation; introns  
 A;Note: Intron positions were determined by comparison of the previously reported cDNA  
 R;Sanchez-Lopez, R.; Nicholson, R.; Gesnel, M.C.; Matrisian, L.M.; Breathnach, R.  
 J. Biol. Chem. 263, 11892-11899, 1988  
 A;Title: Structure-function relationships in the collagenase family member transin.  
 A;Reference number: S22767; MUID:88298869; PMID:2841336  
 A;Contents: annotation; active site; activation  
 A;Note: molecules with mutations in the autoinhibitory region showed a much increased  
 A;Note: mutations of His-216, Glu-217, and His-226 inactivate the enzyme  
 R;Park, A.J.; Matrisian, L.M.; Kells, A.F.; Pearson, R.; Yuan, Z.; Navre, M.  
 J. Biol. Chem. 266, 1584-1590, 1991  
 A;Title: Mutational analysis of the transin (rat stromelysin) autoinhibitor region demo  
 A;Reference number: A43028; MUID:91107652; PMID:1988438  
 A;Contents: annotation; autoinhibitory region  
 A;Note: Arg-89 and Cys-92 are essential for maintaining latency  
 C;Comment: This enzyme degrades various extracellular matrix proteins, including fibron  
 C;Comment: Stromelysin 1 hydrolyzes peptide bonds in plasminogen to yield a fragment wi  
 C;Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activatio  
 C;Comment: Prostromelysin is found in glycosylated and unglycosylated forms, both of wh  
 C;Genetics:  
 A;Introns: 33/3; 115/2; 165/1; 207/1; 262/1; 310/2; 355/1; 408/2; 443/1  
 C;Function:  
 A;Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl s  
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote  
 C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo  
 F;1-17/Domain: signal sequence #status predicted <SIG>  
 F;18-475/Product: prostromelysin 1 #status predicted <PRO>  
 F;18-97/Domain: activation peptide #status predicted <ACT>  
 F;58-262/Domain: matrix metalloproteinase homology <MMP>  
 F;88-95/Region: autoinhibitory  
 F;98-475/Product: stromelysin 1 #status predicted <MAT>  
 F;282-475/Domain: hemopexin repeat homology <PXN>  
 F;90,216,220,226/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status  
 F;118/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;216,220,226/Binding site: zinc, catalytic (His) (active) #status predicted  
 F;217/Active site: Glu #status experimental  
 F;288-475/Disulfide bonds: #status predicted

Alignment Scores:  
 Pred. No.: 3,32e-92 Length: 475  
 Score: 1173.50 Matches: 236  
 Percent Similarity: 64.86% Conservative: 76  
 Best Local Similarity: 49.06% Mismatches: 148  
 Query Match: 40.05% Indels: 21





QY 1098 GATTATCCCAATCATCCAT--ACATTAGGTTTTCAGGACGTGTGAAGAAAATAGAT 115  
Db 358 GlyTyrProLysAspIleHisSerSerPheGlyPheProArgSerValAsnHisIleAasp 377  
QY 1155 GCAGCCGCTGTGTATAGACACCAAAAAACCTACTTCTTTTGCGGCATTTGGTGCTGG 121  
Db 378 AlaAlaValSerGluGluAspThrGlyLysThrTyrrPhePheValAlaAsnLysTyrTrp 397  
QY 1215 AGTTTTGTAAATGACCACCAACCATGACAAGAAGATTCCCGCAGACAGATGGTAACAC 127  
Db 398 ArgTyrAspGluTyrLysArgSerMetAspAlaGlyTyrProLysMetIleGluTyrAsp 417  
QY 1275 TTCTCTGAATCAGTATCCGTTGTTGATGCTGTTCTCCAGTACAAAGATTTCTTTTTC 133  
Db 418 PheProGlyIleGlyAsnLysValAspAlaValPheLysLysAspGlyPhePheTyrPhe 437  
QY 1335 AGCCGTGATCAAGCAANTTGAATCACATTAAGACAAAGAATAATTACCGAATCATG 139  
Db 438 PheHisGlyThrArgGlnTyrLysPheApproLysThrLysArgIleLeuthrLeuGln 457  
QY 1395 AGAACTAATACTTGGTTTCAATGCCAAAGAA 1424  
Db 458 LysAlaAsnSerTrpPheAsnCysArgLys 467

RESULT 11  
KCHUI  
Interstitial collagenase (EC 3.4.24.7) precursor [validated] - human  
N:Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1);  
C:Species: Homo sapiens (man)  
C>Date: 13-Aug-1986 #sequence\_revision 30-Sep-1992 #text change 09-Jul-2004  
S:Accession: A37308; S22766; I57620; A00996; D29157; A45418; S06132; B60964; S  
R:Templeton, N.S.; Brown, P.D.; Levy, A.T.; Margulies, I.M.K.; Liotta, L.A.; S  
Cancer Res. 50, 5431-5437, 1990  
A>Title: Cloning and characterization of human tumor cell interstitial collagege  
A:Reference number: A37308; MUID:90352587; PMID:2167156  
A:Accession: A37308  
A:Molecule type: mRNA  
A:Residues: 1-469 <TEM>  
A:Cross-references: UNIPROT:P03956; GB:X54925; NID:g30125; PIDN:CAA38691.1; PIDN:  
R:Brinckerhoff, C.E.; Ruby, P.L.; Austin, S.D.; Fini, M.E.; White, H.D.  
J. Clin. Invest. 7, 542-546, 1987  
A>Title: Molecular cloning of human synovial cell collagenase and selection of  
A:Reference number: S22766; MUID:87109799; PMID:3027129  
A:Accession: S22766  
A:Molecule type: DNA  
A:Residues: 1-63,65-70 <BRI>  
A:Cross-references: EMBL:M15996; NID:g180666; PIDN:AAA35700.1; PID:g180667  
R:Angel, P.; Baumann, I.; Stein, B.; Delius, H.; Rahmsdorf, H.J.; Herrlich, P.  
Mol. Cell. Biol. 7, 2256-2266, 1987  
A>Title: 12-O-tetradecanoyl-phorbol-13-acetate induction of the human collage  
A:Reference number: I57620; MUID:87257941; PMID:3037355  
A:Accession: I57620  
A>Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA

A;Residues: 1-35 <RES>  
A;Cross-references: GB:M16567; NID:g180668; PIDN:AAAS2033.1; PID:g180669  
R;Goldberg, G.I.; Wilhelm, S.M.; Kronberger, A.; Bauer, E.A.; Grant, G.A.; Eisen, A.Z.  
J. Biol. Chem. 261, 8600-8605, 1986  
A;Title: Human fibroblast collagenase. Complete primary structure and homology to an onc  
A;Reference number: A00996; MUID:86196089; PMID:3009463  
A;Accession: A00996  
A;Molecule type: mRNA  
A;Residues: 1-114, 'R', 116-409, 'S', 411-469 <GOL>  
A;Cross-references: GB:M13509; NID:g180664; PIDN:AAA35699.1; PID:g180665  
A;Note: Part of this sequence was confirmed by protein sequencing of the proenzyme  
R;Whitham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris,  
Biochem. J. 240, 913-916, 1986  
A;Title: Comparison of human stromelysin and collagenase by cloning and sequence analysis  
A;Reference number: A90336; MUID:87156645; PMID:3030290  
A;Accession: D29157  
A;Molecule type: mRNA  
A;Residues: 1-139, 'H', 201-207, 'T', 209-469 <WHI>  
A;Cross-references: EMBL:X05231; NID:g38266; PIDN:CAA28858.1; PID:g38267  
A;Note: Parts of this sequence, including the amino end of the proenzyme and of the matu  
R;Birkedal-Hansen, B.; Moore, W.G.I.; Taylor, R.E.; Bhowan, A.S.; Birkedal-Hansen, H.  
Biochemistry 27, 6751-6758, 1988  
A;Title: Monoclonal antibodies to human fibroblast procollagenase. Inhibition of enzymatic  
end of the activated enzyme.  
A;Reference number: A44518; MUID:89062403; PMID:2461732  
A;Accession: A44518  
A;Molecule type: protein  
A;Residues: 270-305 <BIR>  
R;Clark, I.M.; Watson, T.E.  
Biochem. J. 263, 201-206, 1989  
A;Title: Fragments of human fibroblast collagenase. Purification and characterization.  
A;Reference number: S06133; MUID:90104231; PMID:2557822  
A;Accession: S06132  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 100-102, 'P', 104-107, 'XX', 110-112, 270-277, 'X', 279-280, 'X', 282-287 <CIA>  
R;Lark, M.W.; Walakovits, L.A.; Shah, T.K.; Vanmiddleworth, J.; Cameron, P.M.; Lin, T.Y.  
Connect. Tissue Res. 25, 49-65, 1990  
A;Title: Production and purification of prostromelysin and procollagenase from IL-1 beta  
A;Reference number: A60964; MUID:91059606; PMID:2173990  
A;Accession: B60964  
A;Molecule type: protein  
A;Residues: 24-35; 100-108; 270-272, 'X', 274, 'X', 276 <LAR>  
R;Suzuki, K.; Nagase, H.; Ito, A.; Engbild, J.J.; Salvesen, G.  
Biol. Chem. Hoppe-Seyler 371(Suppl.), 305-310, 1990  
A;Title: The role of matrix metalloproteinase 3 in the stepwise activation of human rheu  
A;Reference number: S10595; MUID:90380300; PMID:2169257  
A;Accession: S10595  
A;Molecule type: protein  
A;Residues: 20-102 <SUZ>  
R;Suzuki, K.; Lees, M.; Newlands, G.P.J.; Nagase, H.; Woolley, D.E.  
Biochem. J. 305, 301-306, 1995  
A;Title: Activation of precursors for matrix metalloproteinases 1 (interstitial collagen  
A;Reference number: S53438; MUID:95126921; PMID:7826345  
A;Accession: S53438  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 20-108 <SUZ>  
R;Springman, E.B.; Angleton, E.L.; Birkedal-Hansen, H.; Van Wart, H.E.  
Proc. Natl. Acad. Sci. U.S.A. 87, 364-368, 1990  
A;Title: Multiple modes of activation of latent human fibroblast collagenase: evidence f  
A;Reference number: A44517; MUID:90115877; PMID:2153297  
A;Contents: annotation, disulfide bond, activation mechanism  
R;Salowe, S.P.; Marcy, A.I.; Cucca, G.C.; Smith, C.K.; Kopka, I.E.; Hagmann, W.K.; Hermes  
Biochemistry 31, 4535-4540, 1992  
A;Title: Characterization of zinc-binding sites in human stromelysin-1: stoichiometry of  
A;Reference number: A43031; MUID:92256384; PMID:1581308  
A;Contents: annotation, zinc ligand in proenzyme  
A;Note: Cys-92 binds zinc in the proenzyme. Both active and proenzyme forms of the catal  
C;Comment: Procollagenase can be activated without removal of the activation peptide. St  
C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi  
C;Genetics:

A;Gene: GDB:MMPL1; CIG  
A;Cross-references: GDB:119783; OMIM:120353  
A;Map position: 11q22.2-11q22.3  
C;Function:  
A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and  
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei  
C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-469/Product: procollagenase #status experimental <PRO>  
F;50-99/Domain: activation peptide #status experimental <ACT>  
F;90-261/Domain: matrix metalloproteinase homology <MMP>  
F;100-469/Product: interstitial collagenase #status experimental <MAT>  
F;272-466/Domain: hemopexin repeat homology <PXN>  
F;120,218,222,228/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status  
F;120,143/Binding site: carboxylate (Asn) (covalent) #status predicted  
F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted  
F;219/Active site: Glu #status predicted  
F;269-270/Cleavage site: Pro-Ile (autolytic) #status experimental  
F;278-466/Disulfide bonds: #status experimental  
Alignment Scores:  
Pred. No.: 3,53e-91 Length: 469  
Score: 1161.50 Matches: 234  
Percent Similarity: 66.45% Conservative: 77  
Best Local Similarity: 50.00% Mismatches: 146  
Query Match: 39.64% Indels: 11  
DB: 1 Gaps: 8  
US-10-729-807-28 (1-1627) x KCHUI (1-469)  
QY 36 CTGCTCTGTGTTGTTCTTTATACATTTCTTCGATTTCCCTAGTCGGATGAG 95  
Db 7 LeuLeuLeuLeuPheTrpGlyValValSerHisSerPheProAlaThrLeuGluThr 26  
QY 96 GAAATGTAAGAAATATGCAATGCGTCAGGCATATCTCAACAGTCTTACTCTCTTGA 155  
Db 27 Gln---GluGlnAspValAspLeuValGlnLysTyrLeuGlnLysTyrTyrAsnLeuLys 45  
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Db 205 AsnAsnPheArgGluTyrAsnLeuHisArgValAlaAlaHisGluLeuGlyHisSerLeu 224  
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Db 225 GlyLeuSerHisSerThrAspIleGlyAlaLeuMetTyrProSerTyrThrPheSerGly 244  
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C;Accession: A37073; A61175; B61175; A36230; S09680; S11026; S19576; S27225; S62  
R;Hasty, K.A.; Pourmotabed, T.F.; Goldberg, G.I.; Thompson, J.P.; Spinella, D.G.; Steve  
J. Biol. Chem. 265, 11421-11424, 1990  
A;Title: Human neutrophil collagenase. A distinct gene product with homology to other ma  
A;Reference number: A37073; MUID:90307647; PMID:2164002  
A;Accession: A37073  
A;Molecule type: mRNA  
A;Residues: 1-467 <HAS>  
A;Cross-references: UNIPROT:P22894; GB:J05556; NID:g180617; PIDN:AAA8021.1; PID:g180618  
R;Devarajan, P.; Mookhtiar, K.; Van Wart, H.; Berliner, N.  
Blood 77, 2731-2738, 1991  
A;Title: Structure and expression of the cDNA encoding human neutrophil collagenase.  
A;Reference number: A61175; MUID:91255696; PMID:1646048

A;Accession: A61175  
A;Status: not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-31, 'I', 33-86, 'E', 88-467 <DEV>  
A;Accession: B61175  
A;Molecule type: protein  
A;Residues: 263-264, 'X', 266-270, 'X', 272-273, 'X', 275, 'X', 277 <DE2>  
R;Mallva, S.K.; Mookhtiar, K.A.; Gao, Y.; Brew, K.; Dioszegi, M.; Birkedal-Hansen, H.; V  
Biochemistry 29, 10628-10634, 1990  
A;Title: Characterization of 58-kilodalton human neutrophil collagenase: comparison with  
A;Reference number: A36230; MUID:91104978; PMID:2176876  
A;Accession: A36230  
A;Molecule type: protein  
A;Residues: 'X', 86-87, 'X', 89-90, 'X', 92-97, 'X', 99-111, 'X', 113-120 <MAL>  
R;Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.  
Eur. J. Biochem. 189, 295-300, 1990  
A;Title: Characterization and activation of procollagenase from human polymorphonuclear  
A;Reference number: S09680; MUID:90249372; PMID:2159879  
A;Accession: S09680  
A;Molecule type: protein  
A;Residues: 21-31, 'I', 33-39, 'I', 41-47, 'V', 49-53, 'I', 55-72, 'G', 74-86, 'E', 88-111, 'X', 113-1  
A;Note: 67-Lys was also found  
R;Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.  
Biochem. Hoppe-Seyler 371, 733, 1990  
A;Title: Corrigendum. Partial amino-acid sequence of human PMN leukocyte procollagenase  
A;Reference number: S11026; MUID:91000455; PMID:2169766  
A;Note: original publication was Biol. Chem. Hoppe-Seyler 371(Suppl.), 295-304, 1990  
A;Accession: S11026  
A;Molecule type: protein  
A;Residues: 21-31, 'I', 33-53, 'I', 55-72, 'G', 74-111, 'X', 113-140;183-203, 'X', 205-209;248-2  
A;Note: 87-Glu was also found  
R;Blaeser, J.; Knaeuper, V.; Osthus, A.; Reinke, H.; Tschesche, H.  
Eur. J. Biochem. 202, 1223-1230, 1991  
A;Title: Mercurial activation of human polymorphonuclear leucocyte procollagenase.  
A;Reference number: S19576; MUID:92111500; PMID:1662606  
A;Accession: S19576  
A;Molecule type: protein  
A;Residues: 69-103 <BL2>  
R;Blaeser, J.; Triebel, S.; Reinke, H.; Tschesche, H.  
FEBS Lett. 313, 59-61, 1992  
A;Title: Formation of a covalent Hg-Cys-bond during mercurial activation of PMNL procol  
A;Reference number: S27225; MUID:93050220; PMID:1330697  
A;Accession: S27225  
A;Molecule type: protein  
A;Residues: 68-103 <BLA>  
R;Knaeuper, V.; Osthus, A.; DeClerck, Y.A.; Langley, K.E.; Blaeser, J.; Tschesche, H.  
Biochem. J. 291, 847-854, 1993  
A;Title: Fragmentation of human polymorphonuclear-leucocyte collagenase.  
A;Reference number: S32527; MUID:93256897; PMID:8489511  
A;Accession: S32527  
A;Molecule type: protein  
A;Residues: 100-112;263-276 <KN3>  
R;Knaeuper, V.; Murphy, G.; Tschesche, H.  
Eur. J. Biochem. 235, 187-191, 1996  
A;Title: Activation of human neutrophil procollagenase by stromelysin 2.  
A;Reference number: S62608; MUID:96202934; PMID:8631328  
A;Accession: S62608  
A;Molecule type: protein  
A;Residues: 21-39, 'I', 41-47, 'V', 49-122 <KN4>  
R;Stams, T.; Spurlino, J.C.; Smith, D.L.; Rubin, B.  
submitted to the Brookhaven Protein Data Bank, January 1994  
A;Reference number: A67078; PDB:1MNC  
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', 106-149, 'G',  
R;Stams, T.; Spurlino, J.C.; Smith, D.L.; Wahl, R.C.; Ho, T.F.; Qoronfleh, M.W.; Banks,  
Nat. Struct. Biol. 1, 119-123, 1994  
A;Title: Structure of human neutrophil collagenase reveals large S1' specificity pocket  
A;Reference number: A58274; MUID:95384762; PMID:7656015  
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', 106-149, 'G',  
C;Comment: This protein is more highly glycosylated than interstitial collagenase and i  
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A;Cross-references: GDB:128173; OMIM:120355  
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 QY 609 GATGAGTGAAGAACTGGCAAGGATGAGGAGGATTCAACTGCTTCTTCTGCTGCTGT 668  
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 DB 258 IleGlnSerLeuTyrGlyAsp---ProLysGluAsnGlnArgLeuProAsnProAspAsn 276  
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 N:Alternate names: matrix metalloproteinase 1 (MMP1); vertebrate collagenase  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 04-Oct-1991 #sequence\_revision 04-Oct-1991 #text\_change 09-Jul-2004  
 C:Accession: A23685  
 R:Quinn, C.O.; Scott, D.K.; Brinckerhoff, C.E.; Matrisian, L.M.; Jeffrey, J.J.; Partridge  
 J. Biol. Chem. 265, 22342-22347, 1990  
 A:Title: Rat collagenase. Cloning, amino acid sequence comparison, and parathyroid hormone  
 A:Reference number: A23685; MUID:91093077; PMID:2176215  
 A:Accession: A23685  
 A:Status: preliminary  
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 DB 47 LeuAlaGlyIleLeuLysLysSerThrValThrSerThrVal---AspArgLeuArgGlu 65  
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GenCore version 5.1.6  
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Searched: 1825181 seqs, 575374646 residues

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2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2752	93.9	513	2	Q6UWK6	Q6UWK6 homo sapien
2	2752	93.9	513	2	AAQ89112	AAQ89112 homo sapien
3	2731	93.2	513	2	Q9H306	Q9H306 homo sapien
4	2347	80.1	512	2	Q9GKE1	Q9GKE1 tupaiia glis
5	1520.5	51.9	472	2	Q93342	Q93342 gallus gall
6	1286.5	43.9	478	2	O6Y4Q5	O6Y4Q5 canis faml
7	1286.5	43.9	478	2	AAO63580	AAO63580 canis fam
8	1271.5	43.4	478	1	MM03_RABIT	MM03_RABIT
9	1254	42.8	477	2	AAH69676	AAH69676 homo sapi
10	1254	42.8	477	2	AAH69716	AAH69716 homo sapi
11	1250	42.7	477	1	MM03_HUMAN	MM03_HUMAN
12	1247	42.6	483	2	Q98857	Q98857 cynops pyrr
13	1244	42.5	477	1	MM03_HORSE	MM03_HORSE
14	1243.5	42.4	476	1	MM10_MOUSE	MM10_MOUSE
15	1238.5	42.3	479	2	Q922W6	Q922W6 mus musculu
16	1237.5	42.2	477	1	MM03_MOUSE	MM03_MOUSE

17	1234	42.1	476	1	MM10_HUMAN	P09238 homo sapien
18	1234	42.1	476	2	AAF36110	AAF36110 homo sapi
19	1229	41.9	472	2	Q10833	Q10833 xenopus lae
20	1219.5	41.6	469	1	MM13_XENLA	Q10835 xenopus lae
21	1205	41.1	469	1	MM01_PIG	P21692 sus scrofa
22	1200.5	41.0	464	1	MM12_RABIT	P79227 oryctolagus
23	1200.5	41.0	464	2	Q9TV75	Q9TV75 oryctolagus
24	1198.5	40.9	476	1	MM10_RAT	P07152 rattus norv
25	1196	40.8	469	1	MM01_HORSE	Q9X825 equus cabal
26	1195	40.8	469	2	Q98858	Q98858 cynops pyrr
27	1190.5	40.6	466	2	Q7SYX1	Q7SYX1 xenopus lae
28	1183.5	40.4	471	2	Q98859	Q98859 cynops pyrr
29	1177.5	40.2	469	1	MM01_BOVIN	P28053 bos taurus
30	1173.5	40.1	475	1	MM03_RAT	P03957 rattus norv
31	1170.5	39.9	468	1	MM01_RABIT	P13943 oryctolagus
32	1167	39.8	467	1	MM18_XENLA	O13065 xenopus lae
33	1161.5	39.6	469	1	MM01_HUMAN	P03956 homo sapien
34	1161.5	39.6	469	2	AAQ35520	AAQ35520 homo sapi
35	1161	39.6	467	1	MM08_HUMAN	P22894 homo sapien
36	1159	39.6	465	2	AAH42742	AAH42742 mus muscu
37	1159	39.6	465	2	BAC40805	BAC40805 mus muscu
38	1158.5	39.5	471	1	MM13_RABIT	O62806 oryctolagus
39	1155	39.4	472	1	MM13_HORSE	O18927 equus cabal
40	1154	39.4	465	2	Q8C209	Q8C209 mus musculu
41	1154	39.4	465	2	Q8C230	Q8C230 mus musculu
42	1150	39.2	465	1	MM08_MOUSE	O70138 mus musculu
43	1143.5	39.0	466	1	MM08_RAT	O88766 rattus norv
44	1141	38.9	471	1	MM13_HUMAN	P45452 homo sapien
45	1141	38.9	471	2	AAH67522	AAH67522 homo sapi

#### ALIGNMENTS

RESULT 1

Q6UWK6	PRELIMINARY;	PRT;	513 AA.
ID	Q6UWK6		
AC	Q6UWK6;		
DT	05-JUL-2004 (TREMBLrel. 27, Created)		
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)		
DE	MP27.		
GN	ORFNames=UNQ2503;		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=22887296; PubMed=12975309;		
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,		
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,		
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,		
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,		
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,		
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,		
RA	Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,		
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,		
RA	Godowski P.;		
RT	"The secreted protein discovery initiative (SPDI), a large-scale		
RT	effort to identify novel human secreted and transmembrane proteins: a		
RT	bioinformatics assessment."		
RL	Genome Res. 13:2265-2270(2003).		
DR	EMBL; AY358752; AAQ89112.1; -		
DR	InterPro; IPR000585; Hemopexin.		
DR	InterPro; IPR006026; Peptidase M.		
DR	InterPro; IPR001818; Pept_M10A_M12B.		
DR	InterPro; IPR006025; Pept_M_Zn_BS.		
DR	Pfam; PF00045; Hemopexin; 4.		
DR	Pfam; PF00413; Peptidase M10; 1.		
DR	Pfam; PF03933; Peptidase M10_N; 1.		
DR	PRINTS; PR00138; MATRXIN.		
DR	SMART; SM00120; HX; 4.		
DR	SMART; SM00235; ZnMc; 1.		



DR PROSITE; PS00546; CYSTEINE SWITCH; 1.  
DR PROSITE; PS00024; HEMOPEXIN; 1.  
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.  
SO SEQUENCE 513 AA; 58394 MW; 1B1D55699553DCD CRC64;

Alignment Scores:		
Pred. No.:	9.1e-236	Length: 513
Score:	2752.00	Matches: 512
Percent Similarity:	99.81%	Conservative: 0
Best Local Similarity:	99.81%	Mismatches: 1
Query Match:	93.92%	Indels: 0
DB:	2	Gaps: 0

US-10-729-807-28 (1-1627) x 06UWK6 (1-513)

QY	24	ATGAAGCGCCTTCTGCTTCTGTGTTTGTGTTTATAACATTTTCTCTGCATTTCCCTTAA	83
Db	1	MetLysArgLeuLeuLeuLeuPheLeuPheLeuThrPheSerSerAlaPheProLeu	20
QY	84	GTCCGGATGACGGAAATGAGAAATATGCACTGGCTCAGGCATATCTCAACAGTTC	143
Db	21	ValArgMetThrGluAsnGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe	40
QY	144	TACTCTCTTGAATAGAAAGGAATCATCTGTTCATAAGCAAGATAGGAGTCTCATAGAT	203
Db	41	TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp	60
QY	204	GACAAATTCGGGAAATGCAAGCATTTTGTGAATTGACAGTCACTGGGAAAACCTGCAGCTCA	263
Db	61	AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer	80
QY	264	AACACCCCTTGAGATCATGAAGACACCCAGGTCTGGGTGCCTGATGTGGCCAGATATGCG	323
Db	81	AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100
QY	324	TACACCTCCCTGGGTGAGAAAATACAACTCACCTACAGATAATAAATATATCTCCG	383
Db	101	TyrThrLeuProGlyTyrPargLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro	120
QY	384	GATATGGCACGAGCTGCTGTGGATGAGGTATCCAAAGAGTTTAGAAGTGTGGAGCAAA	443
Db	121	AspMetAlaArgAlaAlaValAspGluAlaIleGlnGlnGlyLeuGluValTrpSerLys	140
QY	444	GTCACTCCACTAAAATTCACCAAGATTCCAAAGGGATTGCACACATCATGATGCTCTTT	503
Db	141	ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe	160
QY	504	AGGACTCGAGTCCATGTGCGGTGCTCCTCGCTATTTTATGGTGCCTTGGAGTGTGGC	563
Db	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180
QY	564	CATGCTTTCCTTCCTGGTCCGGTCTGGGTGTGTGACCTCATTTTGATGAGGATGAAAC	623
Db	181	HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn	200
QY	624	TGGACCAAGATGGACAGGATTCAACTGTTCTTGTGGCTGCTCATGATTTGCTCAT	683
Db	201	TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis	220
QY	684	GCACCTGGGCTCTCTCACTCCAAATGATCAAAAGCCCTTGATGTTCCCAATATATGTCCTC	743
Db	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
QY	744	CTGGATCCCAAGAAAATACCCACTTTCTCAGGATGATATCAATGGGAATCAGTCCATCTAT	803
Db	241	LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr	260
QY	804	GGAGGTCTCCCTAAAGTACTGCTAAGCCAAAGGAACCCACTATACCCATGCTGTGAC	863
Db	261	GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp	280
QY	864	CCTGACTTGACATTTTGACGCTATCACACTTTCCGCGAGGAAGTAATGTTCTTTAAAGGC	923

Db	281	ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly	300
Qy	924	AGGCACCTATGGAGGATCTATTATGATATCACGGATGTTGAGTTGAATTAATTGCTTCA	983
Db	301	ArgHisLeuTprArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer	320
Qy	984	TTCTGGCCATCTCTGCGAGTGTCTGCAAGCTGCATACGAGAACCCAGAGATAAGATT	1043
Db	321	PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle	340
Qy	1044	CTGGTTTTTAAAGATGAAACTTCTGGATCATCAGAGGATATGCTGCTCCGAGATTAT	1103
Db	341	LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr	360
Qy	1104	CCCAATCCCATCCATACATATTAGGTTTTCCAGGACGCTGGAAGAAAAATAGATGAGCCGCTC	1163
Db	361	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal	380
Qy	1164	TGTGATAAGACCAACAAAAAACCCTACTTCTTTGTGGGCATTTGGTCTCTGAGGTTTGAT	1223
Db	381	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTrpArgPheAsp	400
Qy	1224	GAATGACCCCAACCATCGCAAAAGSNTCCCGCAGAGAGTGTAAACACTTCCCTGGA	1283
Db	401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly	420
Qy	1284	ATCAGTATCCGTGTGTGATGCTGCTTCCAGTACAAAGGATTCCTCTTTTTCAGCCGTGGA	1343
Db	421	IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly	440
Qy	1344	TCAAAGCAATTTGTAATCAACATTAAAGCAAGAATATCCCGAATCATGAGAACTAAT	1403
Db	441	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
Qy	1404	ACTTGGTTTCAATGCAAAAGAACCAAGAACTCCTCATTTGGTTTGTATTCACACAGAA	1463
Db	461	ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu	480
Qy	1464	AAAGCATTTCAGGAGGCATTAACATATTGTATCATAGAAGTGTAAAGCTTGTATTATTTT	1523
Db	481	LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe	500
Qy	1524	GGTATTGTTCATTTGCTGAAACCACTTCTATTATCAAA	1562
Db	501	GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln	513
RESULT 2			
ID	AAQ89112	PRELIMINARY;	PRT; 513 AA.
AC	AAQ89112;		
DT	02-MAR-2004	(Tremblrel. 27, Created)	
DT	02-MAR-2004	(Tremblrel. 27, Last sequence update)	
DE	02-MAR-2004	(Tremblrel. 27, Last annotation update)	
DE	MMF27.		
GN	UNQ02503.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	PubMed=12975309;		
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,		
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,		
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,		
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,		
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,		
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,		
RA	Wandlen R., Watanabe C., Wieland D., Woods K., Xie M.H., Yansura D.,		
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,		
RA	Godowski P.;		
RT	"The Secreted Protein Discovery Initiative (SPDI), a Large-Scale		
RT	Effort to Identify Novel Human Secreted and Transmembrane Proteins: A		

RT Bioinformatics Assessment. ";  
 RL Genome Res. 13:2265-2270(2003).  
 DR EMBL; AY358752; AAQ89112.1; -.  
 SQ SEQUENCE 513 AA; 58994 MW;

Alignment Scores:		
Prod. No.:	9_1e-236	Length: 513
Score:	2752.00	Matches: 512
Percent Similarity:	99.81%	Conservative: 0
Best Local Similarity:	99.81%	Mismatches: 1
Query Match:	93.92%	Indels: 0
DB:	2	Gaps: 0

US-10-729-807-28 (1-1627) x AAQ89112 (1-513)

QY	24	ATGAAGCGCTTCTGCTTCTGTGTGTTTATTAACATTTCTTCGCAATTTCCCTTA	83
DB	1	MetLysArgLeuLeuLeuPheLeuPheIleThrPheSerSerAlaPheProLeu	20
QY	84	GTCCGGATGACGGAAATGAGAAAATATGCACTGGCTCAGGCATATCTCAACAGTTC	143
DB	21	ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe	40
QY	144	TACTCTCTTGAATAGAAGGAATCATCTTGTTCAAAGCAAGAATAGAGTCTCATAGAT	203
DB	41	TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp	60
QY	204	GACAAATTCGGAAATCAAGCATTTTGTGGATTGACAGTGCAGTGGAAAACCTGACTCA	263
DB	61	AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer	80
QY	264	ACACCCCTTGACATCATGAAGACACCCAGGTGTGGGTGGCTGTGATGGGCCAGTATGGC	323
DB	81	AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly	100
QY	324	TACCCCTCCCTGGGTGGAGAAAATACAACTCTACCTACAGAAATAATAAATATACTCCG	383
DB	101	TyrThrLeuProGlyTrpArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro	120
QY	384	GATATGGCAGAGCTGCTGTGTGATGAGGCTATCCAGAAAGTTTAGAAGTGTGAGCAAA	443
DB	121	AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSerLys	140
QY	444	GTCACCTCCACTAAATTCACCAAGATTTCAAAGGGATTGCAGACATCATGATTCCTTT	503
DB	141	ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe	160
QY	504	AGGACTTCGAGTCCATGGTGGGTGCTCCTCGCTATTTTGATGCTCCCTTGGGAGTGCITGGC	563
DB	161	ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly	180
QY	564	CATGCCCTTCTCTGCTGGTCCGGTCTGGGTGGTGACACTCATTTTGATGAGGATGAAGAAC	623
DB	181	HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn	200
QY	624	TGCACCAAGGATGGAGCAGATTCAACTTGTTTCTTGTGGCTGCTCATGAATTTGGTCAT	683
DB	201	TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis	220
QY	684	GCACCTGGGCTCTCTCACTCCAATGATCAAAACAGCCTTGATGTTTCCCAAAATTATGCTCC	743
DB	221	AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer	240
QY	744	CTGGATCCAGAAAATACCCACTTCTCAGAGTATCAATGGAATCCAGTCCACTCAT	803
DB	241	LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr	260
QY	804	GGAGGTCTCCCTAAGGTACTCTGAAGCAAGGAACCCACTATATCCCCATGCTGTGAC	863
DB	261	GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp	280
QY	864	CCTGACTTGACTTTTGAGCTATCAAACTTTCCGACAGAAAGTAATGTCTTTAAAGGC	923

Db	281	ProAspLeuThrPheAspAlaIleThrThrPheArgGluValMetPhePheLysGly	300
Qy	924	AGGCACCTATGGAGGATCTATTATGATATACCGATGTGGTTGAGTTTGAAATTAATGCTTCA	983
Db	301	ArgHisLeuTrpAlaGlyIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer	320
Qy	984	TTCTGGCCATCTCTGCCAGCTGATCTCTCAAGCTCATACGAGAACCCAGAGATAAGATT	1043
Db	321	PheTrpProSerLeuProAlaAspLeuGluAlaIaTyrGluAsnProArgAspLysIle	340
Qy	1044	CTGGTTTTTAAAGATGAAACTTCTGGATGATCAGAGATATGCTGTCTTCCGAGATTAT	1103
Db	341	LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr	360
Qy	1104	CCCAATTCATCCATACATACATTAGGTTTTCCAGGAGCTGTGAAGAAAAATAGATGCAGCCGTC	1163
Db	361	ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal	380
Qy	1164	TGTGATTAAGACCAACAGAAAAACCTACTTCTTGTGTGGCATTGTGGTCTGGAGGTTTGAT	1223
Db	381	CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTTPatrgPheAsp	400
Qy	1224	GAATGACCCAAACCATGGACAAGGATTTCCCGCAGAGAGTGTATAAACACTTTCTCTGGA	1283
Db	401	GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly	420
Qy	1284	ATCAGTATCCGTTGATGCTGCTTCCAGTACAAAGGATTTCTCTTTTTCAGCCGCTGGA	1343
Db	421	IleSerIleArgValAspAlaIlePheGlnTyrLysGlyPhePhePhePheSerArgGly	440
Qy	1344	TCAAGCAATTTCGAATCAACATTAACAGCAAGAAATATTATCCCGAAATCATGAGAACTAAT	1403
Db	441	SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn	460
Qy	1404	ACTTGTTTCAATGCAAAAGAACCAAGAACTCTCATTTGGTTTGTATATCAACAAGAA	1463
Db	461	ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu	480
Qy	1464	AAAGCATTTCAGAGGCATAAAGATATTGATCATAGAGTTTAAAGCTGTGTTATTTT	1523
Db	481	LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe	500
Qy	1524	GGTATTCTTTCATTTGCTGAAAAACACTTCTATTATCAAA	1562
Db	501	GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln	513
RESULT 3			
Q9H306			
ID	Q9H306	PRELIMINARY;	PRT; 513 AA.
AC	Q9H306;		
DT	01-MAR-2001	(T-EMBLrel. 16, Created)	
DT	01-MAR-2001	(T-EMBLrel. 16, Last sequence update)	
DT	01-MAR-2004	(T-EMBLrel. 26, Last annotation update)	
DE	Matrix metalloprotease MMP-27.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Benoit de Coignac A., Elson G., Magistrelli G., Jeannin P.,		
RA	Delneste Y., Aubry J.P., Berthier O., Bonnefoy J.Y., Gauchat J.F.;		
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF195192; AAG28453.1; -		
DR	HSSP; P08254; 1HY7.		
DR	MEROPS; M10.027; -		
DR	Genew; HGNC:14250; MMP27.		
DR	GO; GO:0005578; C:extracellular matrix; IEA.		
DR	GO; GO:0004222; F:metalloendopeptidase activity; IEA.		
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
DR	InterPro; IPR000585; Hemopexin.		
DR	InterPro; IPR006026; Peptidase M.		
DR	InterPro; IPR001818; Pept M10A_M12B.		

DR InterPro; IPR006025; Pept M Zn Bs.  
 DR InterPro; IPR009070; PGSD\_like.  
 DR Pfam; PF00045; Hemopexin; 4.  
 DR Pfam; PF00413; Peptidase M10; 1.  
 DR Pfam; PF03933; Peptidase M10\_N; 1.  
 DR PRINTS; PR00138; MATRIXIN.  
 DR SMART; SM00120; HX; 4.  
 DR SMART; SM00235; ZnMc; 1.  
 DR PROSITE; PS00546; CYSTEINE SWITCH; 1.  
 DR PROSITE; PS00024; HEMOPEXIN; 1.  
 DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN\_1.  
 KW Metalloprotease; Protease.  
 SQ SEQUENCE 513 AA; 59023 MW; ED3C9B175C014683 CRC64;

Alignment Scores:  
 Pred. No.: 6,74e-234 Length: 513  
 Score: 2731.00 Matches: 508  
 Percent Similarity: 99.42% Conservative: 2  
 Best Local Similarity: 99.03% Mismatches: 3  
 Query Match: 93.21% Indels: 0  
 DB: 2 Gaps: 0

US-10-729-807-28 (1-1627) x Q9H306 (1-513)

QY 24 ATGAAGCGCTCTGCTCTGCTGCTGCTCTCTTTATACATTTCTCTCTGCAATTCCTCTTA 83  
 DB 1 MetLysArgLeuLeuLeuLeuPheLeuPhePheLeuPheSerSerAlaPheProLeu 20  
 QY 84 GTCGGATGACGGAATAAGAAATATGCACTGGCTCAGGCATATCTCAACCGATTC 143  
 DB 21 ValArgMetMetGluAsnGluGluAsnValGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40  
 QY 144 TACTCTCTCAATAGAGGATCACTCTGTTCAAGCAAGATAGGACTCTCATAGAT 203  
 DB 41 TyrSerLeuGluLeuGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuLeuAsp 60  
 QY 204 GACAAATTCGGGAATGCAAGCATTTTTCGATTGACAGTCACTGAGTGGAACTGGACTCA 263  
 DB 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
 QY 264 AACACCTTGAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGCCGATATGGC 323  
 DB 81 AsnThrLeuGluLeuMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
 QY 324 TAGACCTCTCGGTGGGAAATACAACTCACTACAGATTAATAAATACTACTCCG 383  
 DB 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleLeuAsnTyrThrPro 120  
 QY 384 GATATGCGACGAGCTGCTGTGAGTGGCTATCCAGAGGTTTAGAAGTGTGGAGCAAA 443  
 DB 121 AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140  
 QY 444 GTCACCTCCATAAATTCACCAAGATTCAAAGGGATTCAGACATCATGATGCTCTTT 503  
 DB 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160  
 QY 504 AGGACTCGAGTCCATGCTCGGTGCTCGCTATTTGATGTCCTTGGAGTGTGGC 563  
 DB 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180  
 QY 564 CATGCTCTCTCTGCTCGGGTCTGGGTGGTGCACACTCATTTTGTATGAGGATGAAAC 623  
 DB 181 HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200  
 QY 624 TGGACCAAGATGAGCAGGATTCACCTGTTCTTGTGGCTGCTCATGATGATGTCAT 683  
 DB 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220  
 QY 684 GCATGGGGCTCTCTCACTCCAAATGATCAACAGCCCTTGATGTTCCCAAAATATGTCCTC 743  
 DB 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240  
 QY 744 CTGGATCCCAAGAAATACCCACTTCTTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803

DB 241 LeuAspProArgLysTyrProLeuSerGlnAspAspIleAsnGlyIleGlnSerIleTyr 260  
 QY 804 GGAGGTCTGCTAAGTACTGCTAAGCCAAAGAACCCACTATACCCCATGCTGTGAC 863  
 DB 261 GlyGlyLeuProLysGluProAlaLysProLysGluProThrIleProHisAlaCysAsp 280  
 QY 864 CCTGACTTGACTTTTTCAGCGCTATCAAACTTTCCGAGAGAGTAATGTTCTTTAAAGGC 923  
 DB 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300  
 QY 924 AGGCACCTATGAGGATCTATTATGATATACCGATGTTTCAGTGAATTAATGCTTCA 983  
 DB 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320  
 QY 984 TTCTGGCATCTCTCCAGCTGATCTGCAGCTGCATACAGAACCCAGAGATAAGATT 1043  
 DB 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340  
 QY 1044 CTGGTTTAAAGATGAAAACTTCTGGATGATCAGAGGATATGCTGCTTTCGCCAGATTAT 1103  
 DB 341 LeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyr 360  
 QY 1104 CCCAAATCCATCATACATTAGCTTTTCCAGGACGTGTGAAGAAATAGATGAGCGCTC 1163  
 DB 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAlaVal 380  
 QY 1164 TGTGATAAGACCAAGAAAACCTACTCTTGTGGGCACTTGTGCTCGAGGTTTGAT 1223  
 DB 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTrpArgPheAsp 400  
 QY 1224 GAAATGACCCAAACCATGGAAGGATTCGCCAGAGAGTGTGTAACCACTTTCTCTGGA 1283  
 DB 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGly 420  
 QY 1284 ATCAGTATCCGTGTTGATGCTGCTTCCAGTACAAAGGATCTCTTTTTCAGCCGTGGA 1343  
 DB 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly 440  
 QY 1344 TCRAAGCAATTTCAATCAACATTAAGACAAAGATATTACCCGAATCATGAGAACTAAT 1403  
 DB 441 SerLysGlnPheGluTyrAspIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460  
 QY 1404 ACTTGGTTTCAATGCAAAAGAACCAAGAACTCTCATTTGGTTTTCATATCAACAAGAA 1463  
 DB 461 ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480  
 QY 1464 AAAGCACTTCAGAGGCATAAAGATATTGTATCATTAAGGTTTAAAGCTTGTATTATTTT 1523  
 DB 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500  
 QY 1524 GGTATTGTTTCATTTGCTGAAAACACCTTCTATTATCA 1562  
 DB 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513

RESULT 4  
 Q9GKE1 PRELIMINARY; PRT; 512 AA.  
 ID Q9GKE1  
 AC Q9GKE1 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DE Matrix metalloproteinase-27.  
 OS Tupia glis belangeri (Common tree shrew).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiia.  
 OX NCBI\_TaxID=37347;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Sklera;  
 RA Guggenheim J.A., To C.H., Frost M.R.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF281673; AAC44844.1; -.

DR HSP; P03956; 1CGL.  
 DR MEROPS; M10\_027; -.  
 DR GO; GO:0005578; C:extracellular matrix; IEA.  
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000585; Hemopexin.  
 DR InterPro; IPR006026; Peptidase M.  
 DR InterPro; IPR001818; Pept M10A\_M12B.  
 DR InterPro; IPR006025; Pept\_M\_Zn\_BS.  
 DR InterPro; IPR009070; PGSD\_like.  
 DR Pfam; PF00045; Hemopexin; 4.  
 DR Pfam; PF00413; Peptidase M10; 1.  
 DR Pfam; PF03933; Peptidase M10\_N; 1.  
 DR PRINTS; PR00138; MATRXIN.  
 DR SMART; SM00120; HX; 4.  
 DR SMART; SM00235; ZnMc; 1.  
 DR PROSITE; PS00546; CYSTEINE\_SWITCH; 1.  
 DR PROSITE; PS00024; HEMOPEXIN; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN 1.  
 DR SEQUENCE 512 AA; 58816 MW; 9CBD89C4F807CEFF5 CRC64;  
 Alignment Scores:  
 Pred. No.: 1,03e-199 Length: 512  
 Score: 2347.00 Matches: 434  
 Percent Similarity: 90.43% Conservative: 29  
 Best Local Similarity: 84.77% Mismatches: 49  
 Query Match: 80.10% Indels: 0  
 DB: 2 Gaps: 0

US-10-729-807-28 (1-1627) x 09GKE1 (1-512)

QY 24 ATGAAGCGCTCTCTGCTCTGTTGTTCTTTATAACATTTTCTTCTGCAATTCCTCTTA 83  
 |||||  
 DB 1 MetLysSerPheLeuLeuLeuPheLeuPheValThrPheSerSerAlaLeuProAla 20  
 |||||  
 QY 84 GTCGGATGACCGAAATATGCAAAATATGCAACTGGCTCAGGCATATCTCAACCAAGTTC 143  
 |||||  
 DB 21 AspGlnLysMetGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40  
 |||||  
 QY 144 TACTCTCTGTAATAGAAGGATCATCTGTTCTCAAGCAAGATAGGAGTCTCATAGAT 203  
 |||||  
 DB 41 TyrSerLeuGluLeuGluGlySerHisLeuValGlnSerLysAsnGlySerLeuLeuAsp 60  
 |||||  
 QY 204 GACAAATTCGGAAATGCAAGCATTTTGTGATTGACAGTCACTGGAAATCTGGACTCA 263  
 |||||  
 DB 61 GlyLysLeuArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyThrLeuAspSer 80  
 |||||  
 QY 264 AACACCTTGAGATCATGAAGACACCCAGTGTGGGTGCTGATGTGGCCAGTATGCG 323  
 |||||  
 DB 81 AsnThrLeuGluLeuMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
 |||||  
 QY 324 TACACCTCCCTGGTGGGAAATATACACCTCCTACAGATATAACTATATCTCTCG 383  
 |||||  
 DB 101 TyrThrLeuProGlyTyrPargLysTyrAsnLeuThrTyrArgileMetAsnTyrThrPro 120  
 |||||  
 QY 384 GATATGGCAGAGTCTGCTGATGAGGTATCCAAAGAGTTTGAAGTGGAGCAAA 443  
 |||||  
 DB 121 AspMetAlaArgAlaAspValaspGluAlaLeuGlnLysAlaLeuGluValIrpSerLys 140  
 |||||  
 QY 444 GTCACCTCACTAAATTCACCAAGATTTCAAAGGGGATTCGACATCATGATTCGCTTT 503  
 |||||  
 DB 141 ValThrProLeuThrPheThrLysIlePheLysGlyIleAlaAspIleMetIleAlaPhe 160  
 |||||  
 QY 504 AGGACTCGAGTCCATGGTGGTGTCTCTGCTATTTTGTAGTGGTCCCTGGAGTGTGGC 563  
 |||||  
 DB 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180  
 |||||  
 QY 564 CATGCTTTCCTCGTCCGGTCTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 623  
 |||||  
 DB 181 HisAlaPheProProGlyLeuGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200  
 |||||  
 QY 624 TGGACCAAGGATGGAGCAGGATTCACCTTGTCTTGTGGCTGCTCATGAATTTGGTCAT 683  
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## RESULT 5

O93342  
 ID O93342 PRELIMINARY; PRT; 472 AA.  
 AC O93342;  
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Matrix metalloproteinase.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;

DB 201 TrpThrLysAspThrAlaGlyPheSerLeuPheLeuValAlaAlaHisGluPheGlyHis 220  
 QY 684 GCAGTGGGCTCTCTCACTCCCAATGATCAACAGCCTTGATGTTGCCAAATATGTCCTCC 743  
 |||||  
 DB 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240  
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 QY 744 CTGGATCCCCAGAAATACCCACCTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803  
 |||||  
 DB 241 LeuAspProSerLysTyrProLeuSerGlnAspAspIleAspGlyIleGlnSerIleTyr 260  
 |||||  
 QY 804 GGAGTCTGCTTAAGGTACTCTGAAGCAAGGAAACCCACTATATCCCATGCTGTGAC 863  
 |||||  
 DB 261 GlyGlyLeuProThrThrProSerLysProLysGlyProLysIleProHisAlaCysasp 280  
 |||||  
 QY 864 CCGACTTTCACCTTTCACCTATCACTTCCGCGAGAGAAGTATGTTCTTTAAAGGC 923  
 |||||  
 DB 281 ProAspLeuThrPheAspAlaIleThrAsnIleArgArgGluValMetPhePheLysGly 300  
 |||||  
 QY 924 AGGCACCTATGAGGATCTATTATGATATCAGGATGTTGAGTTTCAATTAATTTGCTTCA 983  
 |||||  
 DB 301 ArgHisLeuTrpArgIleTyrHisAspIleThrAspValGluPheGluLeuLeuAlaSer 320  
 |||||  
 QY 984 TTCTGCCATCTCTGCCAGTCTGCTCAAGCTGCTACGAGAACCCAGAGATTAAGATT 1043  
 |||||  
 DB 321 PheTrpProSerLeuProAlaAspLeuGlnAlaAlaTyrGluAsnProArgAspLysIle 340  
 |||||  
 QY 1044 CTGGTTTTAAAGATGAAACTTCTGGATGATCAGAGGATATGCTGCTTCCAGATTAT 1103  
 |||||  
 DB 341 LeuValPheLysAspGluAsnPheTrpMetIleGlyAlaTyrAsnValLeuProArgTyr 360  
 |||||  
 QY 1104 CCCAAATCCATCATACATTAGTGTTCAGGACGTGTCAAGAAATAGATGACGCGTC 1163  
 |||||  
 DB 361 ProArgSerIleHisIleLeuGlyPheProArgTyrValLysLysIleAspAlaAlaVal 380  
 |||||  
 QY 1164 TGTGATAAGACACCAAGAAAAACCTACTTCTTTGTGGCATTTGGTGTGGAGTTTGAT 1223  
 |||||  
 DB 381 CysAspGlnAspThrArgLysThrTyrPheValGlyIleTrpCysTrpArgTyrAsp 400  
 |||||  
 QY 1224 GAAATGACCAACCATGACAAAGATTCCCGCAGAGAGTGGTAAACACATTTCTCTGA 1283  
 |||||  
 DB 401 GluMetThrArgThrMetAspArgGlyTyrProGlnArgIleValArgHisPheProGly 420  
 |||||  
 QY 1284 ATCAGTATCCGTGTTGATGCTCTTCCAGTCAAGAGTCTCTCTTTTTCAGCGTGA 1343  
 |||||  
 DB 421 IleGlyLeuArgValAspAlaAlaPheGlnHisLysGlyPhePheTyrPheArgGly 440  
 |||||  
 QY 1344 TCAAGCAATTTGAATACAACTTAAGACAAAGATATTACCCGAATCATGAGAACTAAT 1403  
 |||||  
 DB 441 SerLysGlnPheGluTyrAspIleLysAlaLysSerIleThrArgIleMetArgThrAsn 460  
 |||||  
 QY 1404 ACTTGTTTCATGCAAGAACCAAGACTCTCATTTGGTTTTCATATCAACAGGAA 1463  
 |||||  
 DB 461 ThrTrpPheGlnCysLysGluProLeuAsnSerSerLeuAspPheHisPheAsnGlnGlu 480  
 |||||  
 QY 1464 AAAGCACATTCAGGAGGCATTAAGATATTGTATCATAGAGTTTAAAGCTTGTATTATTT 1523  
 |||||  
 DB 481 LysAlaTyrSerGlyGluValGluThrLeuHisGlnSerLeuSerLeuLeuLeuPhe 500  
 |||||  
 QY 1524 GGTATTGTTCAATTCCTGAAAAACACTTCTATTAT 1559  
 |||||  
 DB 501 GlyIleValHisLeuLeuAsnLysIleCysSerTyr 512  
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Db	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668	669	670	671	672	673	674	675	676</
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Sarcoma;  
 RA Sorensen K.C., Balkin R.G., Ktichell B.E., Siegel A.M., Schaeffer D.;  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AV183143; AA063580.1; -  
 DR InterPro: IPR000585; Hemopexin.  
 DR InterPro: IPR006026; Peptidase M.  
 DR InterPro: IPR001818; Pept M10A M12B.  
 DR InterPro: IPR006025; Pept M Zn\_BS.  
 DR Pfam: PF00045; Hemopexin; 4  
 DR Pfam: PF00413; Peptidase M10; 1.  
 DR Pfam: PF03933; Peptidase M10\_N; 1.  
 DR PRINTS: PR00130; MATRILIX.  
 DR SMART: SM00120; HX; 4.  
 DR SMART: SM00235; ZmC; 1.  
 DR PROSITE: PS00546; CYSTEINE SWITCH; 1.  
 DR PROSITE: PS00024; HEMOPEXIN; 1.  
 DR PROSITE: PS00142; ZINC PROTEASE; UNKNOWN 1.  
 SQ SEQUENCE 478 AA; 53633 MW; 5D1B9DA9D57BC041 CRC64;  
 Alignment Scores:  
 Pred. No.: 2, 62e-105 Length: 478  
 Score: 1286.50 Matches: 254  
 Percent Similarity: 67.29% Conservative: 69  
 Best Local Similarity: 52.92% Mismatches: 140  
 Query Match: 43.91% Indels: 17  
 DB: 2 Gaps: 8  
 US-10-729-807-28 (1-1627) x Q6Y4Q5 (1-478)  
 QY 24 ATGAGCGCTTCTGCTTCTGTTTGTCTTTTAAACATTTCTTCTGATTTCCCTTA 83  
 DB 1 MetGlnAsnLeuProAlaLeuLeuPheCysGlyValValCysSerAlaTyrProVal 20  
 QY 84 GTCGGATGACGGAATGAA---GAAATATGCAACTGGCTCAGGCATATCTCAACCAG 140  
 DB 21 AspArgAlaAlaGluAspGluAsnAsnMetGluLeuThrGlnGlnTyrLeuGluAsn 40  
 QY 141 TTCTACTCTCTGAAATAGAGGAATCATCTTTCAAAGCAAGATAGGAGTCTCAT 200  
 DB 41 TyrTyrAsnLeuGlyLysAspValLysProPheValArgArgAsnSerGlyProVal 60  
 QY 201 GATGACAAATTCGGAAATGCAAGCATTTTGGATTGACAGTGTGAGTGTGAAATCGGAC 260  
 DB 61 ValGluLysIleArgGluMetGlnLysPheLeuGlyLeuGluValThrGlyLysValAsp 80  
 QY 261 TCAACACCCCTTGAGATCATGACACCCAGGTGGGTGGTGGTGGTGGTGGTGGTGGT 320  
 DB 81 SerAspThrLeuAlaMetMetArgProA-gCysGlyValProAspValGlyAspPhe 100  
 QY 321 GGCTACACCTCCCTGGG-----TGGAGAAATACAACTACCTACAGAAATAATA 371  
 DB 101 ---ThrThrPheProGlyMetProLysTyrArgLysThrHisLeuThrTyrArgIleMet 119  
 QY 372 AACTATATCCGGATATGCGAGCTGCTGTGGATGAGGCTATATCAAGAGGTTTAAAG 431  
 DB 120 AsnTyrThrProAspLeuProArgAspAlaValAspSerAlaIleGluLysAlaLeuAsn 139  
 QY 432 GTGTGAGCAAGTCACTCACTAAATCAACCAAGATTTCGAAGGGGATTCGACGATC 491  
 DB 140 ValTrpLysGluValThrProLeuThrPheSerArgThrAspGluGluAlaAspIle 159  
 QY 492 ATGATGCTCTTAGGACTCGAGTCCATGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 551  
 DB 160 LysIleSerPheAlaValArgAspHisGlyAspPhe---AsnProPheAspGlyProGly 178  
 QY 552 GGAGTGTGGCATGCCCTTCTCTGCTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 611  
 DB 179 AsnValLeuGlyHisAlaTyrProProGlyProGlyProGlyIleTyrGlyAspAlaHisPheAsp 198

QY 612 GAGGATGAAACTGGACCAAGGATGAGCAGGAGTTCACATTTGTTTCTTGTGGTGTGCAT 671  
 DB 199 AspAspGluGlnTrpThrSerThrSerGlyThrAsnLeuPheLeuValAlaHis 218  
 QY 672 GAATTTGGTCATGCACTGGGGTCTCTCACTCCAATGATCAAAACAGCGCTTGATGTTCCCA 731  
 DB 219 GluLeuGlyHisSerLeuGlyLeuPheHisSerAlaAspProSerAlaLeuMetTyrPro 238  
 QY 732 AATTAT---GTCTCCCTGGATCCAGAAATACCCATTTCTCAGGATGATATCAATGGA 788  
 DB 239 ValTyrAsnValLeuAlaAspLeuAlaArgPheHisLeuSerGlnAspValAsnGly 258  
 QY 789 ATCCAGTCCATCTATGAGGTCTGCTCAAG-----GTACCTGTCT 827  
 DB 259 IleGlnSerLeuTyrGlyGlyProSerAspSerSerAsnAspProValValProThr 278  
 QY 828 AAG-----CCAAAGGAACCCACTATATACCCCATGCTGTGACCTGACTTGTGAC 881  
 DB 279 GluSerValProGlyProGlyThrProAlaAlaCysAspProThrLeuSerPheAsp 298  
 QY 882 GCTATCACAATTTCCGACAGAGTAATGTTCTTTAAAGGACGACCTATGAGGATC 941  
 DB 299 AlaIleSerThrLeuArgGlyGluPheLeuPhePheLysAspArgHisPheTyrPheLys 318  
 QY 942 TATTATGATATCACGGATGTTGAGTTTGAATTAATGTTCTTCTGCGCATCTCTGCCA 1001  
 DB 319 SerLeuArgThrLeuGluProGlyPheTyrLeuLeuSerSerPheTyrProSerLeuPro 338  
 QY 1002 GCTGATCTCAAGTGCATAC---GAGAACCCAGAGATTAAGATTTCTGTTTAAAGAT 1058  
 DB 339 SerGlyLeuAspAlaAlaTyrGluThrSerLysAspIleValPheIlePheLysGly 358  
 QY 1059 GAAACTTCTGGATGATCAGAGATATGCTGTCTGCCAGATTATCCCAATCCATPCCAT 1118  
 DB 359 AsnGlnPheTyrPhePheValGlyAspLysTyrTyrTrpArgPheAspGluLysArgGlnSer 378  
 QY 1119 ACATTAAGTTTCCAGGAGTGTGAGAAATAGATGACGCGTCTGTGTATGAGACCACA 1178  
 DB 379 ThrLeuGlyPheProThrValLysLysIleAspAlaAlaValPheAspLysGluLys 398  
 QY 1179 AGAAACCTACTCTTTCTGGGCATTTGGTGTGGAGTGTGTGATGAATGACCCAAACC 1238  
 DB 399 LysLysThrTyrPhePheValGlyAspLysTyrTyrTrpArgPheAspGluLysArgGlnSer 418  
 QY 1239 ATGCAAAAGGATCCCGCAGAGTGGTAAACACTTTCTCCTGGAATCAGTATCCGTGTT 1298  
 DB 419 MetGluProGlyPheProLysGlnIleAlaGluAspPheProGlyValAspSerLysVal 438  
 QY 1299 GATGCTGCTTCCAGTACAAAGATTTCTTTTTCAGCGGTGGATCAAGCAATTTGAA 1358  
 DB 439 AspAlaAlaPheGluAlaPheGlyPheTyrTyrPhePheAsnGlySerGlnLeuGlu 458  
 QY 1359 TACAACATTAAAGCAAGAAATATTATCCCGAATCATGAGAACTAATACTTGGTTTCAATGC 1418  
 DB 459 PheAspProAsnAlaLysLysValThrHisValLeuLysSerAsnSerTrpLeuAsnCys 478  
 RESULT 7  
 ID AA063580 PRELIMINARY; PRT; 478 AA.  
 AC AA063580;  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Stromelysin 1.  
 GN MMP3.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Sarcoma;





CC	III, IV, and V; collagens III, IV, X, and IX, and cartilage
CC	proteoglycans. Activates procollagenase.
CC	-I- CATALYTIC ACTIVITY: Preferential cleavage where P1', P2' and P3'
CC	are hydrophobic residues.
CC	-I- COPAFCTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
CC	similarity).
CC	-I- SIMILARITY: Belongs to peptidase family M10A.
CC	-I- SIMILARITY: Contains 1 hemopexin-like domain.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>
CC	or send an email to <a href="mailto:license@sb-sib.ch">license@sb-sib.ch</a> ).
CC	-----
DR	EMBL; M25664; AAA31467.1; --.
DR	PIR; A37306; KCRBS1.
DR	HSP; P08254; IG05.
DR	MEROPS; M10.005; --.
DR	InterPro; IPR000585; Hemopexin.
DR	InterPro; IPR006026; Peptidase M.
DR	InterPro; IPR001818; Pept_M10A_M12B.
DR	InterPro; IPR006025; Pept_M_Zn_BS.
DR	InterPro; IPR009070; PGSD like.
DR	Pfam; PF00045; Hemopexin; 4.
DR	Pfam; PF00413; Peptidase_M10; 1.
DR	Pfam; PF03933; Peptidase_M10_N; 1.
DR	PRINTS; PR00138; MATRXIN.
DR	SMART; SM00120; HX; 4.
DR	SMART; SM00235; ZnMc; 1.
DR	PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR	PROSITE; PS00024; HEMOPEXIN; 1.
DR	PROSITE; PS00142; ZINC_PROTEASE; 1.
DR	Calcium-binding; Collagen degradation; Extracellular matrix; Zinc;
KW	Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
KW	Zymogen.
FT	SIGNAL 1 17
FT	PROPEP 18 100
FT	CHAIN 101 478
FT	DOMAIN 288 478
FT	SITE 93 93
FT	METAL 125 125
FT	METAL 159 159
FT	METAL 169 169
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FT	METAL 439 439

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QY 816 AAGTACCTGCTAAGCCAAAGGACCCACCTATACCCCATGCTGCTGACCTGACT 875  
 Db 278 MetGluProValProGlySerGlyThr---ProValMetCysAspProAspLeuSer 296  
 QY 876 TTTCACCTATCAACACTTTCCGAGAGAGTAAATGTTCTTAAAGCAGCAGCCTATGG 935  
 Db 297 PheAspAlaIleSerThrLeuArgGlyGluLeuPhePhePhePhePhePhePhe 316  
 QY 936 AGGATCTATTATGATATACCGATGTTGAGTTGAATTAATGCTTCATCTGCGCATCT 995  
 Db 317 ArgLysSerLeuArgGlyLeuGluProGluPheHisLeuIleSerSerPheTyrProSer 336  
 QY 996 CTGCCACTGATCTGCAAGCTGCATAGAG---AACCCGAGAGATAGATCTCGTTT 1052  
 Db 337 LeuProSerAlaValAspAlaAlaTyrGluValIleSerArgAspThrValPheIlePhe 356  
 QY 1053 AAAGATGAAAACTCTCGATGATCAGAGGATATGCTGCTTGCAGATTTATCCCAATCC 1112  
 Db 357 LysGlyThrGlnPheTyrPhePheValGluValGlnAlaGlyTyrProArgSer 376  
 QY 1113 ATCCATCATAGTTTCCAGGACGCTGTAAGAAATAGATGAGCGCTCTGTGATAAG 1172  
 Db 377 IleHisThrLeuGlyPheProSerThrIleArgLysIleAspAlaAlaIleSerAspLys 396  
 QY 1173 ACCACAGAAAACTCTTCTGCTGGCATTTGCTGCTGAGGTTTGTGAATGACC 1232  
 Db 397 GluArgLysLysThrPhePheValGluAspLysTyrTyrPheArgPheAspGluLysArg 416  
 QY 1233 CAACACCATGAGCAAGATTCCTCCGAGAGAGTGTAAACACTTCTCTGGAATCAGTATC 1292  
 Db 417 GlnSerLeuGluProGlyPheProArgHisIleAlaGluAspPheProGlyIleAsnPro 436  
 QY 1293 CGTGTGATGCTGCTTCCAGTACAAGGATCTCTTTTTCACGCCGTGATCAAGCAA 1352  
 Db 437 LysIleAspAlaValPheGluAlaPheGlyPhePheTyrPhePheSerGlySerSerGln 456  
 QY 1353 TTTCATACACATTAAGACAAAGATTAATCCGGAATCATGAGAACTAATACTTGGTTT 1412  
 Db 457 SerGluPheAspProAsnAlaLysValThrHisValLeuLysSerAsnSerTyrPhe 476  
 QY 1413 CAATGC 1418  
 Db 477 GlnCys 478  
 RESULT 9  
 AAH69676 PRELIMINARY; PRT; 477 AA.  
 AC AAH69676;  
 DT 20-MAY-2004 (TrEMBLrel. 27, Created)  
 DT 20-MAY-2004 (TrEMBLrel. 27, Last sequence update)  
 DE 20-MAY-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Matrix metalloproteinase 3, preproprotein.  
 GN MMP3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PCR rescued clones;  
 RX MEDLINE=22389257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Iu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PCR rescued clones;  
 RA Strausberg R.;  
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC969676; AAH69676.1; -. 7497490A861DEEA9 CRC64;  
 SQ SEQUENCE 477 AA; 53978 MW; 7497490A861DEEA9 CRC64;

Alignment Scores:  
 Pred. No.: 2,05e-102 Length: 477  
 Score: 1254.00 Matches: 247  
 Percent Similarity: 66.04% Conservative: 70  
 Best Local Similarity: 51.46% Mismatches: 145  
 Query Match: 42.80% Indels: 18  
 DB: 2 Gaps: 9

US-10-729-807-28 (1-1627) x AAH69676 (1-477)

QY 24 ATGAAGCGCCTTCGCTTCTGTTGTTCTTTTATAACATTTCTTCTGCAATTCCTTA 83  
 Db 1 MetLysSerLeuProIleLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 20  
 QY 84 GTCCGATGACGGGAAATGAAGAA---AATATGCACTGGCTCAGGCATATCTCAACAG 140  
 Db 21 AspGlyAlaAlaArgGlyGluAspThrSerMetAsnLeuValGlnLysTyrLeuGluAsn 40  
 QY 141 TTCTACTCTCTGAAATAGAGGGAATCATCTTCTTCAAGCAAGATAGGAGTCTCAT 200  
 Db 41 TyrTyrAspLeuGluLysAspValLysGlnPheValArgLysAspSerGlyProVal 60  
 QY 201 GATCACAATAATCGGAAATCGACAGCATTTTGGATTGACAGTCTGGAAGAACTGGAC 260  
 Db 61 ValLysLysIleArgGluMetGlnLysPheLeuGlyLeuGluValThrGlyLysLeuAsp 80  
 QY 261 TCAACACACCTTGAGATCATGACACACCCAGGTGTGGGTGCTGTATGTGGGCAGTAT 320  
 Db 81 SerAspThrLeuGluValMetArgLysProArgCysGlyValProAspValGlyHisPhe 100  
 QY 321 GGCTACACCTCTCTCTGGG-----TGGAGAAAATACAACTCACTACAGATAATA 371  
 Db 101 ---ArgThrPheProGlyIleProLysTyrArgLysThrHisLeuThrTyrArgIleVal 119  
 QY 372 AACTATATCTCGGATATGGCAGCTGCTGTGGATGAGGCTATCCAGAGAGTTTAGAA 431  
 Db 120 AsnTyrThrProAspLeuProLysAspAlaValAspSerAlaValGluLysAlaLeuLys 139  
 QY 432 GTGTGGAGCAAAAGTCACTCCACTAAAATTTCAACAAAGATTTCAAAGGGGATTCAGACATC 491  
 Db 140 ValTyrGluGluValThrProLeuThrPheSerArgLeuTyrGluGlyGluAlaAspIle 159  
 QY 492 ATGATGCTTTTAGGATCTGAGTCCATGCTCGGTGCTCTCTGCTAT---TTTGATGTCCTC 548  
 Db 160 MetIleSerPheAlaValArgGluHisGly-----AspPheTyrProPheAspGlyPro 177  
 QY 549 TTGGGAGTGTTCGCCATGCTTTCTCTCGGTGCTGGGTGCTGGGTGCTGACACATTTT 608  
 Db 178 GlyAsnValLeuAlaHisAlaTyrAlaProGlyProGlyIleAsnGlyAspAlaHisPhe 197  
 QY 609 GATGAGGATGAAAAGTGGACCAAGGATTCAGAGGATTCACACTTGTCTTCTGCTGCTCT 668  
 Db 198 AspAspAspGluGlnTyrThrLysAspThrThrGlyThrAsnLeuPheLeuValAlaAla 217  
 QY 669 CATGAATTTGGTATGACTGGGCTCTCTCACTCAATGATCAACAGCCCTGATGTC 728  
 Db 218 HisGluIleGlyHisSerLeuGlyLeuPheHisSerAlaAsnThrGluAlaLeuMetTyr 237



Db 198 AspAspAspGluGlnTrpThrLysAspThrGlyThrAsnLeuPheLeuValAlaAa 217  
Qy 669 CATGAATTTGGTCATGCACTGGGGCTCTCTCACTCCAAATGATCAACAGCGCTTGATGTC 728  
Db 218 HisGluIleGlyHisSerLeuGlyLeuPheHisSerAlaAsnThrGluAlaLeuMetTyr 237  
Qy 729 CCAAAATATGTCCTCCG--GATCCAGAGAAATACCACTTCTCAGGATGATATCAAT 785  
Db 238 ProLeuThrHisSerLeuThrAspLeuThrArgPheArgLeuSerGlnAspPileAsn 257  
Qy 786 GGAATCCAGTCCATCTATGGA-----GCTCTGCTCAAGGTACCTGCT 827  
Db 258 GlyIleGlnSerLeuTyrGlyProProAspSerProGluThrProLeuValProThr 277  
Qy 828 AAG-----CCAAAGAACCACTATACCCCATGCCCTGACCTGACCTGACTTTCAC 881  
Db 278 GluProValProGluProGlyThrProAlaAsnCysAspProAlaLeuSerPheAsp 297  
Qy 882 GCTATCACACTTTCGCGCAGAGAGTAAATGTTCTTTAAAGCGACGACCTATGAGGATC 941  
Db 298 AlaValSerThrLeuArgGlyGluIleLeuPheLysAspArgHisPheTrpArgLys 317  
Qy 942 TATTATGATATCAGGATGTTGAGTTTGAATTAATGCTTCCTGCTCCCATCTCTCCCA 1001  
Db 318 SerLeuArgLysLeuGluProGluLeuHisLeuIleSerSerPheTrpProSerLeuPro 337  
Qy 1002 GCTGATCTGCAAGTCTGATCAGAG--AACCAGAGATAGATCTGCTTTTAAAGAT 1058  
Db 338 SerGlyValAlaAlaTyrGluValThrSerLysAspLeuValPheIlePheLysGly 357  
Qy 1059 GAAATCTTGGATGATCAGAGGATGCTGCTGTCGAGATATCCAAATCCATCAT 1118  
Db 358 AsnGlnPheTrpAlaIleArgGlyAsnGluValArgAlaGlyTyrProArgGlyIleHis 377  
Qy 1119 ACATTAGTCTTTCAGGACGCTGTAAGAAATAGATGACGCGCTGTGATAAGACCA 1178  
Db 378 ThrLeuGlyPheProProThrValArgLysIleAspAlaIleSerAspLysGluLys 397  
Qy 1179 AGAAAACTTCTTCTTGGGCGATGTTGGTGGAGTTGAGTTGATGAATGACCAAC 1238  
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Qy 1239 ATGACAAAGATTCGCGCAGAGTGTAAACACTTTCCTGGAATCAGTATCCGTGTT 1298  
Db 418 MetGluProGlyPheProLysGlnIleAlaGluAspPheProGlyIleAspSerLysIle 437  
Qy 1299 GATGCTGCTTTCAGTACAAAGGATCTCTTTTCAGCGCTGGATCAAGCAATTTGAA 1358  
Db 438 AspAlaValPheGluGluPheGlyPhePheTyrPhePheThrGlySerSerGlnLeuGlu 457  
Qy 1359 TACAACATTAAGACAAAGATATATACCGAATCATGAACTATATCTGTTCAATGC 1418  
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RESULT 11  
NM03 HUMAN  
ID NM03 HUMAN STANDARD; PRT; 477 AA.  
AC P08254;  
DC 01-AUG-1988 (Rel. 08, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Stromelysin-1 precursor (EC 3.4.24.17) (Matrix metalloproteinase-3)  
DE (MMP-3) (Transin-1) (St-1).  
GN Name=MMP3; Synonyms=STMY1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-24.  
RX MEDLINE=88198243; PubMed=3360803;  
RA Saus J., Quinones S., Otani Y., Nagase H., Harris E.D. Jr.,  
RA Kurkinen M.;

RT "The complete primary structure of human matrix metalloproteinase-3.  
RT Identity with stromelysin.";  
RL J. Biol. Chem. 263:6742-6745 (1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fibroblast;  
RX MEDLINE=87156645; PubMed=3030290;  
RA Whitam S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A.,  
RA Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;  
RA "Comparison of human stromelysin and collagenase by cloning and  
RT sequence analysis.";  
RL Biochem. J. 240:913-916 (1986).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88016164; PubMed=3477804;  
RA Wilhelm S.M., Collier I.E., Kronberger A., Eisen A.Z., Marmer B.L.,  
RA Grant G.A., Bauer E.A., Goldberg G.I.;  
RA "Human skin fibroblast stromelysin: structure, glycosylation,  
RT substrate specificity, and differential expression in normal and  
RT tumorigenic cells.";  
RL Proc. Natl. Acad. Sci. U.S.A. 84:6725-6729 (1987).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,  
RA Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C.,  
RA Kurdi O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D.,  
RA Heller R., Davis R.W.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A., AND VARIANT GLU-45.  
RX Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,  
RA Nickerson D.A.;  
RA "SeattleSNPs: NHLBI HUG66682 program for genomic applications, UW-  
RT PHRC, Seattle, WA (URL: <http://pga.gs.washington.edu>).";  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP ZYMOGEN ACTIVATION.  
RX MEDLINE=90344802; PubMed=2383557;  
RA Nagase H., Englund J.J., Suzuki K., Salvesen G.;  
RT "Stepwise activation mechanisms of the precursor of matrix  
RT metalloproteinase 3 (stromelysin) by proteinases and (4-  
RT aminophenyl)mercuric acetate.";  
RL Biochemistry 29:5783-5789 (1990).  
RN [7]  
RP STRUCTURE BY NMR OF CATALYTIC DOMAIN.  
RX MEDLINE=95384761; PubMed=7656014;  
RA Gooley P.R., O'Connell J.F., Marcy A.I., Cuca G.C., Salowe S.P.,  
RA Bush B.L., Hermes J.D., Esser C.K., Hagmann W.K., Springer J.P.,  
RA Johnson B.A.;  
RT "The NMR structure of the inhibited catalytic domain of human  
RT stromelysin-1.";  
RL Nat. Struct. Biol. 1:111-118 (1994).  
RN [8]  
RP STRUCTURE BY NMR OF 100-267.  
RX MEDLINE=99043696; PubMed=9827994;  
RA Stockman B.J., Waldon D.J., Gates J.A., Schall T.A.,  
RA Kloosterman D.A., Mizsak S.A., Jacobsen E.J., Belonga K.L.,  
RA Mitchell M.A., Mao B., Petke J.D., Goodman L., Powers E.A.,  
RA Ledbetter S.R., Kaytes P.S., Vogel G., Marshall V.P., Petzold G.L.,  
RA Poorman R.A.;  
RT "Solution structures of stromelysin complexed to thiazole  
RT inhibitors.";  
RL Protein Sci. 7:2281-2286 (1998).  
RN [9]  
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 18-272.  
RX MEDLINE=96117647; PubMed=8535233;  
RA Becker J.W., Marcy A.I., Rokosz L.L., Axel M.G., Burbaum J.J.,  
RA Fitzgerald P.M.D., Cameron P.M., Esser C.K., Hagmann W.K.,  
RA Hermes J.D., Springer J.P.;  
RT "Stromelysin-1: three-dimensional structure of the inhibited catalytic  
RT domain and of the C-truncated proenzyme.";  
RL Protein Sci. 4:1966-1976 (1995).  
RN [10]







Db 122 AspMetAlaGluAlaAspValAspThrAlaIleAArgAlaPheLysValTrpSerAsp 141  
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Db 142 ValThrProLeuThrPheSerArgIleTyrGluGlyThrAlaAspIleGlnIleSerPhe 161  
QY 504 AGGACTCGAGTCATCGGTGGTCTCGCTAT---TTTGATGGTCCCTTGGAGGTCTT 560  
Db 162 GlyAlaGlyValHisGly-----AspPheTyrProPheAspGlyProHisGlyThrLeu 179  
QY 561 GGCCATGCTCTTCCTCGTCCGGTCTGGGTGGTGACACTCATTTGATGAGGATGAA 620  
Db 180 AlaHisAlaPheAlaProGlyAsnSerIleGlyGlyAspAlaHisPheAspGluAspGlu 199  
QY 621 AACTGGACCAAGATGAGGACAGATTCACCTTGTCTTCTTGTGCTGCTCATGAATTGT 680  
Db 200 ThrTrpThrAlaGlySerAlaGlyTyrAsnLeuPheLeuValAlaAlaHisGluPheGly 219  
QY 681 CATGCACTGGGTCTCTCACTCCATGATCAACAGCCTTGATGTTCCCAAAATATATGC 740  
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QY 801 TATGAGGTCTGCCTAAG---GTACTGCTAGCCAAAG----- 836  
Db 260 TyrGlyAlaSerProAsnProValProThrThrProGlnAlaThrThrProThrThrThr 279  
QY 837 -----GAACCACTATATACCCATCCCTGCTGACCCCTGAC 869  
Db 280 ValSerThrThrThrThrThrSerSerProIleAsnProSerIleCysAspProThr 299  
QY 870 TTGACTTTTGAGCTATCAAACTTCCCGAGAGAGTAAATGTTCTTTAAAGCAGGCAC 929  
Db 300 LeuValPheAspAlaIleThrThrLeuArgGlyIleLeuPhePheLysAspSerSer 319  
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QY 990 CATCTCTCCAGCTGATCGAAGCTGCATAGCAGAACCCAGAA---GATAGATTCTG 1046  
Db 340 ProSerLeuProSerGlyIleGlnAlaAlaTyrGluAsnProGluThrAspGlnIlePhe 359  
QY 1047 GTTTTAAAGATGAAAACTCTGGATGATCAGAGATATGCTCTGTCGAGATATATCC 1106  
Db 360 LeuPheLysGlySerLysTyrTrpAlaLeuGlnGlyPheAspIleLeuProAsnTyrPro 379  
QY 1107 AATCATCATCATATAGTTTTCAGGACGCTGTAAGAAATAGATGACGACCGTCTGT 1166  
Db 380 LysAsnIleAspLysLeuGlyPheProArgThrValLysHisIleAsnAlaAlaValTyr 399  
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Db 400 LeuGlnSerThrGlnLysThrTyrPhePheAlaGlyGlnTyrTrpSerTyrAspGlu 419  
QY 1227 ATGACCCAAACCATGAGCAAGATTCCTCCGAGAGATGTTGATAAACAATTTCTCGGAATC 1286  
Db 420 AlaArgLysThrMetAspLysGluSerProArgArgIleGluAspAspPheProGlyIle 439  
QY 1287 AGTATCGTGTGATGCTTTCAGTACAAAGATTCCTCTTTTTCAGCCGCTGATCA 1346  
Db 440 GlyLysLysValHisAlaValPheGluAspAsnGlyLeuLeuTyrPhePheSerGlyHis 459  
QY 1347 AAGCAATTCAATACAACTTATAGACAAAGAAATATACCGAATCATGAGAACTAATACT 1406  
Db 460 LysGlnPheGluPheAsnMetLysSerLysValThrArgThrGlnLysAsnThrSer 479  
QY 1407 TGGTTTCAATGC 1418  
Db 480 TrpLeuGlyCys 483

## RESULT 13

MM03\_HORSE  
ID MM03 HORSE STANDARD; PRT; 477 AA.  
AC Q28397;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 01-OCT-2004 (Rel. 45, Last annotation update)  
DE Stromelysin-1 precursor (EC 3.4.24.17) (Matrix metalloproteinase-3) (MMP-3).  
DE (MMP-3).  
GN Name=MMP3;  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Cartilage;  
RX MEDLINE=99074117; PubMed=9858406;  
RA Richardson D.W., Dodge G.R.;  
RT "Molecular characteristics of equine stromelysin and the tissue inhibitor of metalloproteinase 1.";  
RL Am. J. Vet. Res. 59:1557-1562(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Cartilage;  
RX MEDLINE=98104320; PubMed=9442239;  
RA Balkman C.E., Nixon A.J.;  
RT "Molecular cloning and cartilage gene expression of equine stromelysin 1 (matrix metalloproteinase 3).";  
RL Am. J. Vet. Res. 59:30-36(1998).  
RN [3]  
RP 3D-STRUCTURE MODELING  
RA Mallena S.C., Sharma J.A.R.P.;  
RL "Theoretical model of horse stromelysin.";  
Submitted (MAR-2002) to the PDB data bank.  
CC -!- FUNCTION: Can degrade fibronectin, laminin, gelatins of type I, III, IV, and V; collagens III, IV, X, and IX, and cartilage proteoglycans. Activates procollagenase.  
CC -!- CATALYTIC ACTIVITY: Preferential cleavage where P1', P2' and P3' are hydrophobic residues.  
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By similarity).  
CC -!- SIMILARITY: Belongs to peptidase family M10A.  
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.  
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CC -----  
DR EMBL; U62529; AAB05774.1; -.  
DR PDB; 1L9I; Model; A=100-267.  
DR MEROPS; M10.005; -.  
DR InterPro; IPR000585; Hemopexin.  
DR InterPro; IPR006026; Peptidase M.  
DR InterPro; IPR001818; Pept M10A\_M12B.  
DR InterPro; IPR006025; Pept M\_Zn\_BS.  
DR InterPro; IPR009070; PGBD-like.  
DR Pfam; PF00045; Hemopexin\_4.  
DR Pfam; PF00413; Peptidase M10; 1.  
DR Pfam; PF03933; Peptidase M10\_N; 1.  
DR PRINTS; PR00138; MATRIXIN.  
DR SMART; SM00120; HX; 4.  
DR SMART; SM00235; ZmC; 1.  
DR PROSITE; PS00546; CYSTEINE\_SWITCH; FALSE\_NEG.  
DR PROSITE; PS00024; HEMOPEXIN; 1.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
KW 3D-structure; Calcium-binding; Collagen degradation;  
KW Extracellular matrix; Glycoprotein; Hydrolase; Metal-binding;

KW	Metalloprotease; Signal; Zinc; Zymogen.	1	17	Potential.	
FT	SIGNAL	18	99	Activation peptide.	
FT	PROPEP	100	477	Stromelysin-1.	
FT	CHAIN	287	477	Hemopexin-like.	
FT	DOMAIN	92	92	Cysteine switch (Potential).	
FT	SITE	124	124	Calcium 1 (By similarity).	
FT	METAL	158	158	Calcium 2 (By similarity).	
FT	METAL	168	168	Zinc 1 (By similarity).	
FT	METAL	170	170	Zinc 1 (By similarity).	
FT	METAL	175	175	Calcium 3 (By similarity).	
FT	METAL	176	176	Calcium 3 (via carbonyl oxygen) (By similarity).	
FT	METAL	178	178	Calcium 3 (via carbonyl oxygen) (By similarity).	
FT	METAL	180	180	Calcium 3 (via carbonyl oxygen) (By similarity).	
FT	METAL	183	183	Zinc 1 (By similarity).	
FT	METAL	190	190	Calcium 2 (via carbonyl oxygen) (By similarity).	
FT	METAL	192	192	Calcium 2 (via carbonyl oxygen) (By similarity).	
FT	METAL	194	194	Calcium 2 (By similarity).	
FT	METAL	196	196	Zinc 1 (By similarity).	
FT	METAL	198	198	Calcium 3 (By similarity).	
FT	METAL	199	199	Calcium 1 (By similarity).	
FT	METAL	201	201	Calcium 1 and 3 (By similarity).	
FT	METAL	218	218	Zinc 2 (catalytic) (By similarity).	
FT	ACT_SITE	219	219	By similarity.	
FT	METAL	222	222	Zinc 2 (catalytic) (By similarity).	
FT	METAL	228	228	Zinc 2 (catalytic) (By similarity).	
FT	METAL	297	297	Calcium 4 (via carbonyl oxygen) (By similarity).	
FT	METAL	389	389	Calcium 4 (via carbonyl oxygen) (By similarity).	
FT	METAL	438	438	Calcium 4 (via carbonyl oxygen) (By similarity).	
FT	CARBOHYD	120	120	N-linked (GlcNAc. . .) (Potential).	
FT	DISULFID	290	477	By similarity.	
FT	CONFLICT	346	346	V -> E (in Ref. 2).	
FT	TURN	104	105		
FT	STRAND	113	118		
FT	TURN	123	124		
FT	HELIX	127	144		
FT	STRAND	148	151		
FT	STRAND	159	164		
FT	STRAND	182	184		
FT	TURN	190	193		
FT	STRAND	195	198		
FT	TURN	199	200		
FT	STRAND	203	204		
FT	STRAND	210	211		
FT	HELIX	212	224		
FT	TURN	225	225		
FT	TURN	232	233		
FT	TURN	235	236		
FT	HELIX	253	263		
SQ	SEQUENCE	477 AA;	54190 MW; 361CB1427E09A272 CRC64;		

## Alignment Scores:

Pred. No.:	1.59e-101	Length:	477
Score:	1244.00	Matches:	244
Percent Similarity:	66.04%	Conservative:	73
Best Local Similarity:	50.83%	Mismatches:	145
Query Match:	42.46%	Indels:	18
DB:	1	Gaps:	8

US-10-729-807-28 (1-1627) x MM03\_HORSE (1-477)

QY	24	ATGAAGCGCTCTGCTCTGTGTGTTCTTTATACATTTCTTCTGCATTTCCCTTA	83
Db	1	MetLysAsnLeuProLleLeuLeuLeuLeuCysValAlaLaCysSerAlaTyrProLeu	20

QY	84	GTCCGGATGACGGAAATGAAGAA---AATATGCAACTGGCTCAGGCATATCTCAACCA	140
Db	21	AspArgSerAlaArgAspGluAspSerAsnMetAspLeuLeuGlnAspTyrLeuGluLys	40
QY	141	TTCTACTCTCTTGAATAGAGGAATCATCTTGTCAAAGCAAGAAATGAGGTCTCAT	200
Db	41	TyrTyrAspLeuGlyLysGluMetArgGlnTyrValArgArgLysAspSerGlyProIle	60
QY	201	GATGACAAATTCGGGAAATCAAGCATTTTGGATTGACAGTGAAGTGAAGTGAAC	260
Db	61	VallYsIysIleGlnGluMetGlnLysPheLeuGlyLeuValThrGlyLysLeuAsp	80
QY	261	TCAACACCCCTTGAGATCATGAACACCCAGGTGTGGGTGCTGATGTGGCCAGTAT	320
Db	81	SerAspThrValGluValMetHisLysSerArgCysGlyValProAspValGlyHisPhe	100
QY	321	GGCTACACCTCCCTCGG-----TGGAGAAATACAACTCACCATACAGATAATA	371
Db	101	--ThrThrPheProGlyMetProLysTrpSerLysThrHisLeuThrTyrArgIleVal	119
QY	372	AACATATCTCCGGATATGGACAGCTGCTGTGGATGAGGCTATCCAAAGAGTTTGA	431
Db	120	AsnTyrThrGlnAspLeuProArgAlaValAspSerAspValGluLysAlaLeuLys	139
QY	432	GTGTGGAGCAAGTCACCTCCACTAAATTCACCAAGATTTCAAAGGGATTCGACATC	491
Db	140	IleTrpGluGluValThrProLeuThrPheSerArgIleTyrGluGlyGluAlaAspIle	159
QY	492	ATGATTGCCTTTAGGACTCGAGTCCATGTCGG---TGTCCTGCTATTTTGTGGTCCC	548
Db	160	MetIleThrPheAlaValArgGluHisGlyAspPhePro-----PheAspGlyPro	177
QY	549	TTGGGAGTGTGGCCATGCTTCTCTGCTGGTCCGGGTCTGGGTGAGACACTCATTT	608
Db	178	GlyLysValLeuAlaHisAlaTyrProGlyProGlyProGlyMetAsnGlyAspAlaHisPhe	197
QY	609	GATGAGATGAATAACTGCACCAAGATGGAGCAGATTCACTTGTTCCTGTCGCTGCT	668
Db	198	AspAspAspGluHisTrpThrLysAspAlaSerGlyIleAsnPheLeuValAlaAla	217
QY	669	CATGAATTTGGTCATGCACCTGGGCTCTCTCACTCCAAATCAACAGCCCTTGATGTC	728
Db	218	HisGluLeuGlyHisSerLeuGlyLeuTyrHisSerThrAsnThrGluAlaLeuMetTyr	237
QY	729	CCAAATTTATGTCCTCCCTG---GATCCAGAAATATACCCTTCTCAGGATGATCAAT	785
Db	238	ProLeuTyrAsnThrLeuLysGlyProAlaArgValArgLeuSerGlnAspValThr	257
QY	786	GGAATCCAGTCCATCTATGAGGTCTGCCTAAGGTACTGCTAAGCCAAAGGACCCACT	845
Db	258	GlyIleGlnSerLeuTyrGlyProProAlaSerProAspSerProValGluProSer	277
QY	846	ATACCCCAT-----GCCTGTGACCTGACTTGTGACTTTTGAC	881
Db	278	GluProGluProProAlaProGlyThrLeuAlaMetCysAspProAlaLeuSerPheAsp	297
QY	882	GCTATCACAACTTTCGCAGAGAAATATGTTCTTTAAAGCGCAGCACCTATGGAGATC	941
Db	298	AlaIleSerThrLeuArgGlyGluIleLeuPhePheLysAspArgTyrPheTrpArgLys	317
QY	942	TATTATGATATACGGATGTTGAGTTTGAATTAATGCTTCATCTGGCCATCTCTGCCA	1001
Db	318	ThrPheArgThrLeuValProGluPheHisProIleSerSerPheTrpProSerLeuPro	337
QY	1002	GCTGATCTGCAAGCTGCATACAGAG---AACCCAGAGATAGATTTGTTTTPAAGAT	1058
Db	338	SerGlyIleAspAlaAlaTyrGluValThrSerArgAspSerValPheIlePheLysGly	357
QY	1059	GAATACTTCGGATGATCAGAGGATGCTGCTTCCACGATATATCCCAATCCATCCAT	1118
Db	358	AsnLysPheTrpAlaIleArgGlyAsnGluGluAlaGlyTyrProArgGlyIleHis	377
QY	1119	ACATTAGTTTCCAGGACCGTGTGAAGAAATAGATGTCAGCCGCTCTGTGTAAGACCACA	1178

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Db 378 ThrLeuGlyPheProThrValArgLysIleAspAlaIlePheAspLysGluLys 397
QY 1179 AGAAAAACCTACTCTTTGTGGCATTTGTGCTGGAGTTTGTATGAATACCCAAACC 1238
Db 398 GlnLysThrTyrPhePheValGluAspLysTyrTyrArgPheAspGluLysArgGlnSer 417
QY 1239 ATGGCAAAAGGATCCCGCAGAGAGTGGTAAACACTTTCCTGGATCAGTATCCGTGT 1298
Db 418 MetGluProGlyTyrProLysGlnIleAlaGluAspPheProGlyIleAspSerLysLeu 437
QY 1299 GATGCTGCTTTCAGATACAAAGCATCTCTTTTTCAGCGGTGATCAAGCAATTTGAA 1358
Db 438 AspAlaAlaPheGluSerPheGlyPheTyrPhePheSerGlySerGlnPheGlu 457
QY 1359 TACAACATTAAGCAAAAGAAATATTACCGGAATCATGAGAACTAATACTTGGTTTCAATGC 1418
Db 458 PheAspProAsnAlaLysValThrHisValLeuLysSerAsnSerTrpPheAsnCys 477

RESULT 14
MM10_MOUSE
ID AC MM10_MOUSE STANDARD; PRT; 476 AA.
AD 055123;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Stromelysin-2 precursor (EC 3.4.24.22) (Matrix metalloproteinase-10)
DE (MMP-10) (transin-2) (SL-2).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RC MEDLINE=98087420; PubMed=9427548;
RA Madlener M., Warner S.;
RT "CDNA cloning and expression of the gene encoding murine Stromelysin-2
RL (MMP-10).";
RL Gene 202:75-81 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cecum;
RX MEDLINE=22354683; PubMed=12456851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schorbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Glissi C., Godzik A., Gough J.,
RA Grimmond S., Gustinchik S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perteau G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sakaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
```

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RL Nature 420:563-573 (2002).
CC -!- FUNCTION: Can degrade fibronectin, gelatins of type I, III, IV,
CC and V; weakly collagens III, IV, and V. Activates procollagenase.
CC -!- CATALYTIC ACTIVITY: Similar to Stromelysin 1, but action on
CC collagen types III, IV and V is weak.
CC -!- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
CC -!- TISSUE SPECIFICITY: Expressed in small intestine. Weak levels in
CC heart and lung.
CC -!- INDUCTION: By wounding.
CC -!- SIMILARITY: Belongs to peptidase family M10A.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Y13185; CAAT73641.1; -.
CC EMBL; AK020292; BAB32058.1; -.
CC PIR; JC6505; JC6505.
CC HSSP; P08254; 1G05.
CC MEROPS; M10.006; -.
CC MGD; MGI:97007; Mmp10.
CC InterPro; IPR000585; Hemopexin.
CC InterPro; IPR006026; Peptidase M.
CC InterPro; IPR001843; Pept M10A_M10C.
CC InterPro; IPR001818; Pept M10A_M12B.
CC InterPro; IPR006025; Pept M_Zn_BS.
CC InterPro; IPR009070; PGED_like.
CC Pfam; PF02051; Fragilysin; 1.
CC Pfam; PF00413; Hemopexin; 4.
CC Pfam; PF03933; Peptidase M10_N; 1.
CC PRINTS; PR00138; MATRIXIN.
CC SMART; SM00120; HX; 4.
CC SMART; PS00235; ZNMC; 1.
CC PROSITE; PS00546; CYSTEINE_SWITCH; 1.
CC PROSITE; PS00024; HEMOPEXIN; 1.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
CC Calcium; Collagen degradation; Extracellular matrix; Hydrolase;
KW Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 17 Probable.
FT PROPEP 18 99 Activation peptide (By similarity).
FT CHAIN 100 476 Stromelysin-2.
FT DOMAIN 286 476 Hemopexin-like.
FT SITE 92 92 Cysteine switch (By similarity).
FT METAL 218 218 Zinc (catalytic) (By similarity).
FT ACT_SITE 219 219 By similarity.
FT METAL 222 222 Zinc (catalytic) (By similarity).
FT METAL 228 228 Zinc (catalytic) (By similarity).
FT DISULFID 289 476 By similarity.
SQ SEQUENCE 476 AA; 53911 MW; 2EB1CC41468F0AC6 CRC64;

Alignment Scores:
Pred. No.: 1,76e-101 Length: 476
Score: 1243.50 Matches: 244
Percent Similarity: 66.88% Conservative: 77
Best Local Similarity: 50.83% Mismatches: 140
Query Match: 42.44% Indels: 19
DS: 1 Gaps: 9

US-10-729-807-28 (1-1627) x MM10_MOUSE (1-476)
QY 24 ATGAAGCGCTTCTGCTCTGCTGTTTGTCTTTATACATTTTCTTCGATTCCTCTTA 83
Db 1 MetGluProLeuAlaIleLeuAlaLeuSerLeuProIleCysSerAlaTrpProLeu 20
QY 84 --GTCCGGATGACGGAATAATGAAGAAAATATGCAACTGGCTGAGCATATCTCAACCCAG 140
Db 21 HisGlyAlaValThrGlnGlyHisProSerMetAspLeuAlaGlnGlnTrpLeuGluLys 40
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QY 141 TTCTACTCTCTTGAATAGAGGGAATCATCTTGTTCACAGCAAGATAGGAGTCTATA 200  
 Db TyrTyrAsnPhelYsAsnGluYsGlnIlePhelYsArgLysAspSerProVal 60  
 QY 201 GATGACAAATTCGGGAATCGAACATTTTGGATTGACAGTGCAGTGGAAACCTGGAC 260  
 Db ValIysIleGlnGluMetGlnYsPhelGluYsLeuGluMetThrGlyYsLeuasp 80  
 QY 261 TCAACACCCCTTGAGATCATGAAGACACCCAGGTGTGGGTGCTCTGATGTGGCCAGPAT 320  
 Db SerAsnThrMetGluLeuMetHisYsProArgCysGlyValProaspValGlyGlyPhe 100  
 QY 321 GGCTACACCCCTCCCTGGG-----TGGAGAAATACACACCTCACCTACAGATATA 371  
 Db Ser-----ThrPheProGlySerProIysTrpArgYsSerHisIleThrYrArgIleVal 119  
 QY 372 AACTATCTCCGGATATGGCAGAGCTGCTGTGATGAGGCTATCCAAAGAGTTTGA 431  
 Db AsnTyrThrProaspLeuProargGlnSerValaspSerAlaIleGluYsAlaLeuYs 139  
 QY 432 GTGTGGAGCAAGTCACTCCACTAAATTCACCAAGATTCAAGGGGATTCGACATC 491  
 Db ValTrpGluGluValThrProLeuThrPheSerArgIleSerGluYsGluAlaAspIle 159  
 QY 492 ATGATTGCTTTAGACTCGAGTCAGTCCATGGTCCGTCTCGCTAT---TTTGATGGTCCC 548  
 Db MetIleSerPheAlaValGlyGluHisGly-----AspPheTyrProPheAspGlyPro 177  
 QY 549 TTGGAGTGTGGCCATGCTCTCTCTCGTCCGGTCTGGGTGGTGACACTCATTTT 608  
 Db GlyGlnSerLeuAlaHisAlaTyrProProGlyProGlyPheTyrGlyAspValHisPhe 197  
 QY 609 GATGAGGATGAAACTGACCAAGATGAGGAGGATTCAACTTGTCTTCTGTGGTCTCT 668  
 Db AspAspAspGluYsTrpThrLeuAlaProSerGlyThrAsnLeuPheLeuValAlaAla 217  
 QY 669 CATGAATTTGTGATGCTGGGCTCTCTCAATGATGATCAACAGCTTGATGTC 728  
 Db HisGluLeuGlyHisSerLeuGlyLeuPheHisSerLysLysLeuMetTyr 237  
 QY 729 CCAATATAT---GTCCTCCCTGGATCCCAAAATATCCCACTTCTCAGGATGATCAAT 785  
 Db ProValTyrArgPheSerThrSerProAlaAsnPheHisLeuSerGlnAspAspIleGlu 257  
 QY 786 GGAATCCAGTCACTATAGGAGT-----CTGCCTAAGTA 821  
 Db GlyIleGlnSerLeuTyrGlyAlaGlyProSerSerAspAlaThrValValProValLeu 277  
 QY 822 CTGCTAAGCCAAAGAACCCACTATACCCATGCTGTGACCTGACTTGCATTTTCAC 881  
 Db SerValSerProarg---ProGluThrProaspYsCysAspProAlaLeuSerPheasp 296  
 QY 882 GCTATCACAACTTCCGAGAGAAGTAATGTTTAAAGGAGGAGGACCTATGGAGGATC 941  
 Db SerValSerThrLeuArgGlyGluValLeuPhePheLysAspArgTyrPheTrpArg 316  
 QY 942 TATTATGATATCACGGATGTGAGTTTGAATTAATTTCTTCTGATCTGCGCATCTGCA 1001  
 Db SerHisTrpAsnProGluProGluPheHisLeuIleSerAlaPheTrpProThrLeuPro 336  
 QY 1002 GCTGATCTGCAAGCTGCATACAG---AACCCAGAGATAAGATTCTGTTTTTAAAGAT 1058  
 Db SerAspLeuAspAlaAlaTyrGluAlaHisAsnThrAspSerValLeuIlePheLysGly 356  
 QY 1059 GAAACATTTCTGATGATCAGAGGATATGCTGTTCGAGATATATCCAAATCCATCCAT 1118  
 Db SerGlnPheTrpAlaValArgGlyAsnGluValGlnAlaGlyTyrProLysGlyIleHis 376  
 QY 1119 ACATTAGTGTTCAGGAGCTGTGAAGAAATAGATGAGCGCTCTGTGTATGAAGACCACA 1178  
 Db ThrLeuGlyPheProProThrValIysIleAspAlaAlaValPheGluYsGluYs 396

QY 1179 AGAAAAACCTACTTCTTTGGCGCATTTGGTCTGGAGGTTTGATGAATAGACCAACC 1238  
 Db LysIysThrTyrPhePheValGlyAspLysTyrTrpArgPheaspGluThrArgHisVal 416  
 QY 1239 ATGACAAAGGATTCGCCAGAGAGTGGTAAACACTTCTTCTGGAATCAGTATCGTGT 1298  
 Db MetAspLysGlyPheProArgGlnIleThrAspAspPheProGlyIleGluProGlnVal 436  
 QY 1299 GATCTGCTTCCAGTACAAAGGATCTTCTTTTTCAGCCCGTGGATCAAGCAATTCGA 1358  
 Db AspAlaValLeuHisGluPheGlyPhePheTyrPhePheArgGlySerSerGlnPheGlu 456  
 QY 1359 TACAACATTAAAGACAAAGATATTACCCGATCATGAGAACTAATACTTGGTTTCAATGC 1418  
 Db PheaspProAsnAlaArgThrValThrHisIleLeuYsSerAsnSerTrpLeuLeuCys 476  
 RESULT 15  
 Q922W6 PRELIMINARY; PRT; 479 AA.  
 AC Q922W6  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)  
 DT 01-OCT-2004 (TrEMBLrel. 28, last annotation update)  
 DE Matrix metalloproteinase 3.  
 GN Name=Mmp3;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N;  
 RC TISSUE=Mammary tumor. Metallothionien-TGF alpha model. 10 month old  
 RC virgin mouse. Taken by biopsy.;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
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 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalish U., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
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 DR MGP; MGI:97010; Mmp3.  
 DR GO; GO:0005578; C:extracellular matrix; IEA.  
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.





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GenCore version 5.1.6  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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14: gb vi:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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| 2          | 1625.4 | 99.9    | 1647   | 6  | AX3464058 | Sequence            |
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| 4          | 1600.6 | 98.4    | 1841   | 6  | AX249969  | Sequence            |
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| 6          | 1548   | 95.1    | 1593   | 6  | AX089610  | Sequence            |
| 7          | 1417.8 | 87.1    | 1617   | 6  | AR263900  | Sequence            |
| 8          | 1293.4 | 79.5    | 1488   | 6  | AX249967  | Sequence            |
| 9          | 1257   | 77.3    | 1687   | 4  | AF281673  | Sequence            |
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| 16         | 449.2  | 27.6    | 1988   | 9  | AK024818  | Sequence            |
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| 26 | BC013875 Homo sapi |            |
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| 28 | BT006874 Homo sapi |            |
| 29 | BT007561 Synthetic |            |
| 30 | XO5231 Human mRNA  |            |
| 31 | BC074815 Homo sapi |            |
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| 34 | BC069716 Homo sapi |            |
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| 42 | CQ786689           | Sequence   |
| 43 | CQ819531           | Sequence   |
| 44 | I01070             | Sequence 1 |
| 45 | M13509             | Human skin |

ALIGNMENTS

| RESULT 1                        | LOCUS                                                                                                                       | AX358475    | 1845 bp | DNA | linear | PAT 13-FEB-2002 |
|---------------------------------|-----------------------------------------------------------------------------------------------------------------------------|-------------|---------|-----|--------|-----------------|
| DEFINITION                      | Sequence 1 from Patent WO0190326.                                                                                           |             |         |     |        |                 |
| ACCESSION                       | AX358475                                                                                                                    |             |         |     |        |                 |
| VERSION                         | AX358475.1                                                                                                                  | GI:18675086 |         |     |        |                 |
| KEYWORDS                        | Homo sapiens (human)                                                                                                        |             |         |     |        |                 |
| SOURCE                          | Homo sapiens                                                                                                                |             |         |     |        |                 |
| ORGANISM                        | Homo sapiens                                                                                                                |             |         |     |        |                 |
| REFERENCE                       | Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Rutheria; Primates; Catarrhini; Homnidae; Homo. |             |         |     |        |                 |
| AUTHORS                         | Holmgren,E., Kihlen,M., Wood,T. and Ekblom,J.                                                                               |             |         |     |        |                 |
| TITLE                           | Novel matrix metalloproteinases                                                                                             |             |         |     |        |                 |
| JOURNAL                         | Patent: WO 0190326-A, 1 29-NOV-2001;                                                                                        |             |         |     |        |                 |
| PHARMACIA & UPJOHN COMPANY (US) |                                                                                                                             |             |         |     |        |                 |
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| Best Local Similarity           | 100.0%; Pred. No. 0;                                                                                                        |             |         |     |        |                 |
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## ORIGIN

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ACCESSION AF195192  
VERSION AF195192.1 GI:11066089  
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SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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REFERENCE 1 (bases 1 to 1655)  
AUTHORS Benoit de Coignac, A., Elson, G., Magistrelli, G., Jeannin, P.,  
Delneste, Y., Aubry, J.P., Berthier, O., Bonnefoy, J.Y. and  
Gauchat, J.F.  
TITLE Cloning of a Novel Matrix Metalloproteinase Homologous to  
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JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1655)  
AUTHORS Benoit de Coignac, A., Elson, G., Magistrelli, G., Jeannin, P.,  
Delneste, Y., Aubry, J.P., Berthier, O., Bonnefoy, J.Y. and  
Gauchat, J.F.  
TITLE Direct Submission  
JOURNAL Submitted (15-OCT-1999) Molecular Biology, Pierre-Fabre, 5, Avenue  
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ACCESSION AX089610
VERSION AX089610.1 GI:13443799
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 benoit de Coignac,A., Elson,G. and Gauchat,J.F.
AUTHORS Stromelysin-homologous novel mmp-27 matrix metalloproteinase
TITLE Patent: WO 0116335-A 1 08-MAR-2001;
JOURNAL
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ORIGIN

Query Match 95.1%; Score 1548; DB 6; Length 1583;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 1568; Conservative 0; Mismatches 15; Indels 1; Gaps 1;

QY 10 GAAGAAAGAGAGGATGAAGCGCTTCGCTCTGCTGTTGTTTATACATTTCTT 69  
Db 1 GAAGAAAGAGAGGATGAAGCGCTTCGCTCTGCTGTTTATACATTTCTT 60

QY 70 CTGCAATTCCTTAGTCCGGATGACGGAAATGAAGAAATATGCAACTGGCTCAGGCAT 129  
Db 61 CTGCAATTCCTTAGTCCGGATGATGGAATGAAGAAATATGCAACTGGCTCAGGCAT 120

QY 130 ATCTCAACAGCTTCTCTCTTGAATAGAGGAATCACTTGTTCAAAGCAAGAATA 189  
Db 121 ATCTCAACAGCTTCTCTCTTGAATAGAGGAATCACTTGTTCAAAGCAAGAATA 180

QY 190 GGAGTCTCATAGATGACAAATTCGGGAATGCAAGCAATTTTGGATTGACAGTGACTG 249  
Db 181 GGAGTCTCATAGATGACAAATTCGGGAATGCAAGCAATTTTGGATTGACAGTGACTG 240

QY 250 GAAACTGGAATCAAAACCCCTTCAGATCATGAAGACACCCAGAGTGTGGGTGCTGATG 309  
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QY 310 TGGGCCAGTATGGCTAACCCTCCCTGGGTGAGAAATACAACTCACTACAGATAA 369  
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QY 370 TAAACTATACCTCCGATATGACAGAGCTGCTGTGATGAGCTATCCAAAGGTTTATG 429  
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QY 430 AAGTGTGAGCAAAAGTCACTCACTAAATTCACCAAGATTTCAAAGGGATTCAGACA 489  
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QY 490 TCATGATTCCTTTAGGATCGAGTCATGTCGTCGTCCTATTTGATGTCCT 549  
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QY 610 ATGAGGATGAAATCGGACCAAGGATGAGCAGGATTCAACTTGTTCCTGTCGTC 669  
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QY 670 ATGAATTTGGTCATGCACTGGGCTCTCTCACTCAATGATCAAAACAGCTTGTATTC 729  
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QY 970 AATTAATTTGCTTCAATTCCTGCGCATCTCTGCGCAGCTGATCTGCAAGCTGCATACGAGAACC 1029  
Db 960 AATTAATTTGCTTCAATTCCTGCGCATCTCTGCGCAGCTGATCTGCAAGCTGCATACGAGAACC 1019

QY 1030 CCAGAGATAAGATTCGTGTTTAAAGATGAAGAACTTCGATGATCAGAGATGATGCTG 1089  
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QY 1330 TTTTCAGCGTGGATCAAGCAATTTGAATCAACATTAAGACAAAGAAATATTACCCGAA 1389  
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QY 1390 TCATGAGACTAATACTTGGTTTCAATGCAAGAACCAAGAACTCCTCATTTGTTTGG 1449  
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LOCUS AR263900 1587 bp DNA linear PAT 29-JAN-2003  
DEFINITION Sequence 78 from patent US 6331427.  
ACCESSION AR263900  
VERSION AR263900.1 GI:28075904  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1687)  
AUTHORS Robison,K.E.  
TITLE Protease homologs  
JOURNAL Patent: US 6331427-A 78 18-DEC-2001;  
FEATURES Location/Qualifiers  
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Query Match 87.1%; Score 1417.8; DB 6; Length 1687;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1430; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Db 1680 TCGAGATGACAAAATTCGGGAAATGCAAGCATTTTGGATTGACAGTGAAGTGGAAAAC 1621  
QY 256 TGGACTCAACACACCCCTTGAGATCATGAAGACACCCAGGTGGGGTGCCTGATGTGGGCC 315  
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QY 316 AGTATGGCTACACCCCTCCCTGGGTGGAGAAAATACAACTCAGTACAGAAATATAAAT 375  
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QY 376 ATACTCCGGATATGGACAGCTGCTGTGATCAGGCTATCCAAAGAGTTCCTAGAGTGT 435  
Db 1500 ATACTCCGGATATGGACAGCTGCTGTGATCAGGCTATCCAAAGAGTTCCTAGAGTGT 1441  
QY 436 GGAGCAAGTCACTCCCACTAAAATTCACCAAGATTTCAAAGGGATTCAGACATCATGA 495  
Db 1440 GGAGCAAGTCACTCCCACTAAAATTCACCAAGATTTCAAAGGGATTCAGACATCATGA 1381  
QY 496 TTGCTTTAGGACTCGAGTCCATGCTCGGTGCTCTGCTATTTTGTGCTCCCTGGAG 555  
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Db 1320 TGCTTGGCCATGCTTTCCCTCCTGGTCCGGTCTGGGTGGTGCACCTCATTTTGTAGGAG 1261  
QY 616 ATGAAACTGGACCAAGGATGGAGCAGGATTCAACTGTTTCTGTGGCTGCCTCATGAAT 675  
Db 1260 ATGAAACTGGACCAAGGATGGAGCAGGATTCAACTGTTTCTGTGGCTGCCTCATGAAT 1201  
QY 676 TTGCTCATGCTGAGGCTCTCTCACTCCATGATCAACAGCCTGTGATTTCCCAAT 735  
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QY 736 ATGCTCCCTGGATCCAGAAAATACCACTTCTCAGGATGATCAATGGAAATCCAGT 795  
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Db 540 AGCGTGGATCAAGCAATTTGAATACAACTTAAGACAAAGAAATATATCCCGAATCATG 481  
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Db 480 AGAACTAATACCTTGGTTTCAATGCAAGAACCAAGAACTCTCATTTGTTTGTATC 421  
QY 1455 AACAAAGAAAACACATTCAGGAGCATAAAGATATTTGATCATAGAGTTTAAAGCTTG 1514  
Db 420 AACAAAGAAAACACATTCAGGAGCATAAAGATATTTGATCATAGAGTTTAAAGCTTG 361  
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QY 1575 CCTAAAATAAACCTCAACAGTCTTTTAAATATAAATTTCTGTTCAAAATAGAA 1627  
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RESULT 8  
AX249967  
LOCUS AX249967 1488 bp DNA linear PAT 28-SEP-2001  
DEFINITION Sequence 3 from Patent WO0166766.  
ACCESSION AX249967  
VERSION AX249967.1 GI:15864453  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Fajardo, M.D., Smith, R. and Moss, P.  
TITLE A matrix metalloproteinase (mmp-25) expressed in skin cells  
JOURNAL Patent: WO 0166766-A 3 13-SEP-2001;  
DARWIN MOLECULAR CORPORATION (US)  
FEATURES  
Location/Qualifiers  
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Query Match 79.5%; Score 1293.4; DB 6; Length 1488;  
Best Local Similarity 91.1%; Pred. No. 3.1e-308;  
Matches 1439; Conservative 0; Mismatches 11; Indels 129; Gaps 1;  
QY 7 GCTGAAGAAAGAGAGAAATGAAGCGCTTCTGCTCTGTTGTTGTTTATACATTTT 66  
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QY 67 CTTCTGCATTTCCCTTAGTCCGGATCAAGGAAAATGAAGAAAATATGCAACTGGCTCAGG 126  
Db 96 CTTCTGCATTTCCCTTAGTCCGGATCAAGGAAAATGAAGAAAATATGCAACTGGCTCAGG 155  
QY 127 CATATCTCAACAGTTCTACTCTCTTGAATAGAGGAATCATCTTTGTTCAAGCAAGA 186  
Db 156 CATATCTCAACAGTTCTACTCTCTTGAATAGAGGAATCATCTTTGTTCAAGCAAGA 215  
QY 187 ATAGGAGTCTCATAGATGACAAATTCGGGAATGCAAGCATTTTGGATTGCAGTGA 246  
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QY 247 CTGGAATACTGGACTCAACACCCCTTGCATCATGAAGACACCCAGGTGTGGGTGCTG 306  
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QY 307 ATGTGGCCAGTATGGCTACACCTCCTGGGTGGAGAAAATACAACTCACCTACCTAGAA 366

Db 336 ATGTGGCCAGTATGGCTACACCCCTCCCTGGTGGAGAAAAATACAACTCCTACAGAA 395  
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 QY 427 TAGAAGTGTGGAGCAAGTCACTCCACTAAATTCACCAAGATTTCAAAGGGATTGCGAG 486  
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 AF281673 1667 bp mRNA linear MAM 08-JAN-2001  
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 DEFINITION AF281673  
 ACCESSION AF281673.1 GI:12006363  
 VERSION  
 KEYWORDS  
 SOURCE Tupaia belangeri (northern tree shrew)  
 ORGANISM  
 Tupaia belangeri  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Scandentia; Tupaiidae; Tupiaia.  
 REFERENCE 1 (bases 1 to 1667)  
 AUTHORS Guggenheim, J.A., To, C.H. and Frost, M.R.  
 TITLE Molecular cloning of a novel matrix metalloproteinase (MMP-27) from  
 JOURNAL sciera  
 REFERENCE 2 (bases 1 to 1667)  
 AUTHORS Guggenheim, J.A. and Frost, M.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-JUN-2000) Department of Optometry & Vision Sciences,  
 Cardiff University, King Edward VII Avenue, Cardiff, Wales CF10  
 3NB, UK  
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 Query Match 77.3%; Score 1257; DB 4; Length 1667;  
 Best Local Similarity 86.8%; Pred. No. 3e-299;  
 Matches 1383; Conservative 0; Mismatches 210; Indels 0; Gaps 0;  
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| Q                                                                           | y |  | 1261 | GAGTGGTAAACAACACTTTTCCTGGAAATCAGTATCCGTGTGTGATGCTGCTTTCCAGTACAAAAG | 1320 |
| D                                                                           | b |  | 1331 | GGATAGTGAGACACTTTCCAGGCGATTGGGCTCCGTGTGTGATGCAGCTTTCCAGCACAAAG     | 1390 |
| Q                                                                           | y |  | 1321 | GATTCITCTTTTTCCAGCGTGGATCAAAGCAATTTGNAATACACATTTAAGACACAAAGATA     | 1380 |
| D                                                                           | b |  | 1391 | GTTTCTCTCTAATTTCTTCGTGGATCAAGCAATTTGAATATGACATTTAAGGCCAAAGACA      | 1450 |
| Q                                                                           | y |  | 1381 | TTACCCGAATCATGAGAACTAATACTTTGGTTTCAATGCAAAAGAACCAAAAGAACTCTCTCAT   | 1440 |
| D                                                                           | b |  | 1451 | TTACCCGAATAATGAGAACCAATACITGGTTTCAGTGTAAAGAACCATTAATTAATTCATCAC    | 1510 |
| Q                                                                           | y |  | 1441 | TTCGTTTGTATATCAACAGGAAAAAGCAATTCAGGAGGCATAAAGATATTTGNTATATA        | 1500 |
| D                                                                           | b |  | 1511 | TTGATTTTCATTTCAACCAGGAAAAAGCAATTTTCAGGAGAAGTGGAGACATTTGCACCATC     | 1570 |
| Q                                                                           | y |  | 1501 | AGAGTTTAAAGCTGTTTATTTTGGTATCTGTTTCATTTGCTGAAAAACACATTCATTTATC      | 1560 |
| D                                                                           | b |  | 1571 | AGAGTTTAAAGCTGCTCATTTTCGGTATTTGTCATCTGCTGAATAAATATGTAGCTATT        | 1630 |
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| LOCUS AX249965 833 bp DNA linear PAT 28-SEP-2001                            |   |  |      |                                                                    |      |
| DEFINITION Sequence 1 from Patent WO0166766.                                |   |  |      |                                                                    |      |
| ACCESSION AX249965                                                          |   |  |      |                                                                    |      |
| VERSION AX249965.1 GI:15864451                                              |   |  |      |                                                                    |      |
| KEYWORDS                                                                    |   |  |      |                                                                    |      |
| SOURCE Homo sapiens (human)                                                 |   |  |      |                                                                    |      |
| ORGANISM Homo sapiens                                                       |   |  |      |                                                                    |      |
| REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |   |  |      |                                                                    |      |
| Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.                   |   |  |      |                                                                    |      |
| AUTHORS Fajardo,M.D., Smith,R. and Moss,P.                                  |   |  |      |                                                                    |      |
| TITLE A matrix metalloproteinase (mmp-25) expressed in skin cells           |   |  |      |                                                                    |      |
| JOURNAL Patent: WO 0166766-A 1 13-SEP-2001;                                 |   |  |      |                                                                    |      |
| DARWIN MOLECULAR CORPORATION (US)                                           |   |  |      |                                                                    |      |
| FEATURES Location/Qualifiers                                                |   |  |      |                                                                    |      |
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RESULT 11
AF062392 1587 bp mRNA linear VRT 02-SEP-1998
LOCUS
DEFINITION Gallus gallus matrix metalloproteinase mRNA, complete cds.
ACCESSION AF062392
VERSION AF062392.1 GI:3511148
KEYWORDS
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 1587)
Yang, M. and Kurkinen, M.
Cloning of a novel matrix metalloproteinase (CMMP) from chicken
embryo fibroblasts
J. Biol. Chem. (1998) In press
2 (bases 1 to 1587)
Yang, M. and Kurkinen, M.
Direct Submission
Submitted (29-APR-1998) Center for Molecular Medicine and Genetics,
Wayne State University School of Medicine, 5047 Gullen Mall,
Detroit, MI 48202, USA
FEATURES
Location/Qualifiers
1..1587 source

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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |      |                                                                |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|----------------------------------------------------------------|------|
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 731  | AAATTATGTCCTCCCTGGATCCGAGAAATACCACTTTCTCAGATGATATCAATGGAAT     | 790  |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 773  | CAATTACGCATATATCAGCCCGAGTGAATTTCTCTCTCCAGATGACATAAGTGGCAT      | 832  |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 791  | CCAGTCATCATCTATGGAGGTCGCTAAGGTACCTGTCTAA--GCCAAGGAACCCACTAT    | 847  |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 833  | TCAGTCTATTTATGGTTCTGCAACAAACCCAGGTAAAGGCCAACCGTCCCTACATC       | 892  |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 848  | ACCCATGCTGTGACCTGACTGACTTTTGAAGCTATCACAACTTTCCGAGAGAGT         | 907  |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 893  | ACCTAACACCTGTGGCCCGCCAGATATCTTTTCGATCGCTAACTACACTTCGACGAGAAGT  | 952  |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 908  | AATGTTCTTTAAAGGACGACCTATGAGGATCTATTATGATATCAGGATCTTGATT        | 967  |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 953  | CATATTTCTAAAGGGAAGACACTTTGTGGCAGTCTATCCCTGATTAACCTCAAGATTTGAAC | 1012 |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 968  | TGAATTAATGCTTCAATTTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCATACAGAA   | 1027 |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1013 | TGAATTAATTTCTGCTTCTGGCCATTTCTGCCATCTGGTATTTCAAGCTCGGTATGAA     | 1072 |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1028 | CCCAGAGATAAGATCTGTTTTTAAAGATGAAACTTCTGGATGATCAGAGATATGC        | 1087 |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1073 | CATGAAGATCGGATCTGTTTTTCAAGGCAATAATTTCTGGGTCTGTCAGCGGATATA      | 1132 |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1088 | TGTCCTTCCAGATATATCCCAATCCATCCATCATATTAGGTTTTTCCAGGACGTGTGAGAA  | 1147 |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1133 | GGTGCTACTTGGTTATCCAAAGAACATCAACAGCTAGGTTCCCTAAAGGTGTTAAGAA     | 1192 |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1148 | AATAGATGACGCGCTGTGATAAGACCAACAAGAAAACCTACTTCTTTTGTGGGCAATTTG   | 1207 |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1193 | AATCGATGACGTGTTGTAAACAAAATAACAGGAGACAGACTTCTTTCTAGGTGACAA      | 1252 |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1208 | GTCTGAGAGTTGATGAATGACCCAAACATGGAACAAGGATTCGCGAGAGGTGGT         | 1267 |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1253 | GTACTGGAGTATGATGAAGACCCAGTCCATGGAGAGGTTTACCTTAGGAGGACAGT       | 1312 |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1268 | AAACAACCTTCTCGGAATCAGTATCGGTGTTGATGCTGCTTCCAGTACAAAGATTCCT     | 1327 |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1313 | CAATGATTTCCAGGAATGACGAGGATGATGCTGTTTCCACATTAAGGATATT           | 1372 |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1328 | CTTTTTCAGCGGTGATCAAGCAATTTGAATACAAATTAAGACAAAGAAATATTACCG      | 1387 |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 1373 | CTACTTCTTCCATGATCAAGGACGCTGAAGTTTGACCCCTACTGCTAAAGAGATTATCAG   | 1432 |
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| RESULT 12                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |      |                                                                |      |
| AF148882                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |      |                                                                |      |
| LOCUS                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |      |                                                                |      |
| DEFINITION                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |      |                                                                |      |
| Equis caballus matrix metalloproteinase 1 precursor (MMP1) mRNA, complete cds.                                                                                                                                                                                                                                                                                                                                                                                                      |      |                                                                |      |
| ACCESSION                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |      |                                                                |      |
| AF148882                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |      |                                                                |      |
| VERSION                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |      |                                                                |      |
| AF148882.1 GI:5020115                                                                                                                                                                                                                                                                                                                                                                                                                                                               |      |                                                                |      |
| KEYWORDS                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |      |                                                                |      |
| Equis caballus (horse)                                                                                                                                                                                                                                                                                                                                                                                                                                                              |      |                                                                |      |
| SOURCE                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |      |                                                                |      |
| Equis caballus                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |      |                                                                |      |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.                                                                                                                                                                                                                                                                                                                                                               |      |                                                                |      |
| REFERENCE                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |      |                                                                |      |
| 1 (bases 1 to 1923)                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |      |                                                                |      |
| Richardson,D.W.                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |      |                                                                |      |
| AUTHORS                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |      |                                                                |      |
| Cloning and expression of equine matrix metalloproteinase 1                                                                                                                                                                                                                                                                                                                                                                                                                         |      |                                                                |      |
| TITLE                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |      |                                                                |      |
| Unpublished                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |      |                                                                |      |
| JOURNAL                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |      |                                                                |      |
| 2 (bases 1 to 1923)                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |      |                                                                |      |
| Richardson,D.W.                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |      |                                                                |      |
| AUTHORS                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |      |                                                                |      |
| Direct Submission                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |      |                                                                |      |
| TITLE                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |      |                                                                |      |
| Submitted (06-MAY-1999) Clinical Studies, New Bolton Center, University of Pennsylvania, 382 West Street Road, Kennett Square, PA 19348-1692, USA                                                                                                                                                                                                                                                                                                                                   |      |                                                                |      |
| JOURNAL                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |      |                                                                |      |
| PA 19348-1692, USA                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |      |                                                                |      |
| FEATURES                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |      |                                                                |      |
| source                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |      |                                                                |      |
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| Matches 855; Conservative 0; Mismatches 525; Indels 24; Gaps 6;                                                                                                                                                                                                                                                                                                                                                                                                                     |      |                                                                |      |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 33   | CTTCTGCTCTGCTGTTGTTCTTTTATAACATTTTCTTCTGCAATTCCTTAGTCCGGATG    | 92   |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 68   | CCTCTGCTGCTGCTGCTACTCTGGGGCATGGGCTCTCACAGCTTCCCAACAGTGCCTTCA   | 127  |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 93   | ACGGAAAAATGAAGAAAAATGCAACTGGCTCAGGCATATCTCAACCAAGTTTCTACTCTCT  | 152  |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 128  | GAACACGGAAGAAAGATGGAGATGGTCCAGAAATACCTGGAAAATCTACTACAACCTG     | 187  |
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| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 188  | AAGAGTGATGGAGCAAAATTTGAAAAGCAGACACAGAGCCAGCTGTTGAAAAGCTG       | 247  |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 213  | CGGAAATGCAAGCAATTTTGGATTGACAGTCACTGGAATACTGGAACCAACCCCTT       | 272  |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 248  | AAGCAATGAGGAATTTCTTTGGGCTGAAAGTACTGGGAAGCCAGATGCTGAAACCCCTG    | 307  |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 273  | GAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGGCCAGTATGCTGCTACACC      | 329  |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 308  | AATGCTATGAAGCAGCCAGATGCGGGGTGCTGATGTGGTCAAGTTTGTCTCCACCGAA     | 367  |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 330  | ---CTCCCTGGGTGGAGAAAATACACCTCACCTACAGATAATAAATACTATCTCCGGAT    | 386  |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 368  | GGGAACCCCTCGTGGGAGAACACACCTCACCTACAGGATTGAAAATTTACACACCAT      | 427  |
| QY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 387  | ATGGCAGAGCTCTGCTGGATGAGGCTATCCAGAGAGTTTAGAAGTGTGAGCAAGATC      | 446  |
| Db                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 428  | TTACCAAGACAGATGTGGACACCGGCAATGGAAGAGCCCTTCACTCTCGAGTAATGTC     | 487  |



Db 127 AATGCAACAATCTTTGGGCTGAAAGTAAACGGGAAACACAGACGCTGAAACTCTGAATGT 186  
QY 278 CATGAAGACACACAGGTGTGGGTGCTGATGTGGGCAGTATGGCTACACCC-----T 331  
Db 187 GATGAAGACACCCAGATGTGGAGTTCCTGACGTGGCTGAGTTGTCTCTCACTCCAGGGAA 246  
QY 332 CCCTGGGTGGAGAAATPACAACTTCACCTACAGATAATAAATATATCTCCGATATGGC 391  
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Db 367 CTTGACCTTCACCAAGGTCTCCGAGGCTCAAGCAGACATAATGATATCTTTGTCAAGGG 426  
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QY 632 GGATGAGCAGGATTCAACTGTCTTCTGCTGGCTGCTCATGAATTTGGTCATGCACTGG 691  
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ACCESSION U62529  
VERSION U62529.1 GI:1480745  
KEYWORDS  
SOURCE  
ORGANISM  
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Equus caballus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
REFERENCE  
AUTHORS Richardson,D.W. and Dodge,G.R.  
TITLE Molecular characteristics of equine stromelysin and the tissue  
inhibitor of metalloproteinase 1  
JOURNAL Am. J. Vet. Res. 59 (12), 1557-1562 (1998)  
MEDLINE 99074117  
PUBMED 9858406  
REFERENCE  
AUTHORS Richardson,D.W. and Dodge,G.R.  
TITLE Direct Submission  
JOURNAL Submitted (28-JUN-1996) Clinical Studies, New Bolton Center, School  
of Veterinary Medicine, University of Pennsylvania, 382 West Street  
Road, Kennett Square, PA 19348-1692, USA  
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Best Local Similarity 60.4%; Pred. No. 3.8e-100;  
Matches 868; Conservative 0; Mismatches 526; Indels 42; Gaps 6;  
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VERSION AX393848.1 GI:19701814  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
1. Wang, T. and Fan, L.  
Compositions and methods for the therapy and diagnosis of head and neck cancer  
Patent: WO 0212329-A 237 14-FEB-2002;  
CORIXA CORPORATION (US)  
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Query Match 27.7%; Score 450.4; DB 6; Length 1804;  
Best Local Similarity 60.4%; Pred. No. 3.8e-100;  
Matches 868; Conservative 0; Mismatches 526; Indels 42; Gaps 6;

QY 21 GGAATGAAGCGCCTTCTGCTCTCTGTGTTTGTGTTTAAATTTCTTCGTCATTTCCC 80  
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Job time : 7051 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 13:11:00 ; Search time 833 Seconds

(without alignments)  
10253.071 Million cell updates/sec

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Perfect score: 1627

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Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| 23 | 1625.4 | 99.9 | 1647 | 9 | ADB16524 | Human PRO |
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## ALIGNMENTS

### RESULT 1

AAA37666

ID AAA37666 standard; DNA; 1627 BP.

XX

AC AAA37666;

XX

DT 24-OCT-2000 (first entry)

XX

DE Human peptidase, HPEP-10 coding sequence.

XX

KW Human; peptidase; cell proliferative disorder; arteriosclerosis;

KW psoriasis; myelofibrosis; cancer; autoimmune disorder; Crohn's disease;

KW inflammatory disorder; AIDS; anaemia; allergy; asthma; atherosclerosis;

KW Grave's disease; multiple sclerosis; scleroderma; infection; diabetes;

KW metabolic disorder; Addison's disease; cystic fibrosis; diagnosis;

KW glycogen storage disease; obesity; therapy; HPEP-10; ds.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT CDS 24..1565

FT /\*tag= a

FT /product= "HPEP-10"

XX

WO2000042201-A2.

XX

PD 20-JUL-2000.

XX

PF 11-JAN-2000; 2000WO-US0000641.

XX

PR 11-JAN-1999; 99US-0172247P.

XX

PR 03-MAY-1999; 99US-0132253P.

XX

PR 27-MAY-1999; 99US-0136653P.

XX

(INCY-) INCYTE PHARM INC.

XX

PI Bandman O, Hillman JL, Tang YT, Azimzai Y, Baughn MR, Lal P;

XX

PI Yue H, Lu DM;

XX

XX WPI; 2000-482832/42.

XX

XX P-PSDB; AAY90293.

XX

PT An isolated polypeptide for diagnosis, prevention and treatment of cell proliferative, autoimmune/ inflammatory and metabolic disorders comprises



PT a sequence encoding a human peptidase.  
XX Claim 4; Page 119; 131pp; English.  
PS This sequence encodes the human peptidase, designated HPEP-10. The  
XX invention relates to 18 human peptidases designated HPEP-1 to HPEP-18,  
CC respectively. The peptidases can be used for treating a disease or  
CC condition associated with decreased expression or over expression of  
CC functional human peptidases. The diseases that can be diagnosed,  
CC prevented and treated include cell proliferative disorders (such as  
CC arteriosclerosis, psoriasis, myelofibrosis, and cancers),  
CC autoimmune/inflammatory disorders (such as AIDS, anaemia, allergies,  
CC Crohn's disease, asthma, atherosclerosis, Grave's disease, multiple  
CC sclerosis, and scleroderma), infections, and metabolic disorders (such as  
CC Addison's disease, diabetes, cystic fibrosis, glycogen storage diseases  
XX and obesity)  
SQ Sequence 1627 BP; 483 A; 336 C; 348 G; 460 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1627; DB 3; Length 1627;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1627; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTTCAGCTCAAGAAAGAGAGGAGTGAAGCGCTTCTGCTTCTGTTGTTCTTTATAA 60  
DB 1 GCTTCAGCTGAAGAAAGAGAGGAGTGAAGCGCTTCTGCTTCTGTTGTTCTTTATAA 60  
QY 61 CATTTTCTTCTGATTTCCCTTAGTCCGATGACGGAATGAAGAAATATGCAACTGG 120  
DB 61 CATTTTCTTCTGATTTCCCTTAGTCCGATGACGGAATGAAGAAATATGCAACTGG 120  
QY 121 CTGAGGATATCTCAACAGTTCTACTCTCTTGAATAGAGGAAATCATCTGTTCAAA 180  
DB 121 CTGAGGATATCTCAACAGTTCTACTCTCTTGAATAGAGGAAATCATCTGTTCAAA 180  
QY 181 GCAAGATAGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCAATTTTGGATTGA 240  
DB 181 GCAAGATAGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCAATTTTGGATTGA 240  
QY 241 CAGTGACTGGAATACTGGATCAAAACCTTGAGATCATGAGACACCCAGGTGTTGGG 300  
DB 241 CAGTGACTGGAATACTGGATCAAAACCTTGAGATCATGAGACACCCAGGTGTTGGG 300  
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DB 301 TGCCTGATGTGGGCGAGTATGGCTACACCTCCCTGGGAGGAAATACAACTCACCT 360  
QY 361 ACAGAATAATAAACTATACCTCCGATATGGCAGAGCTGCTGTGGATGAGGCTATCCAAG 420  
DB 361 ACAGAATAATAAACTATACCTCCGATATGGCAGAGCTGCTGTGGATGAGGCTATCCAAG 420  
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DB 421 AAGGTTAGAGTGTGGAGCAAGTCTCACTCAATAAATTCACCAAGATTTCAAAGGGGA 480  
QY 481 TTGAGACATCATGATTTGCTTTAGGACTCGAGTCCATGTCGTCCTGCTATTTTG 540  
DB 481 TTGAGACATCATGATTTGCTTTAGGACTCGAGTCCATGTCGTCCTGCTATTTTG 540  
QY 541 ATGGTCCCTTGGGAGTGTGGCCATGCTTTTCTCTGCTCCGGGCTGCGGTGGTGACA 600  
DB 541 ATGGTCCCTTGGGAGTGTGGCCATGCTTTTCTCTGCTCCGGGCTGCGGTGGTGACA 600  
QY 601 CTCATTTTGTAGAGTGAATACTGGACCAAGGATGGAGCAGGATTCAACTGTTCTTG 660  
DB 601 CTCATTTTGTAGAGTGAATACTGGACCAAGGATGGAGCAGGATTCAACTGTTCTTG 660  
QY 661 TGGCTGCTCATGATTTGCTCATGCACTGGGCTCTCTCACTCCAATGATCAAAAGGCT 720  
DB 661 TGGCTGCTCATGATTTGCTCATGCACTGGGCTCTCTCACTCCAATGATCAAAAGGCT 720  
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DB 721 TGATGTTCCCAAAATATCTCCCTGGATGCCAGAAAATACCCACTTTTCTCAGGATGATA 780  
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DB 781 TCAATGGATCCAGTCCATCTATGAGGCTCTGCTAAGGTACCTGCTAAAGCAAGAAC 840  
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DB 841 CCACTATACCCCATGCTGTGACCCCTGACTTGACTTTTGAACGCTATCACAACTTTCCGCA 900  
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DB 901 GAGAAGTAAATGTTCTTTAAAGGAGGAGGACCTATGAGGAGTCTATATGATATCACGATG 960  
QY 961 TTGAGTTTGAATTAATGTTCTTCAATCTGCGCATCTCTGCCAGTGTATGCTCAAGCTCAT 1020  
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DB 1021 ACCGAGAACCCAGAGATAGATTTCTGGTTTTTAAAGATGAAAACTTCTGGATGATCAGAG 1080  
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DB 1201 GCATTTGCTGCTGGAGGTTTGTGAAATGACCCAAACCATGGACAAAGGATTTCCGCGAGA 1260  
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QY 1321 GATTTCTTTTTCAGCGCTGGATCAAGCAATTTGAATACAACTTAAGACAAAGATA 1380  
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DB 1621 AATAGAA 1627

RESULT 2  
AAD23963  
ID AAD23963 standard; cDNA; 1845 BP.  
XX  
AC AAD23963;  
XX  
DT 16-OCT-2002 (first entry)  
XX Human matrix metalloproteinase MMP1 cDNA.  
DE  
XX

KW Matrix metalloproteinase; MMP; extracellular matrix; ECM;  
 KW embryonic development; morphogenesis; reproduction; tissue repair;  
 KW mental disorder; Alzheimer's disease; multiple sclerosis; obesity;  
 KW Parkinson's disease; motor neuron disease; metabolic disease; retinopathy;  
 KW type 2 diabetes; cardiovascular; dyslipidaemia; adipogenesis; neuropathy;  
 KW nephropathy; proliferative disease; cancer; psoriasis;  
 KW prostate hyperplasia; hormonal disorder; alopecia; Crohn's disease;  
 KW central nervous system disorder; CNS; inflammatory condition; arthritis;  
 KW periodontal disease; wound healing; human; MMP1; ss.  
 XX Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 XX CDS 24..1565  
 XX /\*tag= a  
 XX /product= "Matrix metalloproteinase MMP1"  
 XX  
 XX WO200190326-A2.  
 XX  
 XX 29-NOV-2001.  
 XX  
 XX 22-MAY-2001; 2001WO-US016563.  
 XX  
 XX 22-MAY-2000; 2000US-0206119P.  
 XX  
 XX (PHAA ) PHARMACIA & UPJOHN CO.  
 XX  
 XX Holmgren E, Kihlen M, Wood T, Ekblom J;  
 XX  
 XX WPI; 2002-083105/11.  
 XX P-PSDB; AAE14392.  
 XX  
 XX New matrix metalloproteinases (MMP) genes and polypeptides, useful for  
 XX treating diseases or for screening modulators of MMP to treat such  
 XX diseases, e.g. mental disorders, Parkinson's disease, cancers or  
 XX inflammatory conditions.  
 XX  
 XX Claim 4; Page 59; 94pp; English.  
 XX  
 XX The invention relates to genes encoding matrix metalloproteinases (MMP).  
 XX The MMP genes are useful for producing MMP polypeptides and for screening  
 XX modulators of MMP. The MMPs are useful for breaking down extracellular  
 XX matrix (ECM), which is essential for processes including embryonic  
 XX development, morphogenesis, reproduction, or tissue repair and  
 XX remodelling. The MMPs are particularly useful for identifying compounds  
 XX that modulate the activity of genes to treat pathologies, e.g. mental  
 XX disorders, Alzheimer's disease, multiple sclerosis, Parkinson's disease  
 XX or motor neuron disease. The MMP polypeptides and genes, as well as their  
 XX modulators, are useful for treating metabolic diseases and disorders  
 XX (e.g. type 2 diabetes, obesity, cardiovascular, dyslipidaemias,  
 XX adipogenesis, retinopathies, neuropathies or nephropathies),  
 XX proliferative diseases and cancers (e.g. breast, colon or lung cancer,  
 XX tumour growth, tumour invasion, psoriasis or prostate hyperplasia),  
 XX hormonal disorders (e.g. male/female hormonal replacement, polycystic  
 XX ovarian syndrome or alopecia), central nervous system (CNS) disorders,  
 XX inflammatory conditions (e.g. Crohn's disease or arthritis), periodontal  
 XX diseases or wound healing. The present sequence is human matrix  
 XX metalloproteinase MMP1 cDNA  
 XX  
 XX Sequence 1845 BP; 555 A; 374 C; 379 G; 537 T; 0 U; 0 Other;  
 XX  
 XX Query Match 100.0%; Score 1627; DB 6; Length 1845;  
 XX Best Local Similarity 100.0%; Pred. No. 0;  
 XX Matches 1627; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX QY 1 GCTTCAGCTGAAGAAGAGAGAGGAAATGAAGCGCTTCTGCTTCTGTTGTTCTTTATAA 60  
 XX DB 1 GCTTCAGCTGAAGAAGAGAGGAAATGAAGCGCTTCTGCTTCTGTTGTTCTTTATAA 60  
 XX  
 XX QY 61 CATTTTCTTTCGATTTCCCTTAGTCCGGATGACGGAAATGAAGAAAATGCAACTGG 120  
 XX DB 61 CATTTTCTTTCGATTTCCCTTAGTCCGGATGACGGAAATGAAGAAAATGCAACTGG 120

QY 121 CTCAGGCATATCTCAACAGTTCTACTCTCTTGAATAGAAGGAATCATCTTGTTCAAA 180  
 DB 121 CTCAGGCATATCTCAACAGTTCTACTCTCTTGAATAGAAGGAATCATCTTGTTCAAA 180  
 QY 181 GCAAGAAATAGGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTGGATTGA 240  
 DB 181 GCAAGAAATAGGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTGGATTGA 240  
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 DB 421 AAGGTTTAGAAGTGGAGCAAAAGTCACTCCACTAAAATTCACCAAGATTTCAAAGGGGA 480  
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 QY 541 ATGGTCCCTTGGGAGTGTGGCCATGCTTTTCCTCCTGGTCCGGGTCTGGGTGTGGTGA 600  
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 DB 1081 GATATGCTGTCTTGGCAGATTATCCCAATCCATCCATCATATTAGGTTTTCAGGACGCTG 1140  
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 DB 1141 TGAAGAAATAGATGACGCGCTCTGTGATAGACACCAAGAAAACCTTACTTCTTTGTGG 1200  
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QY      1381 TTACCCGAATCATGAGAACTAATACCTTGGTTTCAATGCAAGAACCAAGAACTCTTCAT 1440
Db      1381 TTACCCGAATCATGAGAACTAATACCTTGGTTTCAATGCAAGAACCAAGAACTCTTCAT 1440
QY      1441 TTGGTTTGTATCAACAAGAAACCAAGCAATTCAGGAGCATAAAGATATTGTATCAT 1500
Db      1441 TTGGTTTGTATCAACAAGAAACCAAGCAATTCAGGAGCATAAAGATATTGTATCAT 1500
QY      1501 AGAGTTTAAAGCTTGTATTTTGGTATTTGTTCAATTTGCTGAAACACATCTTATTTATC 1560
Db      1501 AGAGTTTAAAGCTTGTATTTTGGTATTTGTTCAATTTGCTGAAACACATCTTATTTATC 1560
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Db      1621 AATAGAA 1627
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## RESULT 3

AA521339  
ID AA521339 standard; cDNA; 1647 BP.

XX AC AA521339;

XX DT 24-OCT-2001 (first entry)

XX DE Human cDNA sequence encoding for PR05992 polypeptide.

XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;  
ear; prostate; cervical; tumor necrosis factor-alpha; TNF-alpha; cartilage;  
ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;  
A-peptide; factor VIIA; gene therapy; ss.

XX OS Homo sapiens.

XX PN WC2001140466-A2.

XX PD 07-JUN-2001.

XX PF 01-DEC-2000; 2000WO-US032678.

XX PR 01-DEC-1999; 99WO-US028301.

XX PR 01-DEC-1999; 99WO-US028634.

XX PR 02-DEC-1999; 99WO-US028551.

XX PR 02-DEC-1999; 99WO-US028564.

XX PR 02-DEC-1999; 99WO-US028565.

XX PR 09-DEC-1999; 99US-0170262P.

XX PR 16-DEC-1999; 99WO-US030095.

XX PR 20-DEC-1999; 99WO-US030911.

XX PR 20-DEC-1999; 99WO-US030999.

XX PR 30-DEC-1999; 99WO-US031243.

XX PR 30-DEC-1999; 99WO-US031274.

XX PR 05-JAN-2000; 2000WO-US000219.

XX PR 06-JAN-2000; 2000WO-US000277.

XX PR 06-JAN-2000; 2000WO-US000376.

XX PR 11-FEB-2000; 2000WO-US000356.

XX PR 18-FEB-2000; 2000WO-US000431.

XX PR 18-FEB-2000; 2000WO-US000432.

XX PR 22-FEB-2000; 2000WO-US000441.

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PR 24-FEB-2000; 2000WO-US0004914.  
PR 24-FEB-2000; 2000WO-US0005004.  
PR 01-MAR-2000; 2000WO-US0005601.  
PR 02-MAR-2000; 2000WO-US0005841.  
PR 03-MAR-2000; 2000US-0187202P.  
PR 10-MAR-2000; 2000WO-US0006319.  
PR 15-MAR-2000; 2000WO-US0006884.  
PR 20-MAR-2000; 2000WO-US0007377.  
PR 21-MAR-2000; 2000WO-US0007532.  
PR 30-MAR-2000; 2000WO-US0008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 05-JUN-2000; 2000US-0209832P.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
XX
```

(GETH ) GENENTECH INC.

Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2001-408281/43.

P-PSDB; AAU12267.

Isolated , secretory and transmembrane PRO polypeptide used to detect  
other PRO polypeptides, link bioactive molecules to cells expressing PRO  
polypeptides, and detect the presence of mammalian tumors e.g. lung,  
breast, prostate, cervical.

Claim 3; Fig 191; 813pp; English.

AA521244-AA521518 encode for novel human secretory and transmembrane PRO  
polypeptides. The PRO polypeptides are useful to detect other PRO  
polypeptides, to link bioactive molecules to cells expressing PRO  
polypeptides, to modulate biological activities of cells expressing PRO  
polypeptides, and to detect the presence of mammalian lung, colon,  
breast, prostate, rectal, cervical or liver tumors by comparing PRO  
polypeptide expression in a cell sample to that in a control sample. Some  
of the 275 sequences are also useful to stimulate the release of tumour  
necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or  
differentiation of chondrocytes, the proliferation or gene expression in  
pericyte cells, the release of proteoglycans from cartilage, the  
proliferation of inner ear utricular supporting cells or of T-  
lymphocytes, the release of a cytokine from peripheral blood monocytes  
(PBMCs), or the proliferation of endothelial cells. Some of the PRO  
polypeptides may modulate glucose or free fatty acid uptake by skeletal  
muscle cells or by adipocytes; or inhibit binding of A-peptide to factor  
VIIA. The PRO polypeptides can be used in assays to identify molecules  
involved in binding interactions. The polynucleotides encoding PRO  
polypeptides can be used to generate probes, antisense RNA/DNA,  
transgenic or knock out animals and can be used in gene therapy

XX SQ Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;

Query Match 99.9%; Score 1625.4; DB 4; Length 1647;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTCAGCTCAAGAAAGAGAGAGATGAAGCGCTTCGCTTCGTGTTCTTTCTTTATAA 60

Db 1 GCTTCAGCTCAAGAAAGAGAGAGATGAAGCGCTTCGCTTCGTGTTCTTTCTTTATAA 60

QY 61 CATTTCTTCTGCAATTTCCCTTAGTCGGATGACGGAATGAAGAAAATATGCACTGG 120

Db 61 CATTTCTTCTGCAATTTCCCTTAGTCGGATGACGGAATGAAGAAAATATGCACTGG 120

QY 121 CTCAGGCATATCTCAACAGTTCTACTCTCTTGAAATAGAGGGAATCATCTTGTTCAA 180  
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QY 481 TTGCAGACATCATGATTCCTTTAGGACTCCAGTCCATGGTCCGTTCTCGCTATTTTG 540  
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Db 541 ATGTCCTTGGGAGTGTCTGGCCATGCTTTTCTCTCTGGTCCGGTCTGGGTGGTGACA 600  
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Db 721 TGATGTTCCCAAAATPATGTCCTCTGATGCCAGAAAATACCCACTTTCTCAGGATGATA 780  
QY 781 TCAATGGAATCAGTCCATCTATGAGGCTGCTGCTTAAAGGTACCTGCTAAGCCAAAGGAAC 840  
Db 781 TCAATGGAATCAGTCCATCTATGAGGCTGCTGCTTAAAGGTACCTGCTAAGCCAAAGGAAC 840  
QY 841 CCACATATACCCATGCTGACCTGACCTGACTTTTGAAGCTATCAAACTTTCCGCA 900  
Db 841 CCACATATACCCATGCTGACCTGACCTGACTTTTGAAGCTATCAAACTTTCCGCA 900  
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Db 901 GAGAAGTAATGTTCTTTAAAGCAGGACCTATGAGGATCTATTATGATATCAAGGATG 960  
QY 961 TTGAGTTTGAATTAATGTTCTTAAAGCAGGACCTATGAGGATCTATTATGATATCAAGGATG 1020  
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Db 1021 ACGAGAACCCAGAGATGAATCTTGTTTAAAGATGAAAATCTTCTGGATGATCAGAG 1080  
QY 1081 GATATGCTGCTTGGCAGATTAATCCCAATCCATCCATCAATAGGTTTTCAGGACGTTG 1140  
Db 1081 GATATGCTGCTTGGCAGATTAATCCCAATCCATCCATCAATAGGTTTTCAGGACGTTG 1140  
QY 1141 TGAAGAAAATAGATGAGCGCTGTGTGATAAGACCAAGAAAACCTACTCTTTTGTGG 1200  
Db 1141 TGAAGAAAATAGATGAGCGCTGTGTGATAAGACCAAGAAAACCTACTCTTTTGTGG 1200  
QY 1201 GCATTTGGTGGAGTTTGTATGAATGACCCAAACCATGACAAAGGATTTCCCGCAGA 1260

Db 1201 GCATTTGGTGGAGTTTGTATGAATGACCCAAACCATGACAAAGGATTTCCCGCAGA 1260  
QY 1261 GAGTGGTAAACACATCTTCTCGGAATCAGTATCCGTGTGTGATGCTGCTTTCCAGTACAAG 1320  
Db 1261 GAGTGGTAAACACATCTTCTCGGAATCAGTATCCGTGTGTGATGCTGCTTTCCAGTACAAG 1320  
QY 1321 GATTTCTTTTTCAGCGCTGGATCAAGCAATTTGAATCAACATTAAGACAAAGAATA 1380  
Db 1321 GATTTCTTTTTCAGCGCTGGATCAAGCAATTTGAATCAACATTAAGACAAAGAATA 1380  
QY 1381 TTACCCGAATCATGAGAACTAATACTTTGGTTTCAATGCAAGAAACCAAGAACTCTCAT 1440  
Db 1381 TTACCCGAATCATGAGAACTAATACTTTGGTTTCAATGCAAGAAACCAAGAACTCTCAT 1440  
QY 1441 TTGTTTTGATATCAACAGGAAAAGCAGATTCAGGAGGATTAAGATTTGTATCAT 1500  
Db 1441 TTGTTTTGATATCAACAGGAAAAGCAGATTCAGGAGGATTAAGATTTGTATCAT 1500  
QY 1501 AGAGTTTAAAGCTTTGTTATTTTGGTATTTGTTTCAATTTGCTGAAAACACTTTTATTC 1560  
Db 1501 AGAGTTTAAAGCTTTGTTATTTTGGTATTTGTTTCAATTTGCTGAAAACACTTTTATTC 1560  
QY 1561 AATAAATTCATAGACCTAAAATAAACTCAACAGCTCTTTTAATATAAAATTCGTTCAA 1620  
Db 1561 AATAAATTCATAGACCTAAAATAAACTCAACAGCTCTTTTAATATAAAATTCGTTCAA 1620  
QY 1621 AATAGAA 1627  
Db 1621 AATAGAA 1627

RESULT 4  
ACR03698  
ID ACA03698 standard; cDNA; 1647 BP.  
XX ACA03698;  
XX 23-MAY-2003 (first entry)  
XX  
XX cDNA encoding human PRO polypeptide #96.  
DE Human; PRO polypeptide; secreted and transmembrane protein;  
KW tumour necrosis factor-alpha; TNF-alpha; blood; proliferation;  
KW differentiation; chondrocyte; tumour; genetic disorder; cytostatic; gene;  
KW ss.  
XX Homo sapiens.  
OS  
XX  
XX US2003036180-A1.  
XX  
XX 20-FEB-2003.  
PD  
XX  
XX 09-MAY-2002; 2002US-00143114.  
XX  
XX 31-MAR-1997; 97WO-US005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025106.  
PR 05-JAN-1999; 98WO-US000106.  
PR 08-MAR-1999; 98WO-US005028.  
PR 10-MAR-1999; 98WO-US005190.

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PR 20-APR-1999; 99WO-US0008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 18-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 23-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00815744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.

PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-332040/31.
XX P-PSDB; ABU66665.
XX
XX New secreted and transmembrane PRO nucleic acids, useful for gene
XX therapy, in chromosome and gene mapping, as chromosome markers, in tissue
XX typing, and in chromosome identification.
XX
XX Claim 2; Fig 191; 660pp; English.
XX
XX The present invention relates to the isolation of novel human PRO
XX polypeptides, and the polynucleotide sequences encoding them. The PRO
XX polypeptides are secreted and transmembrane proteins. The PRO
XX polypeptides are useful for detecting other PRO polypeptides, for linking
XX bioactive molecules to cells expressing PRO polypeptides, for modulating
XX biological activities of cells expressing PRO polypeptides, and for
XX identifying agonists or antagonists. The PRO polypeptides are useful for
XX for stimulating the release of tumour necrosis factor (TNF)-alpha from
XX human blood, for stimulating the proliferation or differentiation of
XX chondrocytes, and detecting the presence of tumours. The polynucleotide
XX sequences encoding PRO polypeptides are useful as hybridisation probes,
XX in chromosome and gene mapping, in the generation of antisense RNA and
XX DNA, in the preparation of PRO polypeptides, for generating transgenic
XX animals or knockout animals, for the genetic analysis of individuals with
XX genetic disorders, and in gene therapy. ACA03603-ACA03877 represent cDNAs
XX encoding the human PRO polypeptides of the invention. Note: the sequence
XX data for this patent was obtained in electronic format directly from the
XX USPTO web site at seqdata.uspto.gov/psipdsIDentry.html
XX
XX Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;

Query Match 99.9%; Score 1625.4; DB 8; Length 1647;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTCAGCTGAGAAAGAGAGGAATGAAGCGCTTCTGCTTCTGTGTGTTGTTCTTTATAA 60
DB 1 GCTTCAGCTGAGAAAGAGAGGAATGAAGCGCTTCTGCTTCTGTGTGTTGTTCTTTATAA 60

QY 61 CATTTTCTTCGATTTCCCTTAGTCCGGATGACGAAATGAAGAAATATGCAACTGG 120
DB 61 CATTTTCTTCGATTTCCCTTAGTCCGGATGACGAAATGAAGAAATATGCAACTGG 120

QY 121 CTCAGGCATATCTCAACCAAGTCTACTCTTGAATAGAGGAATCATCTGTTCAA 180
DB 121 CTCAGGCATATCTCAACCAAGTCTACTCTTGAATAGAGGAATCATCTGTTCAA 180

QY 181 GCAAGAATAGGAGTCTCATAGATGACAAAATTCGGGAATGCAAGCATTTTGGATTGA 240
DB 181 GCAAGAATAGGAGTCTCATAGATGACAAAATTCGGGAATGCAAGCATTTTGGATTGA 240

QY 241 CAGTGACTGGAATACTGGACTCAACACCCCTTGAGATCATGAGACACCCAGGTGGGG 300
DB 241 CAGTGACTGGAATACTGGACTCAACACCCCTTGAGATCATGAGACACCCAGGTGGGG 300

QY 301 TGCCTCATGTGGGCCAGTATGGCTACACCTCCCTGGGTGGAGAAATACCACTCACCT 360
DB 301 TGCCTCATGTGGGCCAGTATGGCTACACCTCCCTGGGTGGAGAAATACCACTCACCT 360
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Qy 361 ACAGAAATTAATTAATCTACTCGGATATGGACGAGCTGCTGGATGAGGCTATCCAG 420  
Db 361 ACAGAAATTAATTAATCTACTCGGATATGGACGAGCTGCTGGATGAGGCTATCCAG 420  
Qy 421 AAGGTTTGAAGAGTGGAGCAAGTCACTCCACTAAATTCACCAAGATTTCAAGGGGA 480  
Db 421 AAGGTTTGAAGAGTGGAGCAAGTCACTCCACTAAATTCACCAAGATTTCAAGGGGA 480  
Qy 481 TTGAGACATCATGATTCGCTTTAGGACTCGAGTCCATGCTGGTCCGCTATTTTG 540  
Db 481 TTGAGACATCATGATTCGCTTTAGGACTCGAGTCCATGCTGGTCCGCTATTTTG 540  
Qy 541 ATGCTCCCTGGAGTGGTGGCCCAAGTCTTCCCTGGATCCAGAAATACCCACTTTCTCAGGATGATA 600  
Db 541 ATGCTCCCTGGAGTGGTGGCCCAAGTCTTCCCTGGATCCAGAAATACCCACTTTCTCAGGATGATA 600  
Qy 601 CTCATTTTGGATGAGGATGAAATCTGGACCAAGATGGAGCAGGATTCAACTTTGTTTCTTG 660  
Db 601 CTCATTTTGGATGAGGATGAAATCTGGACCAAGATGGAGCAGGATTCAACTTTGTTTCTTG 660  
Qy 661 TGGCTGCTCATGAATTTGGTCAATGCACTGGGCTCTCTCACTCCCAATGATCAAAAGGCT 720  
Db 661 TGGCTGCTCATGAATTTGGTCAATGCACTGGGCTCTCTCACTCCCAATGATCAAAAGGCT 720  
Qy 721 TGATGTTCCCAATTAATGCTCCCTGGATCCAGAAATACCCACTTTCTCAGGATGATA 780  
Db 721 TGATGTTCCCAATTAATGCTCCCTGGATCCAGAAATACCCACTTTCTCAGGATGATA 780  
Qy 781 TCAATGGAAATCAGTCCATCTATGAGGCTCTGCTTAAGTACTGCTAAGCCAAAGGAAC 840  
Db 781 TCAATGGAAATCAGTCCATCTATGAGGCTCTGCTTAAGTACTGCTAAGCCAAAGGAAC 840  
Qy 841 CCATATACCCCATGCTGAGCCCTGACTTTGACGCTATCAAACTTTCCGCA 900  
Db 841 CCATATACCCCATGCTGAGCCCTGACTTTGACGCTATCAAACTTTCCGCA 900  
Qy 901 GAGAGTAAATGTTCTTAAAGCGGCACTATGAGGATCTATTATGATATCAGGATG 960  
Db 901 GAGAGTAAATGTTCTTAAAGCGGCACTATGAGGATCTATTATGATATCAGGATG 960  
Qy 961 TTGAGTTTGAATTAATTTGCTTCAATCTGGCCATCTGCGAGTCACTGCAAGCTGCAT 1020  
Db 961 TTGAGTTTGAATTAATTTGCTTCAATCTGGCCATCTGCGAGTCACTGCAAGCTGCAT 1020  
Qy 1021 ACGAGAACCCAGAGATAGATTTGGTTTTTAAAGATGAAACTTTGATGATCAGAG 1080  
Db 1021 ACGAGAACCCAGAGATAGATTTGGTTTTTAAAGATGAAACTTTGATGATCAGAG 1080  
Qy 1081 GATATGCTGCTTGGCAGATTAATCCCAATCCATCCATATCCATATTTAGGTTTTCCAGGACGTG 1140  
Db 1081 GATATGCTGCTTGGCAGATTAATCCCAATCCATCCATATTTAGGTTTTCCAGGACGTG 1140  
Qy 1141 TGAAGAAATAGATGAGCGCTGCTGTGTAAGACCAAGAAACCTTCTTTTGG 1200  
Db 1141 TGAAGAAATAGATGAGCGCTGCTGTGTAAGACCAAGAAACCTTCTTTTGG 1200  
Qy 1201 GCATTTGGTGGAGTTTGTATGAAATGACCCAAACCAATGAGCAAGGATTTCCCGCAGA 1260  
Db 1201 GCATTTGGTGGAGTTTGTATGAAATGACCCAAACCAATGAGCAAGGATTTCCCGCAGA 1260  
Qy 1261 GAGTGTAAACACTTTCTCGGATCAGTATCCGTTGATGCTGTTTCCAGTACAAG 1320  
Db 1261 GAGTGTAAACACTTTCTCGGATCAGTATCCGTTGATGCTGTTTCCAGTACAAG 1320  
Qy 1321 GATTCCTCTTTTTCAGCCGTGGATCAAGCAATTTGAATACAACTTAAGACAAAGATA 1380  
Db 1321 GATTCCTCTTTTTCAGCCGTGGATCAAGCAATTTGAATACAACTTAAGACAAAGATA 1380  
Qy 1381 TTAACCGAATCATGAGAACTAATCTTTGGTTTCAATGCAAGAAACCAAGAACTCTCAT 1440  
Db 1381 TTAACCGAATCATGAGAACTAATCTTTGGTTTCAATGCAAGAAACCAAGAACTCTCAT 1440  
Qy 1441 TTGGTTTTGATATCAACAGAGGAAAAAGCAATTCAGAGGCATTAAGATATTTGATCAT 1500

Db 1441 TTGGTTTTGATATCAACAGAGGAAAAAGCAATTCAGAGGCATTAAGATATTTGATCAT 1500  
Qy 1501 AGAGTTTAAAGCTGTTTATTTTGGTATTTGTTCACTTCTGCTGAAAAACACTTCTATTATC 1560  
Db 1501 AGAGTTTAAAGCTGTTTATTTTGGTATTTGTTCACTTCTGCTGAAAAACACTTCTATTATC 1560  
Qy 1561 AATAAATCATAGACCTTAAATAAACCTCAACAGCTCTTTTAAATAAATTCGCTTCAA 1620  
Db 1561 AATAAATCATAGACCTTAAATAAACCTCAACAGCTCTTTTAAATAAATTCGCTTCAA 1620  
Qy 1621 AATAGAA 1627  
Db 1621 AATAGAA 1627  
RESULT 5  
ABX89236  
ID ABX89236 standard; cDNA; 1647 BP.  
XX ABX89236;  
DT 13-MAY-2003 (first entry)  
XX DNA encoding novel secreted and transmembrane protein PRO5992.  
DE Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;  
XX cardiac insufficiency disorder; cancer; tumour; immune response;  
KW adrenal cortical capillary endothelial growth; c-fos induction;  
KW vascular endothelial growth factor inhibition; VEGF inhibition;  
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;  
KW retinal neurons cell survival; rod photoreceptor cell survival;  
KW retinal disorder; retinitis pigmentosa; kidney disorder;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;  
KW chondrocyte redifferentiation; sports injury; arthritis; gene; ss.  
XX Homo sapiens.  
XX US2003017563-A1.  
XX 23-JAN-2003.  
XX 07-MAY-2002; 2002US-00140808.  
XX 31-MAR-1997; 97WO-US005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 98WO-US000106.  
PR 08-MAR-1999; 98WO-US005028.  
PR 10-MAR-1999; 98WO-US005190.  
PR 20-APR-1999; 98WO-US008615.  
PR 02-JUN-1999; 98WO-US010733.  
PR 01-SEP-1999; 98WO-US020111.  
PR 08-SEP-1999; 98WO-US020594.  
PR 13-SEP-1999; 98WO-US020944.  
PR 15-SEP-1999; 98WO-US021090.  
PR 05-OCT-1999; 98WO-US023089.  
PR 29-NOV-1999; 98WO-US028214.





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QY 361 ACAGATAATAAATATCTCCGGATATGCGACGAGCTGCTGGATGAGGCTATCCCAAG 420
Db 361 ACAGATAATAAATATCTCCGGATATGCGACGAGCTGCTGGATGAGGCTATCCCAAG 420
QY 421 AAGGTTTGAAGTGTGGAGCAAGTCACTCCACTAAATTCACCAAGATTTCAAAGGGGA 480
Db 421 AAGGTTTGAAGTGTGGAGCAAGTCACTCCACTAAATTCACCAAGATTTCAAAGGGGA 480
QY 481 TTGCAGACATCATGATTCGCTTTAGGACTCGAGTCAGTCAGTCGCTGCTCCTCTATTTTG 540
Db 481 TTGCAGACATCATGATTCGCTTTAGGACTCGAGTCAGTCAGTCGCTCCTCTATTTTG 540
QY 541 ATGGTCCCTTGGAGTGTCTGGCCATGCTTCCCTCTGCTCGGCTCGGCTGGGTGGTGACA 600
Db 541 ATGGTCCCTTGGAGTGTCTGGCCATGCTTCCCTCTGCTCGGCTCGGCTGGGTGGTGACA 600
QY 601 CTCATTTTGTGAGGATGAATACTGGACCAAGATGGAGCAGGATTCAACTTTGTTCTTG 660
Db 601 CTCATTTTGTGAGGATGAATACTGGACCAAGATGGAGCAGGATTCAACTTTGTTCTTG 660
QY 661 TGGCTGCTCATGAATTTGTCATGCACTGGGCTCTCTCACTCCAATGATCAAAAGCCT 720
Db 661 TGGCTGCTCATGAATTTGTCATGCACTGGGCTCTCTCACTCCAATGATCAAAAGCCT 720
QY 721 TGATGTTCCCAATATGTCCTCTGGATCCCGAATAATACCACTTTCTCAGGATGATA 780
Db 721 TGATGTTCCCAATATGTCCTCTGGATCCCGAATAATACCACTTTCTCAGGATGATA 780
QY 781 TCAATGGAATCCAGTCCATCTATGAGGCTCTGCTAAAGTACTCTGTAAGCCAAAGGAAC 840
Db 781 TCAATGGAATCCAGTCCATCTATGAGGCTCTGCTAAAGTACTCTGTAAGCCAAAGGAAC 840
QY 841 CCACATATACCCATGCTGTCGCTGACCTTGACTTTTGAAGCTATCACACTTTCCGCA 900
Db 841 CCACATATACCCATGCTGTCGCTGACCTTGACTTTTGAAGCTATCACACTTTCCGCA 900
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Db 901 GAGAAGTAAATGTTCTTAAAGCAGCAGCCTATGAGGATCTATTATGATATCAAGGATG 960
QY 961 TTGAGTTTGAATTAATGCTTCTCATCTGSCCATCTCTGCGAGTGAATCTGCAAGCTGCAT 1020
Db 961 TTGAGTTTGAATTAATGCTTCTCATCTGSCCATCTCTGCGAGTGAATCTGCAAGCTGCAT 1020
QY 1021 ACAGAACCCAGAGATAGATCTCTGTTTAAAGATGAAACTTCTGATGATCAGAG 1080
Db 1021 ACAGAACCCAGAGATAGATCTCTGTTTAAAGATGAAACTTCTGATGATCAGAG 1080
QY 1081 GATATGCTCTCTGCGAGATTAATCCCAATCCATCCATACATTTAGGTTTCCAGGACGTG 1140
Db 1081 GATATGCTCTCTGCGAGATTAATCCCAATCCATCCATACATTTAGGTTTCCAGGACGTG 1140
QY 1141 TGAAGAAATAGATGAGCGCTCTGTGATAGACCAAGAAACCTACTCTTTGTTGG 1200
Db 1141 TGAAGAAATAGATGAGCGCTCTGTGATAGACCAAGAAACCTACTCTTTGTTGG 1200
QY 1201 GCATTTGGTCTGGAGTTTGTAGAAATGACCCAAACCAATGACAAAGATTTCCCGCAGA 1260
Db 1201 GCATTTGGTCTGGAGTTTGTAGAAATGACCCAAACCAATGACAAAGATTTCCCGCAGA 1260
QY 1261 GAGTGTGTAACACTTTCTCGAATCAGTATCGTGTGATGCTGTTCCAGTACAAAG 1320
Db 1261 GAGTGTGTAACACTTTCTCGAATCAGTATCGTGTGATGCTGTTCCAGTACAAAG 1320
QY 1321 GATTTCTTTTTCAGCCGTGGATCAAGCAATTTGAATACAACTTAAGACAAAGATA 1380
Db 1321 GATTTCTTTTTCAGCCGTGGATCAAGCAATTTGAATACAACTTAAGACAAAGATA 1380
QY 1381 TTACCCGAATCATAGAACTAATACTTTGTTTCAATGCAAGAACCAAGAACTCTCTAT 1440
Db 1381 TTACCCGAATCATAGAACTAATACTTTGTTTCAATGCAAGAACCAAGAACTCTCTAT 1440
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QY 1441 TTGGTTTGTATCAACAGGAAAAAGCATTTCAGGAGGCATAAAGATTTGTATCAT 1500
Db 1441 TTGGTTTGTATCAACAGGAAAAAGCATTTCAGGAGGCATAAAGATTTGTATCAT 1500
QY 1501 AGAGTTTAAAGCTGTTTATTTTGTGTTTTCATTTGCTGAAAAACACTTCTATTATC 1560
Db 1501 AGAGTTTAAAGCTGTTTATTTTGTGTTTTCATTTGCTGAAAAACACTTCTATTATC 1560
QY 1561 AATTAATTCATAGACCTAAATAAACCCTCAACAGGCTCTTTTAATATAAATTCGCTTCAA 1620
Db 1561 AATTAATTCATAGACCTAAATAAACCCTCAACAGGCTCTTTTAATATAAATTCGCTTCAA 1620
QY 1621 AATAGAA 1627
Db 1621 AATAGAA 1627

RESULT 6
ACD41890
ID ACD41890 standard; cDNA; 1647 BP.
XX
AC ACD41890;
XX
DT 05-SEP-2003 (first entry)
XX
Human secreted/transmembrane protein (PRO) cDNA #96.
XX
Human; ss; gene; PRO; secreted protein; transmembrane protein; tumour;
cytostatic; gene therapy; tumour necrosis factor-alpha; TNF-alpha; blood;
proteoglycan; cartilage; cytokine; peripheral blood mononuclear cell;
PBMC; glucose uptake; FFA; skeletal muscle cell; adipocyte cell;
chondrocyte cell proliferation; chondrocyte cell differentiation;
pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell;
endothelial cell; A-peptide; factor VIIA.
XX
Homo sapiens.
XX
US2003036179-A1.
XX
20-FEB-2003.
XX
10-MAY-2002; 2002US-00142431.
XX
31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 13-SEP-1999; 99WO-US020594.
PR 15-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 05-OCT-1999; 99WO-US021547.
PR 29-NOV-1999; 99WO-US023089.
PR 30-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
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PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 16-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030311.  
PR 20-DEC-1999; 99WO-US030399.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
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PR 18-FEB-2000; 2000WO-US000432.  
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PR 24-FEB-2000; 2000WO-US005004.  
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PR 02-MAR-2000; 2000WO-US005841.  
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PR 21-MAR-2000; 2000WO-US007332.  
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PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
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PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 10-NOV-2000; 2000WO-US030873.  
PR 01-DEC-2000; 2000WO-US032578.  
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PR 20-DEC-2000; 2000WO-US034956.  
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PR 28-FEB-2001; 2001WO-US0006520.  
PR 01-MAR-2001; 2001WO-US006666.  
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PR 14-MAR-2001; 2001US-00806889.  
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PR 10-MAY-2001; 2001US-00854280.  
PR 18-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
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PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
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PR 05-JUN-2001; 2001US-00874503.  
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PR 20-JUN-2001; 2001WO-US019692.  
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PR 19-DEC-2001; 2001US-00028072.  
XX (GETH ) GENENTECH INC.  
PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
XX

PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX  
DR WPI; 2003-466355/44.  
DR P-PSDE; ABO24936.  
XX  
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or  
PT PRO4978, useful in molecular biology, chromosome and gene mapping, in  
PT generating antisense RNA and DNA, and in gene therapy.  
XX  
XX Claim 2; Fig 191; 659pp; English.  
XX  
XX The invention relates to an isolated nucleic acid comprising at least 80%  
CC sequence identity to a PRO (secreted and transmembrane protein) cDNA  
CC comprising a nucleic acid (a) encoding a PRO polypeptide, or its  
CC extracellular domain (with or without its associated signal peptide),  
CC which comprises any of the 275 120-850 residue amino acid sequences,  
CC given in the specification; (b) comprising any of the 275 300-3500  
CC nucleotide sequences, given in the specification; or (c) comprising the  
CC full-length coding sequence of the nucleotide sequences given in the  
CC specification, or of the DNA deposited under any of the American Type  
CC Culture Collection (ATCC) Accession Numbers listed in the specification.  
CC Also included are a vector comprising the novel nucleic acid, a host cell  
CC comprising the vector, producing a PRO polypeptide, the isolated PRO  
CC polypeptides detailed above, a chimaeric molecule comprising the PRO  
CC polypeptide of fused to a heterologous amino acid sequence, an anti-PRO  
CC antibody, detecting a PRO polypeptide in a sample suspected of containing  
CC the PRO polypeptide, linking a bioactive molecule to a cell expressing a  
CC PRO polypeptide, modulating at least one biological activity of a cell  
CC expressing a PRO polypeptide, stimulating the release of tumour necrosis  
CC factor-alpha (TNF-alpha) from human blood, (or proteoglycans from  
CC cartilage or cytokine from peripheral blood mononuclear cells (PBMC)),  
CC modulating the uptake of glucose or FFA by skeletal muscle cells or  
CC adipocyte cells, stimulating the proliferation or differentiation of  
CC chondrocyte cells (or proliferation of or gene expression in pericyte  
CC cells), stimulating the proliferation of inner ear utricular supporting  
CC cells (or of T-lymphocyte cells, or of endothelial cells), inhibiting the  
CC binding of A-peptide to factor VIIA, or differentiation of adipocyte  
CC cells, detecting the presence of a tumour in a mammal and an  
CC oligonucleotide probe derived from any of the nucleotide sequences given  
CC in the specification. The polynucleotide is useful in molecular biology,  
CC including uses as hybridisation probes, in chromosome and gene mapping,  
CC in generating antisense RNA and DNA, and in gene therapy. The  
CC polynucleotide may also be used in preparing PRO polypeptides by  
CC recombinant techniques, and in generating either transgenic animals or  
CC knock-out animals which, in turn, are useful in the development and  
CC screening of therapeutically useful reagents. The PRO polypeptide or the  
CC antibody is used in preparing a medicament for treating a condition  
CC responsive to the polypeptide or antibody, such as tumours, and in  
CC various diagnostic assays. The present sequence encodes a PRO polypeptide  
XX  
SQ Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;

Query Match 99.9%; Score 1625.4; DB 8; Length 1647;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCTTCAGCTCAAGAGAGAGAGATGAGCGCTTCGCTTCTGTTCTGTTCTTTATAA 60  
DB 1 GCTTCAGCTCAAGAGAGAGAGATGAGCGCTTCGCTTCTGTTCTGTTCTTTATAA 60  
QY 61 CATTTTCTTCGATTTCCCTTAGTCGGATGACGGAATAATGAAGAAATATGCAACTGG 120  
DB 61 CATTTTCTTCGATTTCCCTTAGTCGGATGACGGAATAATGAAGAAATATGCAACTGG 120  
QY 121 CTCAGGCATATCTCAACCACTTCTACTCTCTTGAATAGAGGAATCATCTGTTCTCAA 180  
DB 121 CTCAGGCATATCTCAACCACTTCTACTCTCTTGAATAGAGGAATCATCTGTTCTCAA 180  
QY 181 GCAAGATAGGATCTCATAGATGACAAATTCGGAAATCGGAAATGCAAGCAATTTTGGATTGA 240  
DB 181 GCAAGATAGGATCTCATAGATGACAAATTCGGAAATCGGAAATGCAAGCAATTTTGGATTGA 240

QY 241 CAGTGACTGGAACCTGGACTCAAAACACCCCTTGAGATCATGAAGACACCCAGGTGTGGG 300  
DB |||||  
QY 241 CAGTGACTGGAACCTGGACTCAAAACACCCCTTGAGATCATGAAGACACCCAGGTGTGGG 300  
DB |||||  
QY 301 TGCCTGATGTGGGCGAGTATGGCTACACCCCTCCCTGGGTGGGAAAAATACAACTCACCT 360  
DB |||||  
QY 301 TGCCTGATGTGGGCGAGTATGGCTACACCCCTCCCTGGGTGGGAAAAATACAACTCACCT 360  
DB |||||  
QY 361 ACAGATAATAAATCTACTCCGGATATGGCAGAGCTGCTGTGATGGGCTATCCCAAG 420  
DB |||||  
QY 361 ACAGATAATAAATCTACTCCGGATATGGCAGAGCTGCTGTGATGGGCTATCCCAAG 420  
DB |||||  
QY 421 AAGGTTTGAAGTGTGGGAGCAAGTCACTCCACTAAATTTACCAAGATTTCAAAAGGGA 480  
DB |||||  
QY 421 AAGGTTTGAAGTGTGGGAGCAAGTCACTCCACTAAATTTACCAAGATTTCAAAAGGGA 480  
DB |||||  
QY 481 TTGCAGACATCATGATTTGCTTTAGGACTCGAGTCCATGGTCCGCTGCTCGCTATTTTG 540  
DB |||||  
QY 481 TTGCAGACATCATGATTTGCTTTAGGACTCGAGTCCATGGTCCGCTGCTCGCTATTTTG 540  
DB |||||  
QY 541 ATGGTCCCTTGGAGTGTCTGGCCATGCTTTCCCTGCTGCTCGGCTGTGGGTGGTGACA 600  
DB |||||  
QY 541 ATGGTCCCTTGGAGTGTCTGGCCATGCTTTCCCTGCTGCTCGGCTGTGGGTGGTGACA 600  
DB |||||  
QY 601 CTCATTTTATGAGGATGAAAACTGGACCAAGATGGAGCAGATTTCAACTTTGTTCTTG 660  
DB |||||  
QY 601 CTCATTTTATGAGGATGAAAACTGGACCAAGATGGAGCAGATTTCAACTTTGTTCTTG 660  
DB |||||  
QY 661 TGGCTGCTCATGAATTTGGTTCATGCACTGGGCTCTCTCACTCCAATGATCAACAGGCT 720  
DB |||||  
QY 661 TGGCTGCTCATGAATTTGGTTCATGCACTGGGCTCTCTCACTCCAATGATCAACAGGCT 720  
DB |||||  
QY 721 TGATGTTCCCAATTTATGTTCCCTGGATCCAGAAATACCCACTTTCTCAGGATGATA 780  
DB |||||  
QY 721 TGATGTTCCCAATTTATGTTCCCTGGATCCAGAAATACCCACTTTCTCAGGATGATA 780  
DB |||||  
QY 781 TCAATGGAATCCAGTCCATCTATGAGGCTGCTGCTAAAGTACTGCTAAGCCAAAGGAAC 840  
DB |||||  
QY 781 TCAATGGAATCCAGTCCATCTATGAGGCTGCTGCTAAAGTACTGCTAAGCCAAAGGAAC 840  
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DB |||||  
QY 841 CCACATATACCCCATGCTGTGACCCCTGACTTTTGAAGCTATCAAACTTTCCGCA 900  
DB |||||  
QY 901 GAGAGTAAATGTTCTTTAAAGCCAGGACCTATGAGGATCTATTATGATATCAGGATG 960  
DB |||||  
QY 901 GAGAGTAAATGTTCTTTAAAGCCAGGACCTATGAGGATCTATTATGATATCAGGATG 960  
DB |||||  
QY 961 TTGAGTTTGAATTAATTTGCTTCATTTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCAT 1020  
DB |||||  
QY 961 TTGAGTTTGAATTAATTTGCTTCATTTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTGCAT 1020  
DB |||||  
QY 1021 ACGAGAACCCAGAGATGAATTTGTTTAAAGATGAAGAACTTTGATGATGATCAGAG 1080  
DB |||||  
QY 1021 ACGAGAACCCAGAGATGAATTTGTTTAAAGATGAAGAACTTTGATGATGATCAGAG 1080  
DB |||||  
QY 1081 GATATGCTGTCTTGCCAGATATCCCAATCCATCCATACATTTAGGTTTCCAGGACGTT 1140  
DB |||||  
QY 1081 GATATGCTGTCTTGCCAGATATCCCAATCCATCCATACATTTAGGTTTCCAGGACGTT 1140  
DB |||||  
QY 1141 TGAAGAAAATAGATGAGCCGCTGTGTGATAAGACCAAGAAAAAATCTACTTTCTTTGG 1200  
DB |||||  
QY 1141 TGAAGAAAATAGATGAGCCGCTGTGTGATAAGACCAAGAAAAAATCTACTTTCTTTGG 1200  
DB |||||  
QY 1201 GCATTTGGTGTGGAGTTTGAATGAATGACCCAAACCCATGAGCAAGGATTTCCCGCAGA 1260  
DB |||||  
QY 1201 GCATTTGGTGTGGAGTTTGAATGAATGACCCAAACCCATGAGCAAGGATTTCCCGCAGA 1260  
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QY 1261 GAGTGTGTAACACATTTCTCGGATCAGTATCCGTTGATGCTGTTTCCAGTACAAG 1320  
DB |||||  
QY 1261 GAGTGTGTAACACATTTCTCGGATCAGTATCCGTTGATGCTGTTTCCAGTACAAG 1320  
DB |||||  
QY 1321 GATTTCTTTCTTTTTCAGCCGCTGGATCAAGCAATTTTGAATACAACATTAAGACAAAGAATA 1380

DB |||||  
QY 1321 GATTTCTTTCTTTTTCAGCCGCTGGATCAAGCAATTTTGAATACAACATTAAGACAAAGAATA 1380  
DB |||||  
QY 1381 TTACCCGAATCATGAGAACTAATACTTGGTTTCAATGCAAGAAACCAAGAACTCTCTCAT 1440  
DB |||||  
QY 1381 TTACCCGAATCATGAGAACTAATACTTGGTTTCAATGCAAGAAACCAAGAACTCTCTCAT 1440  
DB |||||  
QY 1441 TTGGTTTGTATATCAACAGGAAAGCACATTCAGGAGGCATAAGATATTGTATCATA 1500  
DB |||||  
QY 1441 TTGGTTTGTATATCAACAGGAAAGCACATTCAGGAGGCATAAGATATTGTATCATA 1500  
DB |||||  
QY 1501 AGAGTTTAAAGCTTGTATTTTGGTTATTTGTTTCAATTTGCTGAAAAACACTTTATTTATC 1560  
DB |||||  
QY 1501 AGAGTTTAAAGCTTGTATTTTGGTTATTTTGGTTATTTGTTTCAATTTGCTGAAAAACACTTTATTTATC 1560  
DB |||||  
QY 1561 AATAAATTCATAGACCTAAAAATAAACCTCAACAGGCTCTTTTAATAATAATTCGCTCAA 1620  
DB |||||  
QY 1561 AATAAATTCATAGACCTAAAAATAAACCTCAACAGGCTCTTTTAATAATAATTCGCTCAA 1620  
DB |||||  
QY 1621 AATAGAA 1627  
DB |||||  
QY 1621 AATAGAA 1627  
DB |||||

RESULT 7  
ACA04119  
ID ACA04119 standard; cDNA; 1647 BP.  
XX  
AC ACA04119;  
XX  
DT 27-MAY-2003 (first entry)  
XX  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 191.  
XX  
KW Human; ss; gene; secreted protein; transmembrane protein; PRO;  
KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;  
KW infertility; birth defects; premature aging; AIDS; biosensor;  
KW acquired immunodeficiency syndrome; cancer; diabetic complication;  
KW bioreactor; tumour.  
XX  
OS Homo sapiens.  
XX  
PN US2003032155-A1.  
XX  
PD 13-FEB-2003.  
XX  
PF 03-MAY-2002; 2002US-00137865.  
XX  
PR 31-MAR-1997; 97WO-US005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
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PR 10-SEP-1998; 98WO-US018824.  
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PR 29-OCT-1998; 98WO-US022992.  
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PR 18-FEB-2000; 2000WO-US004342.
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PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
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PR 02-JUN-2000; 2000WO-US015264.
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PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 28-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 01-MAR-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00806889.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 28-MAY-2001; 2001WO-US020192.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001US-00877800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019592.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.

PR 19-DEC-2001; 2001US-00028072.
XX (GETH ) GENENTECH INC.
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
XX Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-331925/31.
XX P-PSDB; ABU66941.
XX New secreted and transmembrane nucleic acids and polypeptides, designated
XX as PRO, useful for treating inflammation, organ failure, atherosclerosis,
XX cardiac injury, infertility, birth defects, premature aging, AIDS, or
XX cancer.
XX Claim 2; Fig 191; 659pp; English.
XX The invention relates to an isolated nucleic acid comprising, or which is
XX at least 80% identical to, or the full-length coding sequence of, any of
XX the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
XX (one of 275 secreted or transmembrane proteins). The nucleic acid further
XX comprises the full-length coding sequence of the DNA deposited under
XX American Type Culture Collection (ATCC) accession number in a list given
XX in the specification. Also included are vectors and host cells for
XX producing PRO proteins, PRO fusion proteins, anti-PRO antibodies, PRO
XX extracellular domains and mature sequences, methods of detecting PRO
XX proteins, methods for stimulating the release of TNF-alpha (tumour
XX necrosis factor alpha) from human blood, (and the proliferation of
XX differentiation of chondrocyte cells, the proliferation of, or gene
XX expression in pericyte cells, the release or proteoglycans from
XX cartilage, proliferation of inner ear articular supporting cells, the
XX proliferation of T-lymphocyte cells, the release of a cytokine from
XX peripheral blood mononuclear cells (PBMC), or the proliferation of
XX endothelial cells), a method for modulating the uptake of glucose or free
XX fatty acid (FFA) by skeletal muscle cells, a method for inhibiting the
XX binding of A-peptide to factor VIIA, or the differentiation of adipocyte
XX cells, a method for detecting the presence of a tumour in a mammal and an
XX oligonucleotide probe derived from any of the nucleotide sequences cited
XX above. The nucleic acids and polypeptides are useful for treating
XX inflammatory diseases, organ failure, atherosclerosis, cardiac injury,
XX infertility, birth defects, premature aging, AIDS (acquired
XX immunodeficiency syndrome), cancer, or diabetic complications. The
XX nucleic acids are useful as hybridisation probes in chromosome and gene
XX mapping, and in generating antisense RNA or DNA. The polypeptides are
XX useful as pharmaceuticals, diagnostics, biosensors or bioeffectors. Both
XX are useful in tissue typing. The present sequence encodes a PRO protein
XX of the invention
XX SQ Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;

Query Match 99.9%; Score 1625.4; DB 8; Length 1647;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTTCAGCTGAAGAAGAGAGAGGAATGAAGCGCCTTCGCTTCTGTTGTTGTTCTTTATAA 60
Db 1 GCTTCAGCTGAAGAAGAGAGAGGAATGAAGCGCCTTCGCTTCTGTTGTTGTTCTTTATAA 60

Qy 61 CATTTTCTTCTGCATTTCCCTTAGTCGCGATGACGGAATAATGAAGAAATATGCAACTGG 120
Db 61 CATTTTCTTCTGCATTTCCCTTAGTCGCGATGACGGAATAATGAAGAAATATGCAACTGG 120

Qy 121 CTCAGGCATATCTCAACCACTTCTACTCTTCTGAAATAGAGGGATCATCTGTTCTAAA 180
Db 121 CTCAGGCATATCTCAACCACTTCTACTCTTCTGAAATAGAGGGATCATCTGTTCTAAA 180

Qy 181 GCAAGATAGAGTCTCATAGATGACAAAATTCGGAAATGCAAGCAATTTTTCGATTGA 240
Db 181 GCAAGATAGAGTCTCATAGATGACAAAATTCGGAAATGCAAGCAATTTTTCGATTGA 240

Qy 241 CAGTGACTGAAATCTGGACTCAAAACCCCTTGAGATCATGAGACACCCAGGTGTGGG 300
Db 241 CAGTGACTGAAATCTGGACTCAAAACCCCTTGAGATCATGAGACACCCAGGTGTGGG 300
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|    |      |        |         |       |        |         |        |        |        |         |        |       |        |       |        |        |      |     |     |     |    |     |     |      |    |    |      |
|----|------|--------|---------|-------|--------|---------|--------|--------|--------|---------|--------|-------|--------|-------|--------|--------|------|-----|-----|-----|----|-----|-----|------|----|----|------|
| Db | 241  | CAGTGA | CTGGAAA | CTGGA | CTCAAA | CACCCTT | GAGAT  | CTATGA | AGACAC | CCAGGTG | TGGGG  | 300   |        |       |        |        |      |     |     |     |    |     |     |      |    |    |      |
| Qy | 301  | TGCCT  | GATG    | TGGG  | CCAGT  | ATATGG  | CTAC   | ACCCT  | CTCC   | TGGGT   | GAGAAA | ATA   | CACCT  | CACCT | 360    |        |      |     |     |     |    |     |     |      |    |    |      |
| Db | 301  | TGCCT  | GATG    | TGGG  | CCAGT  | ATATGG  | CTAC   | ACCCT  | CTCC   | TGGGT   | GAGAAA | ATA   | CACCT  | CACCT | 360    |        |      |     |     |     |    |     |     |      |    |    |      |
| Qy | 361  | ACAGA  | ATAA    | TAAAC | TACTA  | CTCCGG  | ATATGG | CA     | CGAG   | CTGCT   | TGGAT  | ATCCA | AG     | 420   |        |        |      |     |     |     |    |     |     |      |    |    |      |
| Db | 361  | ACAGA  | ATAA    | TAAAC | TACTA  | CTCCGG  | ATATGG | CA     | CGAG   | CTGCT   | TGGAT  | ATCCA | AG     | 420   |        |        |      |     |     |     |    |     |     |      |    |    |      |
| Qy | 421  | AAGG   | TTTTAG  | AGT   | GTGAG  | CA      | AGT    | CTCA   | CTTAA  | AAATTC  | AC     | CMAG  | ATTTCA | AGGGA | 480    |        |      |     |     |     |    |     |     |      |    |    |      |
| Db | 421  | AAGG   | TTTTAG  | AGT   | GTGAG  | CA      | AGT    | CTCA   | CTTAA  | AAATTC  | AC     | CMAG  | ATTTCA | AGGGA | 480    |        |      |     |     |     |    |     |     |      |    |    |      |
| Qy | 481  | TTG    | CAG     | ACAT  | CAT    | GATT    | GGC    | TTTAG  | AGCT   | CGAG    | TCCAT  | CGT   | TCGT   | CGCT  | ATTTTG | 540    |      |     |     |     |    |     |     |      |    |    |      |
| Db | 481  | TTG    | CAG     | ACAT  | CAT    | GATT    | GGC    | TTTAG  | AGCT   | CGAG    | TCCAT  | CGT   | TCGT   | CGCT  | ATTTTG | 540    |      |     |     |     |    |     |     |      |    |    |      |
| Qy | 541  | ATG    | GTCC    | CTT   | GGG    | AGT     | CTT    | GGC    | CAT    | CCCTT   | TCT    | CTG   | TCCGG  | GCT   | GGGTG  | GACA   | 600  |     |     |     |    |     |     |      |    |    |      |
| Db | 541  | ATG    | GTCC    | CTT   | GGG    | AGT     | CTT    | GGC    | CAT    | CCCTT   | TCT    | CTG   | TCCGG  | GCT   | GGGTG  | GACA   | 600  |     |     |     |    |     |     |      |    |    |      |
| Qy | 601  | CTCA   | TTTTG   | TAG   | AGAT   | GA      | AAA    | CTG    | GAC    | CAAG    | ATG    | AG    | TG     | AG    | CAG    | ATTTCA | AGT  | 660 |     |     |    |     |     |      |    |    |      |
| Db | 601  | CTCA   | TTTTG   | TAG   | AGAT   | GA      | AAA    | CTG    | GAC    | CAAG    | ATG    | AG    | TG     | AG    | CAG    | ATTTCA | AGT  | 660 |     |     |    |     |     |      |    |    |      |
| Qy | 661  | TGG    | CTG     | CT    | AT     | GAA     | TTTTGG | T      | CAT    | CACT    | GGG    | GCT   | CT     | CAC   | TCCAA  | TGAT   | CAAA | CAG | 720 |     |    |     |     |      |    |    |      |
| Db | 661  | TGG    | CTG     | CT    | AT     | GAA     | TTTTGG | T      | CAT    | CACT    | GGG    | GCT   | CT     | CAC   | TCCAA  | TGAT   | CAAA | CAG | 720 |     |    |     |     |      |    |    |      |
| Qy | 721  | TGAT   | GT      | TCC   | CAAA   | TAT     | TGT    | CT     | CC     | TGAT    | CCC    | AGAAA | ATA    | CCCA  | CTT    | TTCT   | CAG  | AT  | GAT | 780 |    |     |     |      |    |    |      |
| Db | 721  | TGAT   | GT      | TCC   | CAAA   | TAT     | TGT    | CT     | CC     | TGAT    | CCC    | AGAAA | ATA    | CCCA  | CTT    | TTCT   | CAG  | AT  | GAT | 780 |    |     |     |      |    |    |      |
| Qy | 781  | TCA    | AT      | GAA   | TCC    | AGT     | TCC    | AT     | TG     | AG      | AGT    | CT    | GCT    | TA    | AGT    | AC     | TGCT | TA  | AG  | 840 |    |     |     |      |    |    |      |
| Db | 781  | TCA    | AT      | GAA   | TCC    | AGT     | TCC    | AT     | TG     | AG      | AGT    | CT    | GCT    | TA    | AGT    | AC     | TGCT | TA  | AG  | 840 |    |     |     |      |    |    |      |
| Qy | 841  | CCAT   | TA      | TAC   | CCCA   | T       | GCCT   | GT     | GAC    | CC      | TGAC   | T     | TGAC   | GCT   | TAT    | CAC    | AACT | TT  | TC  | CG  | CA | 900 |     |      |    |    |      |
| Db | 841  | CCAT   | TA      | TAC   | CCCA   | T       | GCCT   | GT     | GAC    | CC      | TGAC   | T     | TGAC   | GCT   | TAT    | CAC    | AACT | TT  | TC  | CG  | CA | 900 |     |      |    |    |      |
| Qy | 901  | GAGA   | AGT     | AA    | TG     | TCT     | TTT    | AA     | AG     | CG      | CAG    | GC    | CA     | CT    | AT     | TAT    | TG   | AT  | T   | CA  | CG | AT  | 960 |      |    |    |      |
| Db | 901  | GAGA   | AGT     | AA    | TG     | TCT     | TTT    | AA     | AG     | CG      | CAG    | GC    | CA     | CT    | AT     | TAT    | TG   | AT  | T   | CA  | CG | AT  | 960 |      |    |    |      |
| Qy | 961  | TTG    | AG      | TTT   | GAA    | TTAA    | TTG    | CT     | TAT    | TC      | GG     | CA    | CT     | CT    | CG     | CA     | CT   | CT  | CG  | CA  | CT | CG  | CA  | 1020 |    |    |      |
| Db | 961  | TTG    | AG      | TTT   | GAA    | TTAA    | TTG    | CT     | TAT    | TC      | GG     | CA    | CT     | CT    | CG     | CA     | CT   | CT  | CG  | CA  | CT | CG  | CA  | 1020 |    |    |      |
| Qy | 1021 | ACG    | AG      | AAC   | CC     | CAG     | AG     | ATA    | GAT    | CT      | TG     | TTTT  | TAA    | GAT   | GAAA   | CT     | CT   | TG  | AT  | GAT | AT | CA  | G   | 1080 |    |    |      |
| Db | 1021 | ACG    | AG      | AAC   | CC     | CAG     | AG     | ATA    | GAT    | CT      | TG     | TTTT  | TAA    | GAT   | GAAA   | CT     | CT   | TG  | AT  | GAT | AT | CA  | G   | 1080 |    |    |      |
| Qy | 1081 | GAT    | AT      | GCT   | GT     | CT      | TG     | CC     | AG     | AT      | TAT    | CC    | CAAA   | T     | CCAT   | CT     | CA   | TAT | T   | AG  | GT | TTT | CC  | AG   | CA | GT | 1140 |
| Db | 1081 | GAT    | AT      | GCT   | GT     | CT      | TG     | CC     | AG     | AT      | TAT    | CC    | CAAA   | T     | CCAT   | CT     | CA   | TAT | T   | AG  | GT | TTT | CC  | AG   | CA | GT | 1140 |
| Qy | 1141 | TGA    | AG      | AAA   | ATA    | GAT     | GC     | AG     | CG     | CT      | GT     |       |        |       |        |        |      |     |     |     |    |     |     |      |    |    |      |

|          |                                                                           |                                                                     |      |
|----------|---------------------------------------------------------------------------|---------------------------------------------------------------------|------|
| Qy       | 1381                                                                      | TTACCCGAATCATGAGAACTAACTACTTGGTTTCAATGCAAGAACCAAGAACTCTCTCAT        | 1444 |
| Db       | 1381                                                                      | TTACCCGAATCATGAGAACTAACTACTTGGTTTCAATGCAAGAACCAAGAACTCTCTCAT        | 1440 |
| Qy       | 1441                                                                      | TTGGTTTGTATATCAACAAGGAAAGACACATTCAGGAGGCATATAAGATATTGTATCATATA      | 1500 |
| Db       | 1441                                                                      | TTGGTTTGTATATCAACAAGGAAAGACACATTCAGGAGGCATATAAGATATTGTATCATATA      | 1500 |
| Qy       | 1501                                                                      | AGAGTTTAAAGCTGTGTTTATTTTGGTATTGTTTCATTTGCTGAAAAACACTTCTATTATTC      | 1560 |
| Db       | 1501                                                                      | AGAGTTTAAAGCTGTGTTTATTTTGGTATTGTTTCATTTGCTGAAAAACACTTCTATTATTC      | 1560 |
| Qy       | 1561                                                                      | AATAAATTCATAGACCTAAATAATAAACCCTCAACAGGTCCTTTTAAATATATAAAATTCGCTTCAA | 1620 |
| Db       | 1561                                                                      | AATAAATTCATAGACCTAAATAATAAACCCTCAACAGGTCCTTTTAAATATATAAAATTCGCTTCAA | 1620 |
| Qy       | 1621                                                                      | AATAGAA 1627                                                        |      |
| Db       | 1621                                                                      | AATAGAA 1627                                                        |      |
| RESULT 8 |                                                                           |                                                                     |      |
| ID       | ADA45710                                                                  | standard; cDNA; 1647 BP.                                            |      |
| XX       | ADA45710;                                                                 |                                                                     |      |
| AC       |                                                                           |                                                                     |      |
| XX       |                                                                           |                                                                     |      |
| DT       |                                                                           |                                                                     |      |
| XX       | 20-NOV-2003 (first entry)                                                 |                                                                     |      |
| XX       | Novel human secreted and transmembrane protein PRO5992 cDNA.              |                                                                     |      |
| DE       |                                                                           |                                                                     |      |
| XX       | Human; secreted and transmembrane protein; PRO; gene; ss;                 |                                                                     |      |
| XX       | Tumour necrosis factor alpha release; TNF-alpha release;                  |                                                                     |      |
| Kw       | glucose uptake modulator; FFA uptake modulator;                           |                                                                     |      |
| Kw       | cell proliferation stimulator; cell differentiation stimulator;           |                                                                     |      |
| Kw       | cell differentiation inhibitor; cytokine release stimulator;              |                                                                     |      |
| Kw       | lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; |                                                                     |      |
| Kw       | cervical tumour; liver tumour; chromosome mapping; gene mapping;          |                                                                     |      |
| Kw       | gene therapy; chromosome identification; chromosome marker.               |                                                                     |      |
| XX       |                                                                           |                                                                     |      |
| XX       | Homo sapiens.                                                             |                                                                     |      |
| XX       |                                                                           |                                                                     |      |
| PN       | US2003022328-A1.                                                          |                                                                     |      |
| XX       |                                                                           |                                                                     |      |
| XX       |                                                                           |                                                                     |      |
| PD       | 30-JAN-2003.                                                              |                                                                     |      |
| XX       |                                                                           |                                                                     |      |
| XX       | 16-APR-2002; 2002US-00123904.                                             |                                                                     |      |
| PF       |                                                                           |                                                                     |      |
| XX       |                                                                           |                                                                     |      |
| PR       | 31-MAR-1997; 97WO-US005230.                                               |                                                                     |      |
| PR       | 12-JUN-1998; 98WO-US012456.                                               |                                                                     |      |
| FR       | 14-JUL-1998; 98WO-US014552.                                               |                                                                     |      |
| PR       | 28-AUG-1998; 98WO-US017888.                                               |                                                                     |      |
| PR       | 10-SEP-1998; 98WO-US018824.                                               |                                                                     |      |
| PR       | 14-SEP-1998; 98WO-US019093.                                               |                                                                     |      |
| PR       | 14-SEP-1998; 98WO-US019094.                                               |                                                                     |      |
| PR       | 14-SEP-1998; 98WO-US019177.                                               |                                                                     |      |
| PR       | 16-SEP-1998; 98WO-US019330.                                               |                                                                     |      |
| PR       | 17-SEP-1998; 98WO-US019437.                                               |                                                                     |      |
| PR       | 07-OCT-1998; 98WO-US021141.                                               |                                                                     |      |
| PR       | 29-OCT-1998; 98WO-US022991.                                               |                                                                     |      |
| PR       | 29-OCT-1998; 98WO-US022992.                                               |                                                                     |      |
| PR       | 20-NOV-1998; 98WO-US024855.                                               |                                                                     |      |
| PR       | 01-DEC-1998; 98WO-US025108.                                               |                                                                     |      |
| PR       | 05-JAN-1999; 99WO-US000106.                                               |                                                                     |      |
| PR       | 08-MAR-1999; 99WO-US005028.                                               |                                                                     |      |
| PR       | 10-MAR-1999; 99WO-US005190.                                               |                                                                     |      |
| PR       | 20-APR-1999; 99WO-US008615.                                               |                                                                     |      |
| PR       | 14-MAY-1999; 99WO-US010733.                                               |                                                                     |      |
| PR       | 02-JUN-1999; 99WO-US012252.                                               |                                                                     |      |
| PR       | 01-SEP-1999; 99WO-US020111.                                               |                                                                     |      |
| PR       | 08-SEP-1999; 99WO-US020594.                                               |                                                                     |      |
| PR       | 13-SEP-1999; 99WO-US020944.                                               |                                                                     |      |



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PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005501.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00806889.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 23-JUN-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.

PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
FA (GETH ) GENENTECH INC.
XX
PI Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI; 2003-584997/55.
DR P-PSDB; ADA45711.
XX
XX Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX
XX Claim 2; Fig 191; 659pp; English.
XX
XX The invention describes 305 nucleic acids encoding PRO (secreted and
CC transmembrane) polypeptides (I). (I) is useful for stimulating the
CC release of TNF-alpha from human blood, for modulating the uptake of
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC stimulating the proliferation or differentiation of chondrocyte cells,
CC for stimulating the proliferation of or gene expression in pericyte
CC cells, for stimulating the release of proteoglycans from cartilage, for
CC stimulating the proliferation of inner ear utricular supporting cells,
CC for stimulating the proliferation of T-lymphocyte cells, for stimulating
CC the release of a cytokine from BMC cells, for inhibiting the binding of
CC A-peptide to factor VIIa, for inhibiting the differentiation of adipocyte
CC cells, for stimulating proliferation of endothelial cells, for detecting
CC the presence of tumour in a mammal. The tumour is lung, colon, breast,
CC prostate, rectal, cervical or liver tumour. The oligonucleotide probes
CC are useful for isolating genomic and cDNA nucleotide sequences or
CC antisense probes. (I) is also useful as therapeutic agent. PRO is useful
CC in assays to identify other proteins or molecules involved in binding
CC interaction. A polynucleotide (II) encoding (I) is useful in chromosome
CC and gene mapping, in generation of antisense RNA and DNA, in the
CC preparation of PRO polypeptide, for generating transgenic animals or
CC knockout animals which in turn are useful in the development and
CC screening of therapeutically useful reagents, in gene therapy, for
CC chromosome identification, as chromosome marker, and for generating
CC probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.
CC detecting its expression in specific cells, tissues or serum, and for
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. (I) and (II) are useful for tissue typing. This sequence encodes
CC a novel human secreted and transmembrane PRO polypeptide.
XX
SQ Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;

Query Match          99.9%; Score 1625.4; DB 9; Length 1647;
Best Local Similarity 99.9%; Pred No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTTCAGCTGAAGAAGAGAGAGGAATGAAGCGCCCTCTGCTCTGTGTGTTGTTCTTTATAA 60
Db 1 GCTTCAGCTGAAGAAGAGAGAGGAATGAAGCGCCCTCTGCTCTGTGTGTTGTTCTTTATAA 60
Qy 61 CATTTTCTTGTCATTTCCCTTAGTCGGGATGACGGAAATGAGAAATATGCAACTGG 120
Db 61 CATTTTCTTGTCATTTCCCTTAGTCGGGATGACGGAAATGAGAAATATGCAACTGG 120
Qy 121 CTCAGGCATATCTCAACAGCTTCTACTCTCTTGAATAGAGAGGAATCATCTTGTTCAAA 180
Db 121 CTCAGGCATATCTCAACAGCTTCTACTCTCTTGAATAGAGAGGAATCATCTTGTTCAAA 180
Qy 181 GCAAGAATAGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTGTGATGA 240
Db 181 GCAAGAATAGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTGTGATGA 240
Qy 241 CAGTGAAGTGAAGTGGACTCAACACCCCTTCAGATCATGAGACACCCAGGTTGGGG 300
Db 241 CAGTGAAGTGAAGTGGACTCAACACCCCTTCAGATCATGAGACACCCAGGTTGGGG 300
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QY 301 TGCCTGATGTGGCCAGTAGTGGCTACACCTCCCTGGGTGGAGAAATACAACTCACCT 360
Db 301 TGCCTGATGTGGCCAGTAGTGGCTACACCTCCCTGGGTGGAGAAATACAACTCACCT 360
QY 361 ACAGAATAATAAATATATATCCGGATATGCGAGAGCTGCTGTGGATGAGGCTATCCAAG 420
Db 361 ACAGAATAATAAATATATATCCGGATATGCGAGAGCTGCTGTGGATGAGGCTATCCAAG 420
QY 421 AAGGTTTGAAGTGTGGAGCAAGTCACTCCCAATAAATTCACCAAGATTTCAAAGGGA 480
Db 421 AAGGTTTGAAGTGTGGAGCAAGTCACTCCCAATAAATTCACCAAGATTTCAAAGGGA 480
QY 481 TTGCAGACATCATGATTGCTTTAGGACTCGAGTCCATGGTCCGTCCTCGCTATTTTG 540
Db 481 TTGCAGACATCATGATTGCTTTAGGACTCGAGTCCATGGTCCGTCCTCGCTATTTTG 540
QY 541 ATGGTCCCTTGGGAGTGTGGCCATGCTTTCCTCCTCGTCCGGTCTGGGTGGTGACA 600
Db 541 ATGGTCCCTTGGGAGTGTGGCCATGCTTTCCTCCTCGTCCGGTCTGGGTGGTGACA 600
QY 601 CTCATTTTCATGAGGATGAATCTGACCAAGATGGAGCAGATTCACCTTTCTTTG 660
Db 601 CTCATTTTCATGAGGATGAATCTGACCAAGATGGAGCAGATTCACCTTTCTTTG 660
QY 661 TGGCTGCTCATGAATTTGGTCTATGCTACCTGGGCTCTCTCACTCCAATGATCAACAGCCT 720
Db 661 TGGCTGCTCATGAATTTGGTCTATGCTACCTGGGCTCTCTCACTCCAATGATCAACAGCCT 720
QY 721 TGAATGTTCCAAATATATGTTCTCCCTGGATCCCGAGAAATACCCACTTTCTCAGGATGATA 780
Db 721 TGAATGTTCCAAATATATGTTCTCCCTGGATCCCGAGAAATACCCACTTTCTCAGGATGATA 780
QY 781 TCAATGGATCCAGTCCATCTATGAGGCTGCTCTTAACTGCTAGTACCTAGCCAAAGAAC 840
Db 781 TCAATGGATCCAGTCCATCTATGAGGCTGCTCTTAACTGCTAGTACCTAGCCAAAGAAC 840
QY 841 CCACATATACCCCATGCTGTGACCTGCTGACTTTTCAAGCTATCACACTTTCCGCA 900
Db 841 CCACATATACCCCATGCTGTGACCTGCTGACTTTTCAAGCTATCACACTTTCCGCA 900
QY 901 GAGAAGTAAATGTTCTTTAAAGCAGGACCTATGAGGATCTATTATGATATACCGATG 960
Db 901 GAGAAGTAAATGTTCTTTAAAGCAGGACCTATGAGGATCTATTATGATATACCGATG 960
QY 961 TTGAGTTTGAATTAATGCTTCAATCTGCCATCTCTGCCAGTGTCTGGAAGCTGAT 1020
Db 961 TTGAGTTTGAATTAATGCTTCAATCTGCCATCTCTGCCAGTGTCTGGAAGCTGAT 1020
QY 1021 ACGAGAACCCAGAGATAGATTCTGGTTTAAAGATGAAAACCTTCTGGATGATCAGAG 1080
Db 1021 ACGAGAACCCAGAGATAGATTCTGGTTTAAAGATGAAAACCTTCTGGATGATCAGAG 1080
QY 1081 GATATGCTGTCTTGGCAGATATCCCAATCCATCCATATAGATTTTCCAGGACGTTG 1140
Db 1081 GATATGCTGTCTTGGCAGATATCCCAATCCATCCATATAGATTTTCCAGGACGTTG 1140
QY 1141 TGAAGAAATAGATCGAGCGTCTGTGATGACACACAGAAACCTTCTTTTGG 1200
Db 1141 TGAAGAAATAGATCGAGCGTCTGTGATGACACACAGAAACCTTCTTTTGG 1200
QY 1201 GCATTTGGTGTGGAGGTTTGTATGAAATGACCAACATGACAAAGGATTTCCCGCAGA 1260
Db 1201 GCATTTGGTGTGGAGGTTTGTATGAAATGACCAACATGACAAAGGATTTCCCGCAGA 1260
QY 1261 GAGTGGTAAAAACATTTCTCGAAATCAGTATCCGTTGATGCTGTTTCCAGTACAAG 1320
Db 1261 GAGTGGTAAAAACATTTCTCGAAATCAGTATCCGTTGATGCTGTTTCCAGTACAAG 1320
QY 1321 GATTCTCTTTTTCAGCGTGTGATCAAGCAATTTGAATACAACTTAAGACAAAGATA 1380
Db 1321 GATTCTCTTTTTCAGCGTGTGATCAAGCAATTTGAATACAACTTAAGACAAAGATA 1380
QY 1381 TTACCGGAATCATGAGAACTAATACTTGGTTTCAATGCAAGAACCAAGAACTCCTCAT 1440
Db 1381 TTACCGGAATCATGAGAACTAATACTTGGTTTCAATGCAAGAACCAAGAACTCCTCAT 1440

1381 TTACCGGAATCATGAGAACTAATACTTGGTTTCAATGCAAGAACCAAGAACTCCTCAT 1440
1441 TTGGTTTTGATATCAACAGGAAAAGACATTCAGGAGGCATAAAGATATTGTATCATA 1500
1441 TTGGTTTTGATATCAACAGGAAAAGACATTCAGGAGGCATAAAGATATTGTATCATA 1500
1501 AAGGTTTAAAGCTGTTTATTTTGGTATTTGTTTCATTTGCTGAAAAACACTTCTATTATC 1560
1501 AAGGTTTAAAGCTGTTTATTTTGGTATTTGTTTCATTTGCTGAAAAACACTTCTATTATC 1560
1561 AATAAATTCATAGACCTTAAATAAATCAACAGGCTCTTTTAATATAAATCTGCTTCAA 1620
1561 AATAAATTCATAGACCTTAAATAAATCAACAGGCTCTTTTAATATAAATCTGCTTCAA 1620
1621 AATAGAA 1627
1621 AATAGAA 1627

RESULT 9
ADA76141
ID ADA76141 standard; cDNA; 1647 BP.
XX
AC ADA76141;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human PRO polynucleotide #96.
XX
Human; gene; ss; PRO; secreted polypeptide; TNF-alpha; chondrocyte cell; tumour;
tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;
cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;
liver; microvascular endothelial cell; glucose; FFA;
skeletal muscle cell; adipocyte cell; pericyte cell;
inner ear utricular supporting cell; T-lymphocyte cell;
endothelial cell tube formation; bone disorder; cartilage disorder;
sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
rheumatoid arthritis; haemoglobin-associated disorder thalassemia;
immune system cell infiltration.
XX
OS Homo sapiens.
XX
PN US2003073212-A1.
XX
PD 17-APR-2003.
XX
PF 16-APR-2002; 2002US-00123903.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 10-MAR-1999; 99WO-US005190.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
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PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 30-NOV-1999; 99WO-US028409.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030311.
PR 20-DEC-1999; 99WO-US030399.
PR 22-DEC-1999; 99WO-US030720.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003365.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 24-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUN-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032878.
PR 20-DEC-2000; 2000US-00747259.
PR 28-FEB-2001; 2001US-00796498.
PR 01-MAR-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006566.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 01-JUN-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
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PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.

PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX (GETH ) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-687639/65.
DR P-PSDB; ADA76142.
XX
XX New isolated nucleic acid encoding a secreted and transmembrane
PT polypeptide, designated e.g. PRO1114 or PRO4978, useful in chromosome and
PT gene mapping, in generating antisense RNA and DNA, and in gene therapy.
XX Claim 2; Fig 191; 659pp; English.
XX
XX The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for modulating the uptake of
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC stimulating differentiation of adipocyte cells, for stimulating
CC proliferation of or gene expression in pericyte cells, for stimulating
CC cells, for inducing endothelial cell tube formation and for treating
CC various bone and/or cartilage disorders such as sports injuries and
CC arthritis. PRO polypeptides which stimulate the release of proteoglycans
CC from cartilage are useful for treating sports-related joint problems,
CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
CC polypeptides are also useful for treating various mammalian haemoglobin-
CC associated disorders such as various thalassaemias and conditions which
CC may benefit from enhanced local immune system cell infiltration. This
CC sequence represents a human PRO polynucleotide of the invention. Note:
CC The sequence data for this patent is also available in electronic format
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;

Query Match          99.9%; Score 1625.4; DB 9; Length 1647;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTTTGTCTTTATAA 60
Db 1 GCTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTTTGTCTTTATAA 60

Qy 61 CATTTTCTTCGCAATTTCCCTTAGTCCGGATGACGGAATGAAGAAAATATGCAACTGG 120
Db 61 CATTTTCTTCGCAATTTCCCTTAGTCCGGATGACGGAATGAAGAAAATATGCAACTGG 120

Qy 121 CTCAGGCATATCTCAACAGGTTCTACTCTCTTGAATAGAGGGAATCATCTGTTCTCAA 180
Db 121 CTCAGGCATATCTCAACAGGTTCTACTCTCTTGAATAGAGGGAATCATCTGTTCTCAA 180

Qy 181 GCAAGATAGAGGTTCTCATAGATGACAAAATTCGGGAATTCGGAATCTTTTGGATTGA 240
Db 181 GCAAGATAGAGGTTCTCATAGATGACAAAATTCGGGAATTCGGAATCTTTTGGATTGA 240
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QY 241 CAGTGACTGGAACCTGGACTCAACACACCTTTGAGATCATGAGACACCCAGGTGTGGGG 300
Db 241 CAGTGACTGGAACCTGGACTCAACACACCTTTGAGATCATGAGACACCCAGGTGTGGGG 300
QY 301 TGCCTGATGTGGGCCAGTAGTGGCTACACCCCTCCCTGGGTGGAGAAATACAACTCACCT 360
Db 301 TGCCTGATGTGGGCCAGTAGTGGCTACACCCCTCCCTGGGTGGAGAAATACAACTCACCT 360
QY 361 ACAGAAATAAATATATATCTCCGGATATGGCAGAGCTGCTGTGGATGAGGCTATCCAAG 420
Db 361 ACAGAAATAAATATATATCTCCGGATATGGCAGAGCTGCTGTGGATGAGGCTATCCAAG 420
QY 421 AAGGTTTGAAGTGGGCAAGTCACTCCATATAAATTCACCAAGATTCARAGGGGA 480
Db 421 AAGGTTTGAAGTGGGCAAGTCACTCCATATAAATTCACCAAGATTCARAGGGGA 480
QY 481 TTGCAGACATCATGATTTGCTTTAGGACTCGAGTCCATGGTGGTCTCGCTATTTTG 540
Db 481 TTGCAGACATCATGATTTGCTTTAGGACTCGAGTCCATGGTGGTCTCGCTATTTTG 540
QY 541 ATGGTCCCTTGGGAGTGTGGCCATGCTTCCCTCTGGTCCGGTCTGGGTGGTGACA 600
Db 541 ATGGTCCCTTGGGAGTGTGGCCATGCTTCCCTCTGGTCCGGTCTGGGTGGTGACA 600
QY 601 CTCATTTTCATGAGGATGAATCTGACCAAGATGGAGCAGGATTCAACTTGTTCCTTG 660
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QY 661 TGGCTGCTCATGAATTTGGTCTATGCTACTGGGGCTCTCTCACTCCAATGATCAACAGCCT 720
Db 661 TGGCTGCTCATGAATTTGGTCTATGCTACTGGGGCTCTCTCACTCCAATGATCAACAGCCT 720
QY 721 TGAATGTTCCCAATATATGTTCTCCCTGGATCCAGAAATACCCACATTTCTCAGGATGATA 780
Db 721 TGAATGTTCCCAATATATGTTCTCCCTGGATCCAGAAATACCCACATTTCTCAGGATGATA 780
QY 781 TCAATGGAAATCAGTCCATCTATGAGGCTGCTTAAGGTACTGCTAGCCCAAGGAAAC 840
Db 781 TCAATGGAAATCAGTCCATCTATGAGGCTGCTTAAGGTACTGCTAGCCCAAGGAAAC 840
QY 841 CCACATATACCCATGCTGTGACCTCTGACTTTTGAAGCTATCAAACTTCCGCA 900
Db 841 CCACATATACCCATGCTGTGACCTCTGACTTTTGAAGCTATCAAACTTCCGCA 900
QY 901 GAGAGTAATGTTCTTTAAAGCAGGCACTATGAGGATCTATTATGATATCAAGGATG 960
Db 901 GAGAGTAATGTTCTTTAAAGCAGGCACTATGAGGATCTATTATGATATCAAGGATG 960
QY 961 TTGAGTTTGAAATTAATTTGCTTCAATCTGCGCATCTCTGCGAGTCTGCAAGCTGCAT 1020
Db 961 TTGAGTTTGAAATTAATTTGCTTCAATCTGCGCATCTCTGCGAGTCTGCAAGCTGCAT 1020
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Db 1021 ACGAGAACCCAGAGATAAGATTCTGGTTTAAAGATGAAACTTCTGGATGATCAGAG 1080
QY 1081 GATATGCTGCTTTGCGAGATTTCCAAATTCATTCATCATTTAGGTTTTCAGGACGTTG 1140
Db 1081 GATATGCTGCTTTGCGAGATTTCCAAATTCATTCATCATTTAGGTTTTCAGGACGTTG 1140
QY 1141 TGAAGAAATATAGATGACGCGCTGTGTGATAAGACCAAGAAACCTACTTCTTTGTCG 1200
Db 1141 TGAAGAAATATAGATGACGCGCTGTGTGATAAGACCAAGAAACCTACTTCTTTGTCG 1200
QY 1201 GCATTTGGTGTGGAGTTTGTATGAATGACCCAAACCTGACAAAGGATTCCTGCGACA 1260
Db 1201 GCATTTGGTGTGGAGTTTGTATGAATGACCCAAACCTGACAAAGGATTCCTGCGACA 1260
QY 1261 GAGTGTGTAACACATTTCTCGAAATCAGTATCCGTTGATGCTGTTTCCAGTACAAAG 1320
Db 1261 GAGTGTGTAACACATTTCTCGAAATCAGTATCCGTTGATGCTGTTTCCAGTACAAAG 1320
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QY 1321 GATTCTCTCTTTTTCAGCCGTGGATCAAGCAATTTGAATACACATTTAAGACAAAGAATA 1380
Db 1321 GATTCTCTCTTTTTCAGCCGTGGATCAAGCAATTTGAATACACATTTAAGACAAAGAATA 1380
QY 1381 TTACCCGGAATCATGAGAACTAATACTTGGTTTCAATGCAAAAGAACCAAGAACTCTCTCAT 1440
Db 1381 TTACCCGGAATCATGAGAACTAATACTTGGTTTCAATGCAAAAGAACCAAGAACTCTCTCAT 1440
QY 1441 TTGGTTTTGATATCAACAAAGGAAAGACATTCAGGAGGCAATAAGATATTGTATATA 1500
Db 1441 TTGGTTTTGATATCAACAAAGGAAAGACATTCAGGAGGCAATAAGATATTGTATATA 1500
QY 1501 AGAGTTTAAAGCTTGTATTTTGGTTATTTGTTCAATTTGCTGAAACACCTTCTATTATTC 1560
Db 1501 AGAGTTTAAAGCTTGTATTTTGGTTATTTGTTCAATTTGCTGAAACACCTTCTATTATTC 1560
QY 1561 AATAAATTCATAGACCTTAAATAAACCTCAACAGAGTCTTTTAAATATAAATTTCTGCTTCAA 1620
Db 1561 AATAAATTCATAGACCTTAAATAAACCTCAACAGAGTCTTTTAAATATAAATTTCTGCTTCAA 1620
QY 1621 AATAGAA 1627
Db 1621 AATAGAA 1627

RESULT 10
ADA18791
ID ADA18791 standard; cDNA; 1647 BP.
XX
AC ADA18791;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human PRO polynucleotide #96.
XX
KW Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
tumour necrosis factor-alpha; TNF-alpha; blood; chondrocyte cell; lung;
colon; breast; prostate; rectum; cervix; liver; tumour; cancer;
glucose uptake; FFA; adipocyte cell; pericyte cell; proteoglycan;
cartilage; inner ear utricular supporting cell; cytokine; A-peptide;
factor VIIA; endothelial cell.
XX
OS Homo sapiens.
XX
PN US2003054517-A1.
XX
PD 20-MAR-2003.
XX
PF 08-MAY-2002; 2002US-00141755.
XX
PR 31-MAR-1997; 97WO-US005230.
PR 12-JUN-1998; 98WO-US012456.
PR 14-JUL-1998; 98WO-US014552.
PR 28-AUG-1998; 98WO-US017888.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019093.
PR 14-SEP-1998; 98WO-US019094.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 29-OCT-1998; 98WO-US022991.
PR 29-OCT-1998; 98WO-US022992.
PR 20-NOV-1998; 98WO-US024855.
PR 01-DEC-1998; 98WO-US025108.
PR 08-MAR-1999; 99WO-US000106.
PR 10-MAR-1999; 99WO-US005028.
PR 20-APR-1999; 99WO-US008615.
PR 14-MAY-1999; 99WO-US010733.
PR 02-JUN-1999; 99WO-US012252.
PR 01-SEP-1999; 99WO-US020111.
PR 08-SEP-1999; 99WO-US020594.
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PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 05-OCT-1999; 99WO-US023089.  
PR 29-NOV-1999; 99WO-US028214.  
PR 30-NOV-1999; 99WO-US028313.  
PR 30-NOV-1999; 99WO-US028409.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 02-DEC-1999; 99WO-US028551.  
PR 02-DEC-1999; 99WO-US028564.  
PR 02-DEC-1999; 99WO-US028565.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030311.  
PR 20-DEC-1999; 99WO-US030399.  
PR 22-DEC-1999; 99WO-US030720.  
PR 30-DEC-1999; 99WO-US031243.  
PR 30-DEC-1999; 99WO-US031274.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000277.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 18-FEB-2000; 2000WO-US004342.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 01-MAR-2000; 2000WO-US005601.  
PR 02-MAR-2000; 2000WO-US005746.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006684.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 21-MAR-2000; 2000WO-US007532.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUN-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 08-NOV-2000; 2000WO-US023328.  
PR 10-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US030873.  
PR 20-DEC-2000; 2000WO-US032678.  
PR 20-DEC-2000; 2000US-00747259.  
PR 28-FEB-2001; 2000WO-US034956.  
PR 28-FEB-2001; 2001US-00796498.  
PR 01-MAR-2001; 2001WO-US0006520.  
PR 01-MAR-2001; 2001WO-US006666.  
PR 09-MAR-2001; 2001US-00802706.  
PR 14-MAR-2001; 2001US-00808689.  
PR 22-MAR-2001; 2001US-00816744.  
PR 05-APR-2001; 2001US-00828366.  
PR 10-MAY-2001; 2001US-00854208.  
PR 18-MAY-2001; 2001US-00860216.  
PR 25-MAY-2001; 2001US-00866028.  
PR 25-MAY-2001; 2001US-00866034.  
PR 25-MAY-2001; 2001WO-US017092.  
PR 01-JUN-2001; 2001US-00872035.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 05-JUN-2001; 2001US-00874503.  
PR 14-JUN-2001; 2001US-00882636.  
PR 19-JUN-2001; 2001US-00886342.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 21-JUN-2001; 2001US-00887879.  
PR 22-JUN-2001; 2001WO-US020116.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 18-JUL-2001; 2001US-00908827.  
PR 06-AUG-2001; 2001US-00924419.

PR 09-AUG-2001; 2001US-00927796.  
PR 16-AUG-2001; 2001US-00931836.  
PR 19-DEC-2001; 2001US-00028072.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX  
XX WPI; 2003-521854/49.  
DR P-PSDB; ADA18792.  
XX  
XX New PRO nucleic acid, useful for preparing a composition for treating  
PT e.g., tumors.  
XX  
XX Claim 2; Fig 191; 660pp; English.  
XX  
XX The invention relates to isolated human PRO polypeptides (secreted and  
CC transmembrane polypeptides) and the polynucleotides encoding them. The  
CC invention also relates to an antibody which specifically binds to a PRO  
CC polypeptide, a method for stimulating the release of tumour necrosis  
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the  
CC proliferation or differentiation of chondrocyte cells and a method for  
CC detecting the presence of a tumour in a mammal (e.g. lung, colon, breast,  
CC prostate, rectal, cervical and liver tumours). The polynucleotides are  
CC useful in molecular biology, including uses as hybridisation probes, in  
CC chromosome and gene mapping, in generating antisense RNA and DNA and in  
CC gene therapy. The polynucleotides may also be used in preparing PRO  
CC polypeptides by recombinant techniques and in generating either  
CC transgenic animals or knock-out animals which are useful in the  
CC development and screening of therapeutically useful reagents. The PRO  
CC polypeptides or antibodies are used in preparing a medicament for  
CC treating a condition responsive to the polypeptides or antibodies, such  
CC as tumours, for modulating the uptake of glucose or FFA by adipocyte  
CC cells, for stimulating the proliferation of or gene expression in  
CC pericyte cells, for stimulating the release of proteoglycans from  
CC cartilage, for stimulating the proliferation of inner ear utricular  
CC supporting cells, for stimulating the release of cytokines from PMMC  
CC cells, for inhibiting the binding of A-peptide to factor VIIA, for  
CC inhibiting the differentiation of adipocyte cells and for stimulating the  
CC proliferation of endothelial cells. This sequence represents a human PRO  
CC polynucleotide of the invention. Note: The sequence data for this patent  
CC is also available in electronic format from USPTO at  
CC seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;  
Query Match 99.9%; Score 1625.4; DB 9; Length 1647;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 GCTTCAGCTGAAGAAGAGAGAGGAATGAAGCGCCTCTGCTTCTGTGTGTTGTTCTTTATAA 60  
Db 1 GCTTCAGCTGAAGAAGAGAGAGGAATGAAGCGCCTCTGCTTCTGTGTGTTGTTCTTTATAA 60  
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Qy 241 CAGTGACTGGAAAACTGGACTCAACACCTCTGAGATCATGACACACCCAGGTTGGGG 300  
Db 241 CAGTGACTGGAAAACCTGGACTCAACACCTCTGAGATCATGACACACCCAGGTTGGGG 300  
Qy 301 TGCCGTGATGGGCCAGTATGGGTACACCTTCCTGGGTGGAGAAAATACAACTCACT 360

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301 TGCCTGATGGCGAGTATGGCTACACCTCCCTGGGTGGGAAATACAACTCACT 360  
QY  
361 ACAGATAATAAATCTACTCCGATATGGCAGCGAGCTGCTGTGGATGAGCTATCCAA 420  
Db  
361 ACAGATAATAAATCTACTCCGATATGGCAGCGAGCTGCTGTGGATGAGCTATCCAA 420  
QY  
421 AAGGTTTAAAGTGTGGAGCAAGTCACTCCACTTAAATTCACCAAGATTTCAAGGGGA 480  
Db  
421 AAGGTTTAAAGTGTGGAGCAAGTCACTCCACTTAAATTCACCAAGATTTCAAGGGGA 480  
QY  
481 TTGAGACATCATGATTCCTTTAGGACTCCAGTCCATGGTCCGTTGCTCGCTATTTTG 540  
Db  
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QY  
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601 CTCATTTTGATGAGATGAATACTGGACCAAGGATGGAGCAGGATTCAACTGTTCTTG 660  
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661 TGGCTGCTCATGAATTTGGTCATGCACTGGGCTCTCTCACTCCCAATGATCAACAGCCT 720  
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661 TGGCTGCTCATGAATTTGGTCATGCACTGGGCTCTCTCACTCCCAATGATCAACAGCCT 720  
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841 CCACATATACCCATCCCTGTGACCTCTGACCTTTTGACGCTATCAAACTTTCCGCA 900  
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QY  
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Db  
1141 TGAAGAAATAGATGACGCGCTGTGATAAGACACACAGAAACCTACTTTCTTTGG 1200  
QY  
1201 GCATTTGGTGTGGAGTTTGTATGAAATGACCAACCATGACAAAGGATTTCCGCGAGA 1260  
Db  
1201 GCATTTGGTGTGGAGTTTGTATGAAATGACCAACCATGACAAAGGATTTCCGCGAGA 1260  
QY  
1261 GAGTGGTAAACACTTTCTCGAAATCAGTATCCGTTGATGCTGTTTCCAGTACAAG 1320  
Db  
1261 GAGTGGTAAACACTTTCTCGAAATCAGTATCCGTTGATGCTGTTTCCAGTACAAG 1320  
QY  
1321 GATTCCTCTTTTACGCGGTGATCAAGCAATTTGAATACAAATTAAGAACAAGATA 1380  
Db  
1321 GATTCCTCTTTTACGCGGTGATCAAGCAATTTGAATACAAATTAAGAACAAGATA 1380  
QY  
1381 TTACCCGAATCATGAGAACTAATCTGTTTCAATGCAAGAACCAAGAACTCTCTCAT 1440  
|||||

1381 TTACCCGAATCATGAGAACTAATCTGTTTCAATGCAAGAACCAAGAACTCTCTCAT 1440  
QY  
1441 TTGTTTTGATATCAACAGGAAAAAGCACATTCAGGAGGATTAAGATATTTGATCAT 1500  
Db  
1441 TTGTTTTGATATCAACAGGAAAAAGCACATTCAGGAGGATTAAGATATTTGATCAT 1500  
QY  
1501 AGAGTTTAAAGTGTGTTTATTTTGGTATTTGTTTCATTTGCTGAAAAACACTTCTATTATC 1560  
Db  
1501 AGAGTTTAAAGTGTGTTTATTTTGGTATTTGTTTCATTTGCTGAAAAACACTTCTATTATC 1560  
QY  
1561 AATAAATTCATAGACCTAAAAATAAACCTCAACAGTCTTTTAAATAAATTCGTTCAA 1620  
Db  
1561 AATAAATTCATAGACCTAAAAATAAACCTCAACAGTCTTTTAAATAAATTCGTTCAA 1620  
QY  
1621 AATAGAA 1627  
Db  
1621 AATAGAA 1627  
RESULT 11  
ADA61414  
ID ADA61414 standard; cDNA; 1647 BP.  
XX  
AC ADA61414;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Homo sapiens.  
XX  
KW Human; secreted and transmembrane protein; PRO; gene; ss;  
KW Tumour necrosis factor alpha release; TNF-alpha release;  
KW glucose uptake modulator; PFA uptake modulator;  
KW cell proliferation stimulator; cell differentiation stimulator;  
KW lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;  
KW cervical tumour; liver tumour; chromosome mapping; gene mapping;  
KW gene therapy; chromosome identification; chromosome marker.  
XX  
OS Novel.  
OS human.  
OS secreted.  
OS and.  
OS transmembrane.  
OS protein.  
OS PRO5992.  
OS cDNA.  
XX  
US2003049816-A1.  
PN  
XX  
PD 13-MAR-2003.  
XX  
PF 15-APR-2002; 2002US-00123262.  
XX  
PR 31-MAR-1997; 97WO-US005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.





Db 241 CAGTGACTGAAAACCTGGACTCAACACCCCTTGAGATCATGAAGACACCCAGGTGTGGG 300  
Qy 301 TGCCCTGATGGGCGAGTATGGCTACACCCCTCCCTGGGTGGAGAAAATAACAACCTCACCT 360  
Db 301 TGCCCTGATGGGCGAGTATGGCTACACCCCTCCCTGGGTGGAGAAAATAACAACCTCACCT 360  
Qy 361 ACAGAAATAAATATCTACTCCGATATGGACAGCTGCTGTGGATGAGGCTATCCAAG 420  
Db 361 ACAGAAATAAATATCTACTCCGATATGGACAGCTGCTGTGGATGAGGCTATCCAAG 420  
Qy 421 AAGGTTTAGAAGTGTGGAGCAAGTCACTCCACTAAATTCACCAAGATTTCAAGGGGA 480  
Db 421 AAGGTTTAGAAGTGTGGAGCAAGTCACTCCACTAAATTCACCAAGATTTCAAGGGGA 480  
Qy 481 TTGCAGACATCATGATTCGCTTTAGGACTCGAGTCCATGGTCCGCTCGCTGCTATTTTG 540  
Db 481 TTGCAGACATCATGATTCGCTTTAGGACTCGAGTCCATGGTCCGCTCGCTGCTATTTTG 540  
Qy 541 ATGGTCCCTTGGGAGTGTGGCCATGGCTTCCCTGCTGGTCCGGTCTGGGTGGTGACA 600  
Db 541 ATGGTCCCTTGGGAGTGTGGCCATGGCTTCCCTGCTGGTCCGGTCTGGGTGGTGACA 600  
Qy 601 CTCATTTTGATGAGGATGAAAACCTGGACCAAGGATGGAGCAGGATTCAACTTTGTTCTTG 660  
Db 601 CTCATTTTGATGAGGATGAAAACCTGGACCAAGGATGGAGCAGGATTCAACTTTGTTCTTG 660  
Qy 661 TGGCTGCTCATGAATTTGGTCAATGCACTGGGGCTCTCTCACTCCAAATGATCAAAACAGCT 720  
Db 661 TGGCTGCTCATGAATTTGGTCAATGCACTGGGGCTCTCTCACTCCAAATGATCAAAACAGCT 720  
Qy 721 TGATGTTCCCAATATGCTCCCTGGATCCAGAAATACCCACTTTCAGAGATGATA 780  
Db 721 TGATGTTCCCAATATGCTCCCTGGATCCAGAAATACCCACTTTCAGAGATGATA 780  
Qy 781 TCAATGGAATCCAGTCCATCTATGGAGTCTGCCTTAAGTACCTGCTAAGCAAGCAAGAAC 840  
Db 781 TCAATGGAATCCAGTCCATCTATGGAGTCTGCCTTAAGTACCTGCTAAGCAAGCAAGAAC 840  
Qy 841 CCATATACCCCATGCTGAGCCTGACTTTGAGCGCTATCAAACTTTCCGCA 900  
Db 841 CCATATACCCCATGCTGAGCCTGACTTTGAGCGCTATCAAACTTTCCGCA 900  
Qy 901 GAGAGTAAATGCTTTAAAGCGGACGACCTATGGAGATCTATATGATATCAAGGATG 960  
Db 901 GAGAGTAAATGCTTTAAAGCGGACGACCTATGGAGATCTATATGATATCAAGGATG 960  
Qy 961 TTGAGTTTGAATTAATTCCTTCATTCGCGCATCTCTGCCAGCTGATCGCAAGCTGCAT 1020  
Db 961 TTGAGTTTGAATTAATTCCTTCATTCGCGCATCTCTGCCAGCTGATCGCAAGCTGCAT 1020  
Qy 1021 ACAGAAACCCAGAGATAAGATTTCTGGTTTTTAAAGATGAAAACCTTCTGGATGATCAGAG 1080  
Db 1021 ACAGAAACCCAGAGATAAGATTTCTGGTTTTTAAAGATGAAAACCTTCTGGATGATCAGAG 1080  
Qy 1081 GATATGCTGCTTCCAGATATCCCAATCCATCCATACATAGGTTTTCCAGAGCTG 1140  
Db 1081 GATATGCTGCTTCCAGATATCCCAATCCATCCATACATAGGTTTTCCAGAGCTG 1140  
Qy 1141 TGAAGAAATAGATGACGCGCTGCTGTATGATGATGATGATGATGATGATGATGATGATG 1200  
Db 1141 TGAAGAAATAGATGACGCGCTGCTGTATGATGATGATGATGATGATGATGATGATGATG 1200  
Qy 1201 GCATTTGGTGTGGAGTTTGTATGAAATGACCCAAACCATGGACAAAGGATTCGCCGAGA 1260  
Db 1201 GCATTTGGTGTGGAGTTTGTATGAAATGACCCAAACCATGGACAAAGGATTCGCCGAGA 1260  
Qy 1261 GAGTGGTAAACACATTTCTGGAATCAGTATCCGTTGATGCTGCTTCCAGTACAAG 1320  
Db 1261 GAGTGGTAAACACATTTCTGGAATCAGTATCCGTTGATGCTGCTTCCAGTACAAG 1320  
Qy 1321 GATTCCTCTTTTTCAGCGGTGATCAAGAGCAATTTGAATACAACTTAAGACAAAGAATA 1380

Db 1321 GATTCCTCTTTTTCAGCGGTGATCAAGCAATTTGAATACAACTTAAGACAAAGAATA 1380  
Qy 1381 TTACCCGAATCATGAGAACTAATACTTTGGTTTCAATGCAAGAACCAAGAACTCCTCAT 1440  
Db 1381 TTACCCGAATCATGAGAACTAATACTTTGGTTTCAATGCAAGAACCAAGAACTCCTCAT 1440  
Qy 1441 TTGGTTTGTATATCAACAAGGAAAAGCAATTCAGGAGGCATAAAGATATTGTATCATA 1500  
Db 1441 TTGGTTTGTATATCAACAAGGAAAAGCAATTCAGGAGGCATAAAGATATTGTATCATA 1500  
Qy 1501 AGAGTTTAAAGCTTTTATTTTGGTATGTTCAATTTGCTGAAAAACACTTCTATTATTC 1560  
Db 1501 AGAGTTTAAAGCTTTTATTTTGGTATGTTCAATTTGCTGAAAAACACTTCTATTATTC 1560  
Qy 1561 AATAAATTCATAGACCTTAAATTAACCTCAACAGTCTTTTAAATATAAATTCGCTTCAA 1620  
Db 1561 AATAAATTCATAGACCTTAAATTAACCTCAACAGTCTTTTAAATATAAATTCGCTTCAA 1620  
Qy 1621 AATAAGAA 1627  
Db 1621 AATAAGAA 1627

RESULT 12  
ADBI9199  
ID ADBI9199 standard; cDNA; 1647 BP.  
XX ADBI9199;  
XX 20-NOV-2003 (first entry)  
XX Novel human secreted and transmembrane protein PRO5992 cDNA.  
XX Human; secreted and transmembrane protein; PRO; gene; ss;  
KW Tumour necrosis factor alpha release; TNF-alpha release;  
KW glucose uptake modulator; FFA uptake modulator;  
KW cell proliferation stimulator; cell differentiation stimulator;  
KW cell differentiation inhibitor; cytokin.  
XX Homo sapiens.  
XX US2003068796-A1.  
XX 10-APR-2003.  
XX 15-APR-2002; 2002US-00123261.  
XX 31-MAR-1997; 97WO-US005230.  
PR 12-JUN-1998; 98WO-US012456.  
PR 14-JUL-1998; 98WO-US014552.  
PR 28-AUG-1998; 98WO-US017888.  
PR 10-SEP-1998; 98WO-US018824.  
PR 14-SEP-1998; 98WO-US019093.  
PR 14-SEP-1998; 98WO-US019094.  
PR 14-SEP-1998; 98WO-US019177.  
PR 16-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 29-OCT-1998; 98WO-US022991.  
PR 29-OCT-1998; 98WO-US022992.  
PR 20-NOV-1998; 98WO-US024855.  
PR 01-DEC-1998; 98WO-US025108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 10-MAR-1999; 99WO-US005190.  
PR 20-APR-1999; 99WO-US008615.  
PR 14-MAY-1999; 99WO-US010733.  
PR 02-JUN-1999; 99WO-US012352.  
PR 01-SEP-1999; 99WO-US020111.  
PR 08-SEP-1999; 99WO-US020594.  
PR 13-SEP-1999; 99WO-US020944.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.

|    |              |                  |    |                                                                          |
|----|--------------|------------------|----|--------------------------------------------------------------------------|
| PR | 05-OCT-1999; | 99WO-US023089.   | XX | (GETH ) GENENTECH INC.                                                   |
| PR | 29-NOV-1999; | 99WO-US028214.   | PA |                                                                          |
| PR | 30-NOV-1999; | 99WO-US028313.   | XX |                                                                          |
| PR | 30-NOV-1999; | 99WO-US028409.   | PI | Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;        |
| PR | 01-DEC-1999; | 99WO-US028301.   | PI | Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;             |
| PR | 01-DEC-1999; | 99WO-US028634.   | PI | Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;             |
| PR | 02-DEC-1999; | 99WO-US028551.   | XX |                                                                          |
| PR | 02-DEC-1999; | 99WO-US028564.   | DR | WPI; 2003-695927/66.                                                     |
| PR | 02-DEC-1999; | 99WO-US028565.   | DR | P-PSDB; ADB19200.                                                        |
| PR | 16-DEC-1999; | 99WO-US030095.   | XX |                                                                          |
| PR | 20-DEC-1999; | 99WO-US030911.   | PT | Novel secreted and transmembrane PRO polypeptides useful for stimulating |
| PR | 20-DEC-1999; | 99WO-US030999.   | PT | the release of tumor necrosis factor alpha and detecting the presence of |
| PR | 22-DEC-1999; | 99WO-US030720.   | PT | a tumor in a mammal.                                                     |
| PR | 30-DEC-1999; | 99WO-US031243.   | XX |                                                                          |
| PR | 30-DEC-1999; | 99WO-US031274.   | XX | Claim 2; Fig 191; 660pp; English.                                        |
| PR | 05-JAN-2000; | 2000WO-US000219. | XX |                                                                          |
| PR | 06-JAN-2000; | 2000WO-US000277. | CC | The invention describes 305 nucleic acids encoding PRO (secreted and     |
| PR | 06-JAN-2000; | 2000WO-US000376. | CC | transmembrane) polypeptides (I). (I) is useful for stimulating the       |
| PR | 11-FEB-2000; | 2000WO-US003565. | CC | release of TNF-alpha from human blood, for modulating the uptake of      |
| PR | 18-FEB-2000; | 2000WO-US004341. | CC | glucose or FFA by skeletal muscle cells or adipocyt                      |
| PR | 18-FEB-2000; | 2000WO-US004342. | XX |                                                                          |
| PR | 22-FEB-2000; | 2000WO-US004414. | SQ | Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;              |
| PR | 24-FEB-2000; | 2000WO-US004914. |    |                                                                          |
| PR | 24-FEB-2000; | 2000WO-US005004. |    | Query Match 99.9%; Score 1625.4; DB 9; Length 1647;                      |
| PR | 01-MAR-2000; | 2000WO-US005601. |    | Best Local Similarity 99.9%; Pred. No. 0;                                |
| PR | 02-MAR-2000; | 2000WO-US005746. |    | Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;            |
| PR | 02-MAR-2000; | 2000WO-US005841. |    |                                                                          |
| PR | 10-MAR-2000; | 2000WO-US006319. | QY | 1 GCTTCAGCTGAAGAAAGAGAGAGAAATGAAGCGCTTCTGTTCTGTTGTTGTTTATATAA 60         |
| PR | 15-MAR-2000; | 2000WO-US006884. | Db | 1 GCTTCAGCTGAAGAAAGAGAGAAATGAAGCGCTTCTGTTCTGTTGTTTATATAA 60              |
| PR | 20-MAR-2000; | 2000WO-US007377. |    |                                                                          |
| PR | 21-MAR-2000; | 2000WO-US007532. | QY | 61 CATTTTCTTCGATTTCCTTAGTCGGATGAGGAAATGAGGAAATGAGGAAATGCAACTGG 120       |
| PR | 30-MAR-2000; | 2000WO-US008439. | Db | 61 CATTTTCTTCGATTTCCTTAGTCGGATGAGGAAATGAGGAAATGAGGAAATGCAACTGG 120       |
| PR | 17-MAY-2000; | 2000WO-US013705. | QY | 121 CTCAGGCATATCTCAACCAAGTTCTACTCTCTTGAATAGAGGGAATCATCTTGTTCAAA 180      |
| PR | 22-MAY-2000; | 2000WO-US014042. | Db | 121 CTCAGGCATATCTCAACCAAGTTCTACTCTTCTTGAATAGAGGGAATCATCTTGTTCAAA 180     |
| PR | 02-JUN-2000; | 2000WO-US015264. | QY | 181 GCAAGAAATAGGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTGGATTGA 240      |
| PR | 28-JUL-2000; | 2000WO-US020710. | Db | 181 GCAAGAAATAGGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTGGATTGA 240      |
| PR | 11-AUG-2000; | 2000WO-US022031. | QY | 241 CAGTGACTGGAAGAACTGGAGTCAACACCCCTTGAGTATGAGATCAAGACACCCAGGTGGGG 300   |
| PR | 23-AUG-2000; | 2000WO-US023328. | Db | 241 CAGTGACTGGAAGAACTGGAGTCAACACCCCTTGAGTATGAGATCAAGACACCCAGGTGGGG 300   |
| PR | 08-NOV-2000; | 2000WO-US030952. | QY | 301 TGCCTGATGTGGGCCAGTATGGCTACACCCCTCCCTGGGTGGAGAAATAACAACCTCACCT 360    |
| PR | 10-NOV-2000; | 2000WO-US030873. | Db | 301 TGCCTGATGTGGGCCAGTATGGCTACACCCCTCCCTGGGTGGAGAAATAACAACCTCACCT 360    |
| PR | 01-DEC-2000; | 2000WO-US032678. | QY | 361 ACAGAATAATAACTATATCTCCGGATATGGCAGAGCTGCTGTGGATGAGGCTATCCAAG 420      |
| PR | 20-DEC-2000; | 2000US-00747259. | Db | 361 ACAGAATAATAACTATATCTCCGGATATGGCAGAGCTGCTGTGGATGAGGCTATCCAAG 420      |
| PR | 28-DEC-2000; | 2000WO-US034956. | QY | 421 AAGGTTTACAAGTGTGGAGCAAGTCACTCCATTAATTTCCACCAAGATTTCAAGGGGA 480       |
| PR | 28-FEB-2001; | 2001US-00796498. | Db | 421 AAGGTTTACAAGTGTGGAGCAAGTCACTCCATTAATTTCCACCAAGATTTCAAGGGGA 480       |
| PR | 01-MAR-2001; | 2001WO-US006520. | QY | 481 TTGCGACATCATGATTTGCTTTTAGGACTCGAGTCCATGCTCGGTCTCGGTATTTTGG 540       |
| PR | 09-MAR-2001; | 2001US-00806666. | Db | 481 TTGCGACATCATGATTTGCTTTTAGGACTCGAGTCCATGCTCGGTCTCGGTATTTTGG 540       |
| PR | 14-MAR-2001; | 2001US-00808689. | QY | 541 ATGGTCCCTTGGGAGTGTGGCCATGCTTTTCTGCTCGGTCTCGGTCTCGGTGTTGACA 600       |
| PR | 22-MAR-2001; | 2001US-00815744. | Db | 541 ATGGTCCCTTGGGAGTGTGGCCATGCTTTTCTGCTCGGTCTCGGTCTCGGTGTTGACA 600       |
| PR | 05-APR-2001; | 2001US-00828366. | QY | 601 CTCATTTTCATGAGGATGAAACTGGACCAAGATGGAGCAGGATTCACATTTGTTCTTG 660       |
| PR | 10-MAY-2001; | 2001US-00854208. | Db | 601 CTCATTTTCATGAGGATGAAACTGGACCAAGATGGAGCAGGATTCACATTTGTTCTTG 660       |
| PR | 10-MAY-2001; | 2001US-00854280. | QY | 661 TGGCTGCTCATGAAATTTGTCATGCACTGGGCTCTCTCACTCCAAATGATCAAAACGCCT 720     |
| PR | 18-MAY-2001; | 2001US-00860216. | Db |                                                                          |
| PR | 25-MAY-2001; | 2001US-00866028. |    |                                                                          |
| PR | 25-MAY-2001; | 2001US-00866034. |    |                                                                          |
| PR | 25-MAY-2001; | 2001WO-US017092. |    |                                                                          |
| PR | 01-JUN-2001; | 2001US-00872035. |    |                                                                          |
| PR | 01-JUN-2001; | 2001WO-US017800. |    |                                                                          |
| PR | 05-JUN-2001; | 2001US-00874503. |    |                                                                          |
| PR | 14-JUN-2001; | 2001US-00882636. |    |                                                                          |
| PR | 19-JUN-2001; | 2001US-00886342. |    |                                                                          |
| PR | 20-JUN-2001; | 2001WO-US019692. |    |                                                                          |
| PR | 21-JUN-2001; | 2001US-00887879. |    |                                                                          |
| PR | 22-JUN-2001; | 2001WO-US020116. |    |                                                                          |
| PR | 29-JUN-2001; | 2001WO-US021066. |    |                                                                          |
| PR | 09-JUL-2001; | 2001WO-US021735. |    |                                                                          |
| PR | 18-JUL-2001; | 2001US-00908827. |    |                                                                          |
| PR | 06-AUG-2001; | 2001US-00924419. |    |                                                                          |
| PR | 09-AUG-2001; | 2001US-00927796. |    |                                                                          |
| PR | 16-AUG-2001; | 2001US-00931836. |    |                                                                          |
| PR | 19-DEC-2001; | 2001US-00028072. |    |                                                                          |

Db 661 TGGCTGCTCATGAATTTGGTTCATGCACTGGGGCTCTCTCACTCCAAATGATCAAAACAGCCT 720  
Qy 721 TGATGTTCCCAAATATGCTCTCCCTGGATCCAGAAAATATCCCACTTCTCAGATGATA 780  
Db 721 TGATGTTCCCAAATATGCTCTCCCTGGATCCAGAAAATATCCCACTTCTCAGATGATA 780  
Qy 781 TCAATGGAATCCAGTCCATCTATGAGGCTCTGCTTAAGTACCTGCTAAGCCAAAGGAAC 840  
Db 781 TCAATGGAATCCAGTCCATCTATGAGGCTCTGCTTAAGTACCTGCTAAGCCAAAGGAAC 840  
Qy 841 CCACATATACCCCATGCTGTCGACCTGATGCTGCTTTTGAAGCTATACAACTTTCGCGA 900  
Db 841 CCACATATACCCCATGCTGTCGACCTGATGCTGCTTTTGAAGCTATACAACTTTCGCGA 900  
Qy 901 GAGAAGTAATGCTTTTAAAGCCAGGCACCTATGAGGATCTATATGATATCAGGATG 960  
Db 901 GAGAAGTAATGCTTTTAAAGCCAGGCACCTATGAGGATCTATATGATATCAGGATG 960  
Qy 961 TTGAGTTTGAATTAATTTGCTTTCATTTCTGCCCATCTCTGCCAGCTGATCGCAAGCTGCAT 1020  
Db 961 TTGAGTTTGAATTAATTTGCTTTCATTTCTGCCCATCTCTGCCAGCTGATCGCAAGCTGCAT 1020  
Qy 1021 ACGAGAACCCAGAGATAAGATTTCTGGTTTTTAAAGATGAAACCTTCTGGATGATCAGAG 1080  
Db 1021 ACGAGAACCCAGAGATAAGATTTCTGGTTTTTAAAGATGAAACCTTCTGGATGATCAGAG 1080  
Qy 1081 GATATGCTGCTTGGCAGATATCCCAATCCATCCATACATAGTGTTCAGGACCTG 1140  
Db 1081 GATATGCTGCTTGGCAGATATCCCAATCCATCCATACATAGTGTTCAGGACCTG 1140  
Qy 1141 TGAAGAAAATAGATGACCGCTGTGTGATGACACACAAAGAAAACCTTCTTTTGG 1200  
Db 1141 TGAAGAAAATAGATGACCGCTGTGTGATGACACACAAAGAAAACCTTCTTTTGG 1200  
Qy 1201 GCATTTGGTGTGGAGSTTTGATGAAATGACCCAAACCATGACAAAGGATTCGCGAGA 1260  
Db 1201 GCATTTGGTGTGGAGSTTTGATGAAATGACCCAAACCATGACAAAGGATTCGCGAGA 1260  
Qy 1261 GAGTGGTAAACACATTTCTCTGGAATCAGTATCCGTTGTGATGCTGCTTTCAGTACAAG 1320  
Db 1261 GAGTGGTAAACACATTTCTCTGGAATCAGTATCCGTTGTGATGCTGCTTTCAGTACAAG 1320  
Qy 1321 GATTTCTTTTTCAGCGCTGATCAAAAGCAATTTGAATCAACATTAAGACAAAGAATA 1380  
Db 1321 GATTTCTTTTTCAGCGCTGATCAAAAGCAATTTGAATCAACATTAAGACAAAGAATA 1380  
Qy 1381 TTACCCGAATCATGAGAACTAATCTTGGTTTCAATGCAAAAGAACCCAAAGAACTCTCAT 1440  
Db 1381 TTACCCGAATCATGAGAACTAATCTTGGTTTCAATGCAAAAGAACCCAAAGAACTCTCAT 1440  
Qy 1441 TTGGTTTGTATATCAACAGGAAAGCACATTCAGGAGGATTAAGATATTGTATCATATA 1500  
Db 1441 TTGGTTTGTATATCAACAGGAAAGCACATTCAGGAGGATTAAGATATTGTATCATATA 1500  
Qy 1501 AGAGTTTAAAGCTGTTTATTTTGTATGTTTCAATTTGCTGAAAAACCTTCTATTATC 1560  
Db 1501 AGAGTTTAAAGCTGTTTATTTTGTATGTTTCAATTTGCTGAAAAACCTTCTATTATC 1560  
Qy 1561 AATAAATTCATAGACCTAAAAATAAACCTCAACAGCTCTTTTAATAATAAATTCGCTTCAA 1620  
Db 1561 AATAAATTCATAGACCTAAAAATAAACCTCAACAGCTCTTTTAATAATAAATTCGCTTCAA 1620  
Qy 1621 AATAGAA 1627  
Db 1621 AATAGAA 1627

RESULT 13

ADB27740

ID ADB27740 standard; cDNA; 1647 BP.

XX

AC

ADB27740;

XX

20-NOV-2003 (first entry)  
cDNA encoding human PRO polypeptide #96.  
Human; gene; ss; PRO; secreted polypeptide; transmembrane polypeptide; tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour; cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix; liver; microvascular endothelial cell; glucose; FFA; skeletal muscle cell; adipocyte cell; pericyte cell; inner ear utricular supporting cell; T-lymphocyte cell; endothelial cell tube formation; bone disorder; cartilage disorder; sports injury; proteoglycan; articular cartilage defect; osteoarthritis; rheumatoid arthritis; haemoglobin-associated disorder thalassaemia; immune system cell infiltration.  
Homo sapiens.  
US2003082704-A1.  
01-MAY-2003.  
24-APR-2002; 2002US-00131819.  
09-DEC-1999; 99US-0170262P.  
01-DEC-2000; 2000WO-US032678.  
19-DEC-2001; 2001US-00028072.  
(GETH ) GENENTECH INC.  
Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W; Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
WPI; 2003-765415/72.  
P-PSDB; ADB27741.  
New PRO nucleic acid, useful for preparing a composition for treating e.g., tumor or for tissue typing.  
Claim 2; Fig 191; 637pp; English.  
The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalassaemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence encodes a human PRO polypeptide of the invention. Note: The sequence data for this patent is also available in electronic format from



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PF 16-MAY-2002; 2002US-00147508.
XX
PR 02-JUL-1998; 98US-0091519P.
PR 02-JUN-1999; 99WO-US012252.
PR 07-JUL-1999; 99US-0143048P.
PR 25-AUG-1999; 99US-00380137.
PR 30-MAR-2000; 2000WO-US008439.
PR 01-DEC-2000; 2000WO-US032678.
PR 19-DEC-2001; 2001US-00028072.
XX
PA (GETH ) GENENTECH INC.
XX
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W,
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX WPI; 2003-786914/74.
DR P-PSDB; ADA86220.
XX
XX New PRO nucleic acid, useful for preparing a composition for treating
PT e.g., tumor or for tissue typing.
XX
PS Claim 2; Fig 191; 637pp; English.
XX
CC The invention describes 305 nucleic acids encoding PRO (secreted and
CC transmembrane) polypeptides (I). (I) is useful for stimulating the
CC release of TNF-alpha from human blood, for modulating the uptake of
CC glucose or FFA by skeletal muscle cells or adipocyte cells, for
CC stimulating the proliferation or differentiation of chondrocyte cells,
CC for stimulating the proliferation of or gene expression in pericyte
CC cells, for stimulating the release of proteoglycans from cartilage, for
CC stimulating the proliferation of inner ear utricular supporting cells,
CC for stimulating the proliferation of T-lymphocyte cells, for stimulating
CC the release of a cytokine from PBM cells, for inhibiting the binding of
CC A-peptide to factor VIIA, for inhibiting the differentiation of adipocyte
CC cells, for stimulating proliferation of endothelial cells, for detecting
CC the presence of tumour in a mammal. The tumour is lung, colon, breast,
CC prostate, rectal, cervical or liver tumour. The oligonucleotide probes
CC are useful for isolating genomic and cDNA nucleotide sequences or
CC antisense probes. (I) is also useful as therapeutic agent. PRO is useful
CC in assays to identify other proteins or molecules involved in binding
CC interaction. A polynucleotide (II) encoding (I) is useful in chromosome
CC and gene mapping, in generation of antisense RNA and DNA, in the
CC preparation of PRO polypeptide, for generating transgenic animals or
CC knockout animals which in turn are useful in the development and
CC screening of therapeutically useful reagents, in gene therapy, for
CC chromosome identification, as chromosome marker, and for generating
CC probes. An anti-(I)-antibody is useful in diagnostic assays for PRO, e.g.
CC detecting its expression in specific cells, tissues or serum, and for
CC affinity purification of PRO from recombinant cell culture or natural
CC sources. (I) and (II) are useful for tissue typing. This sequence encodes
CC a novel human secreted and transmembrane PRO polypeptide.
XX
SQ Sequence 1647 BP; 492 A; 341 C; 347 G; 467 T; 0 U; 0 Other;
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Best Local Similarity 99.9%; Pred. NO. 0;
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DB 1 GCTTCAGCTGAAGAAGAGAGAGGAATGAAGCGCTTCCTGCTTCCTGTTGTTGTTCTTATAA 60
QY 61 CATTTTCTTCGATTTCCCTTAGTCCGATGACGGAATGAAGAAATGAAGAAATGCAACTGG 120
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DB 121 CTCAGGCATATCTCAACAGTCTACTCTCTGAATAGAGGAATCATCTGTGTTCAA 180
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Job time : 841 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 13:11:05 ; Search time 155 Seconds  
(without alignments)  
7460.990 Million cell updates/sec

Title: US-10-729-807-28

Perfect score: 1627

Sequence: 1 gcttcagctgaagaagaga.....aattcgttcaaatagaa 1627

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:\*

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2: /cgn2.6/prodata/1/ina/5B COMB.seq:\*

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5: /cgn2.6/prodata/1/ina/PCUS COMB.seq:\*

6: /cgn2.6/prodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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| 1          | 1627   | 100.0       | 1845   | US-09-862-631-1    | Sequence 1, Appli |
| 2          | 1625.4 | 99.9        | 1847   | US-10-140-002-191  | Sequence 191, App |
| 3          | 1417.8 | 87.1        | 1687   | US-09-280-116-78   | Sequence 78, Appl |
| 4          | 447.6  | 27.5        | 1970   | US-09-023-655-1264 | Sequence 1264, Ap |
| 5          | 447.6  | 27.5        | 1981   | US-09-484-970B-62  | Sequence 62, Appl |
| 6          | 445.6  | 27.4        | 1801   | US-09-023-655-1374 | Sequence 1374, Ap |
| 7          | 442.6  | 27.2        | 1434   | US-09-023-655-1174 | Sequence 1174, Ap |
| 8          | 435.6  | 26.8        | 2223   | US-09-178-002-3    | Sequence 3, Appli |
| 9          | 435.6  | 26.8        | 2223   | US-09-023-655-1040 | Sequence 1040, Ap |
| 10         | 425.4  | 26.1        | 2314   | US-09-178-002-1    | Sequence 1, Appli |
| 11         | 423    | 26.0        | 474    | US-09-280-116-77   | Sequence 77, Appl |
| 12         | 389.4  | 23.9        | 1410   | US-08-068-392-1    | Sequence 1, Appli |
| 13         | 389.4  | 23.9        | 1410   | US-08-396-988-1    | Sequence 1, Appli |
| 14         | 379.2  | 23.3        | 1717   | US-08-229-515A-12  | Sequence 12, Appl |
| 15         | 379.2  | 23.3        | 1717   | US-08-645-865-12   | Sequence 12, Appl |
| 16         | 373.2  | 22.9        | 1521   | US-08-994-689C-18  | Sequence 18, Appl |
| 17         | 373.2  | 22.9        | 2792   | US-08-994-689C-8   | Sequence 8, Appli |
| 18         | 360.8  | 22.2        | 1160   | US-07-780-973-15   | Sequence 15, Appl |
| 19         | 184    | 11.3        | 837    | US-08-371-082-1    | Sequence 1, Appli |
| 20         | 184    | 11.3        | 1078   | US-09-492-543-28   | Sequence 28, Appl |
| 21         | 184    | 11.3        | 1078   | US-09-492-543-29   | Sequence 29, Appl |
| 22         | 184    | 11.3        | 1078   | US-09-023-655-1368 | Sequence 1368, Ap |
| 23         | 141.8  | 8.7         | 989    | US-09-862-631-2    | Sequence 2, Appli |
| 24         | 141.8  | 8.7         | 999    | US-09-862-631-7    | Sequence 7, Appli |
| 25         | 141.8  | 8.7         | 1035   | US-09-009-156-4    | Sequence 4, Appli |
| 26         | 141.8  | 8.7         | 1035   | US-09-372-154-4    | Sequence 4, Appli |
| 27         | 140.8  | 8.7         | 1010   | US-09-009-156-20   | Sequence 20, Appl |

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28 140.8 8.7 1010 3 US-09-372-154-20 Sequence 20, Appl
29 140.2 8.6 825 3 US-08-896-062-1 Sequence 1, Appli
30 131 8.1 2123 4 US-09-194-468A-29 Sequence 29, Appl
31 122.2 7.5 536 1 US-08-303-270-3 Sequence 3, Appli
32 101.6 6.2 1923 3 US-09-294-841-1 Sequence 1, Appli
33 91 5.6 2116 3 US-09-000-041A-1 Sequence 1, Appli
34 91 5.6 2116 4 US-09-734-002-1 Sequence 1, Appli
35 86.8 5.3 2247 4 US-09-023-655-1410 Sequence 1410, Ap
36 86.8 5.3 2256 1 US-07-794-393-1 Sequence 1, Appli
37 86.8 5.1 2256 1 US-08-001-711-1 Sequence 1, Appli
38 83.6 5.1 2260 1 US-07-794-393-3 Sequence 3, Appli
39 83.6 5.1 2260 1 US-08-001-711-3 Sequence 3, Appli
40 80.8 5.0 2177 4 US-09-919-039-124 Sequence 124, App
41 80.4 4.9 3530 3 US-08-704-711A-10 Sequence 10, Appl
42 80.4 4.9 3530 3 US-09-521-220-10 Sequence 10, Appl
43 79.2 4.9 2109 4 US-09-799-451-345 Sequence 345, App
44 79.2 4.9 2333 1 US-08-392-678-33 Sequence 33, Appli
45 79.2 4.9 2334 1 US-08-457-304A-33 Sequence 33, Appli

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#### ALIGNMENTS

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RESULT 1
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; Sequence 1, Application US/09862631
; Patent No: 6734005
; GENERAL INFORMATION:
; APPLICANT: Holmgren, Erik
; APPLICANT: Kihlen, Mats
; APPLICANT: Wood, Tim
; APPLICANT: Ekblom, Jonas
; TITLE OF INVENTION: No. 6734005el Matrix Metalloproteinases
; FILE REFERENCE: 00014regus
; CURRENT APPLICATION NUMBER: US/09/862,631
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 206119
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 1
; LENGTH: 1845
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-862-631-1

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1627; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|    |      |                                                                 |      |
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| Db | 1261 | GAGTGGTAAACACATTTCTGGAATCAGTATCCGTTGATGCTGCTTCCAGTACAAG         | 1320 |
| QY | 1321 | GATTTCTTTTTCAGCGTGGATCAAGCAATTTGAATACAACTTAAGACAAAGAAATA        | 1380 |
| Db | 1321 | GATTTCTTTTTCAGCGTGGATCAAGCAATTTGAATACAACTTAAGACAAAGAAATA        | 1380 |
| QY | 1381 | TTACCCGATCATGAGAACTAATACTTGGTTTCAATGCAAGAACCAAGAACTCTCAT        | 1440 |
| Db | 1381 | TTACCCGATCATGAGAACTAATACTTGGTTTCAATGCAAGAACCAAGAACTCTCAT        | 1440 |

|    |      |                                                                |      |
|----|------|----------------------------------------------------------------|------|
| QY | 1441 | TTGGTTTGTATCAACAAGAAAAAGCATTTCAGGAGCATATAAGATATTGTATCATA       | 1500 |
| Db | 1441 | TTGGTTTGTATCAACAAGAAAAAGCATTTCAGGAGCATATAAGATATTGTATCATA       | 1500 |
| QY | 1501 | AGAGTTTAAGCTTGTGTTATTTTGGTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG     | 1560 |
| Db | 1501 | AGAGTTTAAGCTTGTGTTATTTTGGTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG     | 1560 |
| QY | 1561 | AATAAATTCATAGACCTTAAATTAACCTCAACAGGCTCTTTTAAATATAAATTCCTGTTCAA | 1620 |
| Db | 1561 | AATAAATTCATAGACCTTAAATTAACCTCAACAGGCTCTTTTAAATATAAATTCCTGTTCAA | 1620 |
| QY | 1621 | AATAGAA 1627                                                   |      |
| Db | 1621 | AATAGAA 1627                                                   |      |

RESULT 2

US-10-140-002-191

Sequence 191, Application US/10140002

Patent No. 6725730

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tamas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R1C59

CURRENT APPLICATION NUMBER: US/10/140,002

CURRENT FILING DATE: 2002-05-06

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 191

LENGTH: 1647

TYPE: DNA

ORGANISM: Homo Sapien

US-10-140-002-191

Query Match 99.9%; Score 1625.4; DB 4; Length 1647;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |     |                                                             |     |
|----|-----|-------------------------------------------------------------|-----|
| QY | 1   | GCTTCAGCTGAGAAAGAGAGAGGATGAAGCGCTTCTGCTTCTGTTGTTGTTCTTTATAA | 60  |
| Db | 1   | GCTTCAGCTGAGAAAGAGAGAGGATGAAGCGCTTCTGCTTCTGTTGTTGTTCTTTATAA | 60  |
| QY | 61  | CATTTTCTTCTGCAATTCCTTAGTCGAGTACGCGAAATGAAGAAATATGCACTGG     | 120 |
| Db | 61  | CATTTTCTTCTGCAATTCCTTAGTCGAGTACGCGAAATGAAGAAATATGCACTGG     | 120 |
| QY | 121 | CTCAGGATATCTCAACAGTCTACTCTCTTGAATAGAGGGAATCATCTTGTTCAAA     | 180 |
| Db | 121 | CTCAGGATATCTCAACAGTCTACTCTCTTGAATAGAGGGAATCATCTTGTTCAAA     | 180 |
| QY | 181 | GCAAGAAATAGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTGGATGA   | 240 |
| Db | 181 | GCAAGAAATAGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTGGATGA   | 240 |
| QY | 241 | CAGTGACTGGAAAACTGGACTCAACACCCCTTGAGATCATGAGACACCAGGTGTGGG   | 300 |

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Db 241 |||||CAGTGACTGGAAACTGGACTCAAAACACCCCTTGAGATCATGAGACACCCAGGTGTGGG 300
QY 301 |||||TGCCTGATGTGGCCAGTAGTGGCTACACCGTCCCTGGGTGGAGAAATCAACCTCACCT 360
Db 301 |||||TGCCTGATGTGGCCAGTAGTGGCTACACCGTCCCTGGGTGGAGAAATCAACCTCACCT 360
QY 361 |||||ACAGATAATAAATACTACTCCGGATATGCGAGAGCTGCTGGAGATGAGGCTATCCAAG 420
Db 361 |||||ACAGATAATAAATACTACTCCGGATATGCGAGAGCTGCTGGAGATGAGGCTATCCAAG 420
QY 421 |||||AAGGTTTGAAGTGTGGCAAAAGTCACTCCACTAAATTCACCAAGATTTCAAAGGGGA 480
Db 421 |||||AAGGTTTGAAGTGTGGCAAAAGTCACTCCACTAAATTCACCAAGATTTCAAAGGGGA 480
QY 481 |||||TTGCAGACATCATGATGCTTTAGACATCGAGTCAATGGTGGTCTCGCTATTTTG 540
Db 481 |||||TTGCAGACATCATGATGCTTTAGACATCGAGTCAATGGTGGTCTCGCTATTTTG 540
QY 541 |||||ATGCTCCCTTGGAGTGTCTGGCCATGCTCTTCTCTGCTCGGCTCTGGGTGTGACA 600
Db 541 |||||ATGCTCCCTTGGAGTGTCTGGCCATGCTCTTCTCTGCTCGGCTCTGGGTGTGACA 600
QY 601 |||||CTCATTTTGAATGAGGATGAAACTGCGCAAGTGAAGGAGGAGGAGGATTCACCTTTG 660
Db 601 |||||CTCATTTTGAATGAGGATGAAACTGCGCAAGTGAAGGAGGAGGAGGATTCACCTTTG 660
QY 661 |||||TGGCTGCTCATGAATTTGGTCTATGCTACCTGGGCTCTCTCACTCCAATGATCAACAGCCT 720
Db 661 |||||TGGCTGCTCATGAATTTGGTCTATGCTACCTGGGCTCTCTCACTCCAATGATCAACAGCCT 720
QY 721 |||||TGATGTTCCCAATATATGCTCCCTGGATCCAGAAATACCCACATTTCTCAGGATGATA 780
Db 721 |||||TGATGTTCCCAATATATGCTCCCTGGATCCAGAAATACCCACATTTCTCAGGATGATA 780
QY 781 |||||TCAATGGAAATCAGTCCATCTATGAGGCTGTCCCTAAGGTACCTGCTAAGGCCAAAGGAAC 840
Db 781 |||||TCAATGGAAATCAGTCCATCTATGAGGCTGTCCCTAAGGTACCTGCTAAGGCCAAAGGAAC 840
QY 841 |||||CCACTATACCCCATGCTGTGACCTGTGACCTTTGACGGTATCAACAATTTCCGCA 900
Db 841 |||||CCACTATACCCCATGCTGTGACCTGTGACCTTTGACGGTATCAACAATTTCCGCA 900
QY 901 |||||GAGAGTAGTATGTTCTTAAAGGAGGCTGTGAGGATCTATGATGATATCAAGGATG 960
Db 901 |||||GAGAGTAGTATGTTCTTAAAGGAGGCTGTGAGGATCTATGATGATATCAAGGATG 960
QY 961 |||||TTGAGTTTGAATTAATTTGCTTCATCTGCGCATCTCTGCGCATCTCTGCGCATCTG 1020
Db 961 |||||TTGAGTTTGAATTAATTTGCTTCATCTGCGCATCTCTGCGCATCTCTGCGCATCTG 1020
QY 1021 |||||ACGAGAACCCAGAGATTAAGTCTGTTTAAAGATGAAACTCTGGATGATCAGAG 1080
Db 1021 |||||ACGAGAACCCAGAGATTAAGTCTGTTTAAAGATGAAACTCTGGATGATCAGAG 1080
QY 1081 |||||GATATGCTGTCTGCGCAGATTAATCCAAATCCATCCATATCTAGTCTTTCAGAGCTG 1140
Db 1081 |||||GATATGCTGTCTGCGCAGATTAATCCAAATCCATCCATATCTAGTCTTTCAGAGCTG 1140
QY 1141 |||||TGAAGAAATATAGATGACGCGCTGTGTGATGAGACCAAGAAACCTACTTTCTTTGG 1200
Db 1141 |||||TGAAGAAATATAGATGACGCGCTGTGTGATGAGACCAAGAAACCTACTTTCTTTGG 1200
QY 1201 |||||GCATTTGGTGTGGAGTTTGAATGAATGACCCCAACCAAGAGAGATTTCCCGCAGA 1260
Db 1201 |||||GCATTTGGTGTGGAGTTTGAATGAATGACCCCAACCAAGAGAGATTTCCCGCAGA 1260
QY 1261 |||||GAGTGTGTAACACATTTCTCTGAAATCAGTATCCGTTGATGCTGTTTCCAGTACAAG 1320
Db 1261 |||||GAGTGTGTAACACATTTCTCTGAAATCAGTATCCGTTGATGCTGTTTCCAGTACAAG 1320
QY 1321 |||||GATTTCTTTTTCAGCGCTGGATCAAGCAATTTGAATCAACATTAAGACAAAGAAATA 1380
|||||
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Db 1321 |||||GATTTCTTTTTCAGCGCTGGATCAAGCAATTTGAATACACATTAAGACAAAGATA 1380
QY 1381 |||||TTACCCGAATCATGAGAACTAATACTTGGTTTCAATGCGAAAGAACCAAGAACTCTCAT 1440
Db 1381 |||||TTACCCGAATCATGAGAACTAATACTTGGTTTCAATGCGAAAGAACCAAGAACTCTCAT 1440
QY 1441 |||||TTGGTTTTCATATCAACAGGAAAGACACATTCAGAGGCGATAAAGATATTCATCATTA 1500
Db 1441 |||||TTGGTTTTCATATCAACAGGAAAGACACATTCAGAGGCGATAAAGATATTCATCATTA 1500
QY 1501 |||||AGAGTTTAAAGCTTGTATTTATTTTGGTATTTGTTCAATTTGCTGAAAAACACTTTCTATTATC 1560
Db 1501 |||||AGAGTTTAAAGCTTGTATTTATTTTGGTATTTGTTCAATTTGCTGAAAAACACTTTCTATTATC 1560
QY 1561 |||||ATAAATTCATGAGACCTTAAATTAACCTCAACAGGCTTTTAAATATAAATTTCTGCTTCAA 1620
Db 1561 |||||ATAAATTCATGAGACCTTAAATTAACCTCAACAGGCTTTTAAATATAAATTTCTGCTTCAA 1620
QY 1621 |||||AATAGAA 1627
Db 1621 |||||AATAGAA 1627

RESULT 3
US-09-280-116-78/c
; Sequence 78, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 1687
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: matrix metalloproteases
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(1687)
; OTHER INFORMATION: n = a, t, c or g
US-09-280-116-78

Query Match 87.1%; Score 1417.8; DB 3; Length 1687;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1430; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 136 TCATAGATGACAAAATTCGGGAAATGCAAGCAATTTTGGATTGACAGTGAAGTGGAAAC 255
Db 1680 TCCGAGATGACAAAATTCGGGAAATGCAAGCAATTTTGGATTGACAGTGAAGTGGAAAC 1621
QY 256 TGGACTCAAAACACCTCTGAGATCATGAGACACCCAGGTGGGTGCTGATGTGGGCC 315
Db 1620 TGGACTCAAAACACCTCTGAGATCATGAGACACCCAGGTGGGTGCTGATGTGGGCC 1561
QY 316 AGTATGGCTACACCTCCCTGGGTGGAGAAAATCAACCTCACCTACAGAAATATAAATCT 375
Db 1560 AGTATGGCTACACCTCCCTGGGTGGAGAAAATCAACCTCACCTACAGAAATATAAATCT 1501
QY 376 ATACTCCGATATGACAGAGCTGCTGTGGATGAGGCTATCCAAGAGGTTTGAAGTGT 435
Db 1500 ATACTCCGATATGACAGAGCTGCTGTGGATGAGGCTATCCAAGAGGTTTGAAGTGT 1441
QY 436 GGAGCAAAAGTCACTCCACTTAAATTCACCAAGATTTCAAAGGGGATTCAGACATCATGA 495
Db 1440 GGAGCAAAAGTCACTCCACTTAAATTCACCAAGATTTCAAAGGGGATTCAGACATCATGA 1381
QY 496 TTGCTCTTTAGGACTCGAGTCCATGGTGGTGTCTCGCTATTTTTCATGCTCCCTTGGGAG 555
|||||
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Db 1380 TTCCCTTTAGGACTCGAGTCCATGGTCCGTGTCCTCGCTATTTTGTGGTCCCTTGGGAG 1321
QY 556 TGCTTGCCCATGCTTTTCTCTCGTCCGGTCTGGGTGGTGAACATTCATTTTGTGATGAGG 615
Db 1320 TGCTTGCCCATGCTTTTCTCTCGTCCGGTCTGGGTGGTGAACATTCATTTTGTGATGAGG 1261
QY 616 ATGAATACTGGACCAAGGATGGAGCAGGATCAACTTGTTCCTGGCTGCTCATGAAT 675
Db 1260 ATGAATACTGGACCAAGGATGGAGCAGGATCAACTTGTTCCTGGCTGCTCATGAAT 1201
QY 676 TTGCTCATGACCTGGGCTCTCTCACTCCATGATCAACAGCCTTCATGTTCCCAAT 735
Db 1200 TTGCTCATGACCTGGGCTCTCTCACTCCATGATCAACAGCCTTCATGTTCCCAAT 1141
QY 736 ATGCTCCCTGGATCCAGAAATACCCACTTTCTCAGGATGATCAATGGAATCCAGT 795
Db 1140 ATGCTCCCTGGATCCAGAAATACCCACTTTCTCAGGATGATCAATGGAATCCAGT 1081
QY 796 CCATCTATGAGGTCTGCTAAGGTACCTGCTAAGCCAAAGGACCCACTATACCCCATG 855
Db 1080 CCATCTATGAGGTCTGCTAAGGTACCTGCTAAGCCAAAGGACCCACTATACCCCATG 1021
QY 856 CTTGTGACCTGACTTCACTTTTCACTGCTATCAAACTTTCCGAGAGAGTAATGTCT 915
Db 1020 CTTGTGACCTGACTTCACTTTTCACTGCTATCAAACTTTCCGAGAGAGTAATGTCT 961
QY 916 TTAAGGACGACCTATGAGGAGTCTATTATGATATCAGGATGTTGAGTTGAATTA 975
Db 960 TTAAGGACGACCTATGAGGAGTCTATTATGATATCAGGATGTTGAGTTGAATTA 901
QY 976 TTGCTTCATTTGCGCATCTGCGCATCTGCGCATCTGCGCATCTGCGCATCTGCGCAT 1035
Db 900 TTGCTTCATTTGCGCATCTGCGCATCTGCGCATCTGCGCATCTGCGCATCTGCGCAT 841
QY 1036 ATAGATTTCTGTTTAAAGATGAAATCTCTGATGATCAGAGGATATCTCTCTTTC 1095
Db 840 ATAGATTTCTGTTTAAAGATGAAATCTCTGATGATCAGAGGATATCTCTCTTTC 781
QY 1096 CAGATTTATCCAAATCCATCATATAGTTTTCAGGA-CGTGTGAAGAAATAGAT 1154
Db 780 CAGATTTATCCAAATCCATCATATAGTTTTCAGGA-CGTGTGTGAAGAAATAGAT 721
QY 1155 GCAGCGCTGTGATAGACACACAGAAACCTTCTTTTGGGCAATTTGGTGTGG 1214
Db 720 GCAGCGCTGTGATAGACACACAGAAACCTTCTTTTGGGCAATTTGGTGTGG 661
QY 1215 AGGTTTGTATGAATGACCCAAACCATGGACAAAGATTTCCCGCAGAGAGTGTAACAC 1274
Db 660 AGGTTTGTATGAATGACCCAAACCATGGACAAAGATTTCCCGCAGAGAGTGTAACAC 601
QY 1275 TTTCTGTGAATCAGTATCCGTTGTGATGCTGCTTTCCAGTACAAAGGATTTCTTTTTC 1334
Db 600 TTTCTGTGAATCAGTATCCGTTGTGATGCTGCTTTCCAGTACAAAGGATTTCTTTTTC 541
QY 1335 AGCGTGTGATCAAGCAATTTGAATACAACTTAAGACAAAGAAATATTACCGCAATCATG 1394
Db 540 AGCGTGTGATCAAGCAATTTGAATACAACTTAAGACAAAGAAATATTACCGCAATCATG 481
QY 1395 AGAACTAATCTTGGTTTCAATGCAAGAAACCAAGAACTCCTCATTTGGTTTGTATC 1454
Db 480 AGAACTAATCTTGGTTTCAATGCAAGAAACCAAGAACTCCTCATTTGGTTTGTATC 421
QY 1455 AACAGGAAAAGACATTCAGGAGGATTAAGATATTGTATCATAGAGTTTAAAGCTTG 1514
Db 420 AACAGGAAAAGACATTCAGGAGGATTAAGATATTGTATCATAGAGTTTAAAGCTTG 361
QY 1515 TTTATTTTGTATTTGTTTCTGCTGAAAACACTTCTATTATTAATTAATTAATTAATTA 1574
Db 360 TTTATTTTGTATTTGTTTCTGCTGAAAACACTTCTATTATTAATTAATTAATTAATTA 301
QY 1575 CTTAAATTAACCTCAACAGGCTTTTAAATTAATTAATTAATTAATTAATTAATTAATTA 1627
Db 300 CTTAAATTAACCTCAACAGGCTTTTAAATTAATTAATTAATTAATTAATTAATTAATTA 248
```

## RESULT 4

```
US-09-023-655-1264
; Sequence 1264, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1264:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1970 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g30125
US-09-023-655-1264
```

```
Query Match 27.5%; Score 447.6; DB 4; Length 1970;
Best Local Similarity 61.1%; Pred. No. 5.1e-121;
Matches 837; Conservative 0; Mismatches 509; Indels 24; Gaps 6;

QY 98 AAATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACCACTTCTACTCTCTTGAAT 157
Db 146 ACAAGACCAAGTGTGACTTAGTCCAGAAATACCTGGAAAAATACACACCTGAAGAA 205
QY 158 AGAAGGGAATCATCTTGTTCAAAGCAAGATAGGAGTCTCATAGATGACAAAATTCGGGA 217
Db 206 TGATGGGAGGCAAGTTGAAAAAGCGAGAAATAGTGGCCAGTGGTTGAAAAATTTGAAGCA 265
QY 218 AATGCAAGCATTTTTCGATTGACAGTGCACCTGGAACCTGACCTCAACACCTTTGAGAT 277
Db 266 AATGAGGAATTCCTTGGGCTGAAAGTACTGGGAAACCAAGATGCTGAAACCTTGAAGGT 325
QY 278 CATGAAGACACCCAGGTGTGGGTGCTGTGATGTGGGCCAGTATGGCTACAC-----CCT 331
Db 326 GATGAAGCAGCCAGATGTGGAGTGCCTGATGTGGCTCAGTTTGTCTCTCACTGAGGGAA 385
QY 332 CCCTGGGTGGAGAAATACACCTCACTACAGAAATATAACTATCTCCGATATGGC 391
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386 CCCTCGTGGGAGCAACACATCTGACCTACAGGATTTGAAATTTACACGCCAGATTTGCC 445  
392 ACCAGCTGCTGTGATGAGCTATCCAAAGAGTTTGAAGTGTGGAGCAAGTCACTCC 451  
446 AAGAGCAGATGTGACCATGCGCATTTGAGAAAGCCTTCCAATCTTGGAGTAATGTGCACAC 505  
452 ACTAAATTCACCAAGATTTCAAAGGGATTTGACACATCATGATTCCTTTAGGACTCG 511  
506 TCTGACATTCACCAAGTCTCTGAGGTCAAGCAGACATCATGATATCTTTGTGACGGG 565  
512 AGTCCATGTGCGGTCTCTCGCTATTTTGAAGTTCCTTGGAGTGTCTGGCCATGCCCTT 571  
566 AGATCATCGGAGCAACTCTCC---TTTGTAGTACCTGGAGGAAATCTTCTCATGCTTT 622  
572 TCCTCTGTGTCGGGTCTGGGTGTGACATCATTTTGTAGTGAAGTGAAGTGAAGTGAAG 631  
623 TCAACAGGCCAGGATTTGGAGGGATGCTCAATTTTGTGAAGATGAAGTGAAGTGAAG 682  
632 GGATGAGCAGGATTTCAACTTGTCTTGTGGTGTCTCATGAATTTGGTCAATGACCTGGG 691  
683 CAATTTTCAAGAGTACAACTTACATCTGTGTGGGTCTGAACTCGGCCATTTCTCTGG 742  
692 GCTCTCTCACTCAATGATCAACAGCCTTGTGATGTTCCCAAAATATGTCTCCCTGGATCC 751  
743 ACTCTCCCATTTCTACTGATATCGGGGCTTTGATGTACCTTAGCTACACCTTCACTG--- 798  
752 CAGAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTATGAGGTCT 811  
799 --GTGATGTTAGTACGTAGCTAGTACATGATGATGATGATGATGATGATGATGATGAT 856  
812 GCTAAGTACCTGTGAGCAAGGAACCCACTATACCCCATGCTGTGACCCCTGACCT 871  
857 CCAAAA---TCTGTCTCAGCCATCGGCCACAAACCCCAAGCATGTGACAGTAAGCT 913  
872 GACTTTGAGCTATCACAACTTTCGAGAGAAAGTAATGTTCTTTAAAGCAGGACCT 931  
914 AACTTTGATGATATCACTACGATTCGGGAGAGTGAATGTTCTTTAAAGCAGATTTCTA 973  
932 ATGGAGATCTATTATGATATACGAGTGTGAGTTTGAATTTGCTTTCATTTCTGGCC 991  
974 CATGGCAAAATCCCTTACCCGAGTGTGAGTCAATTTCTTTCTTGTGTTCTGGCC 1033  
992 ATCTCTGCCAGTGTCTCAAGCTGCATACGA---GAACCCCAAGAGTAAGTCTGTG 1048  
1034 ACACTGCCAATGGCTTGAAGCTCTTACGAATTTGGCAGAGATGAAGTCCGTT 1093  
1049 TTTTAAAGATGAACCTTCTGATGATCAGAGATGCTGTTTCCAGATTTATCCCAA 1108  
1094 TTTCAAAGGGAATAAGTACTGGGCTGTTTCAAGGACAGAAATGTCTACACGGATACCCCAA 1153  
1109 ATCCATCCATA---CATTAGTGTTCAGGACGTGTGAAGAAATAGATGCGAGCGTCTG 1165  
1154 GGACATCTACAGTCTCTTGGCTTCCCTAGACTGTGAAGCATATCGATGCTGCTTTTC 1213  
1166 TGATAAGCACAAGAAAAACCTTCTTTTGGGCATTTGGTGTGAGGTTTGTATGA 1225  
1214 TCAGGAAAAACACTGAAAAACCTTCTTCTTGTGTAACAATACTGGAGTATGATGA 1273  
1226 AATGACCCAAACCATGGACAAGGATTCGCCAGAGAGTGGTGAACAATTTCTTGGAAAT 1285  
1274 ATATAAAGCATATATGGATTCAGGTTATCCCAAAATGATAGCAGATGATTTCTCTGGAAT 1333  
1286 CAGTATCCGTGTGATGCTGTTCCAGTACAAAGGATTTCTTTTTCAGCGGTGGATC 1345  
1334 TGGCCACAAGTGTGAGTGTTCATGAAGATGATTTTCTATTTCTTTTCATGGAAC 1393  
1346 AAAGCAATTTGAATACAACTTAAGACAAGAAATATTAACCGAATCATGAGAACTAATAC 1405  
1394 AAGACAAATACAAATTTGATCTCTTAAACGAAGAAATTTTGTCTCTCCAGAAAGCTAATG 1453  
1406 TTGGTTTCAATGGAAGAAACCAAGAACTCTCTCATTTGGTTTGTATATCA 1455  
1454 CTGGTTCACTGACGAAAAAATTTGAATTAATTAATTTGAATGGAACAA 1503

## RESULT 5

US-09-484-970B-62  
; Sequence 62, Application US/09484970B  
; Patent No. 6426186  
; GENERAL INFORMATION:  
; APPLICANT: Jones, Karen A.  
; APPLICANT: Volkmut, Wayne  
; APPLICANT: Walker, Michael G.  
; TITLE OF INVENTION: BONE REMODELING GENES  
; FILE REFERENCE: PB-0014 US  
; CURRENT APPLICATION NUMBER: US/09/484,970B  
; CURRENT FILING DATE: 2000-01-18  
; NUMBER OF SEQ ID NOS: 172  
; SOFTWARE: PERL Program  
; SEQ ID NO 62  
; LENGTH: 1981  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6426186 245334.1  
US-09-484-970B-62

Query Match 27.5%; Score 447.6; DB 4; Length 1981;  
Best Local Similarity 61.1%; Pred. No. 5.1e-121;  
Matches 837; Conservative 0; Mismatches 509; Indels 24; Gaps 6;

QY 98 AATGAAGAAAAATATGCAACTGGCTCAGCATATCTCAACCCAGTCTTACTCTCTTGAAT 157  
DB 157 ACNAGAGCAGATGTGGACTTAGTCCGAAATACCTTGGAAAAATATCAACCTGAAGAA 216  
QY 158 AGAAGGAATCATCTTTGTTCAAAGCAAGAAATAGGAGTCTCATAGATGACAAATTCGGGA 217  
DB 217 TGATGGGCGCAAGTTGAAAAGCGGAGAAATAGTGGCCAGTGGTTGAAAAATTTGAAGCA 276  
QY 218 AATGCAAGCATTTTGTGATTTGACAGTGTGACAGTGTGAAAACTGGAACTCAACACCCCTGAGAT 277  
DB 277 AATGCAAGCAATTTCTTTGGCTGAAAGTGTGCTGGGAAACAGATGCTGAAACCCCTGAAGCT 336  
QY 278 CATGAAGACACCCAGTGTGGGTGCTGATGTGGCCAGTATGGCTACAC-----CCT 331  
DB 337 GATGAAGACGCCAGATGTGGAGTGCCTGATGTGGCTCAGTTTGTCTCCTCAGTAGGGGAA 396  
QY 332 CCTGGGTGGAGAAAAATACAACTCACTACAGAAATAATAAACTATCTCCGGATATGGC 391  
DB 397 CCTGCTGGGAGCAACACATCTGACCTACAGGATTTGAAATTTACACGCCAGATTTGCC 456  
QY 392 ACGAGTCTGTGTGATGAGGCTATCCAGAAAGTTTAGAAGTGTGGAGCAAGTCACTCC 451  
DB 457 AAGACAGATGTGGACCAATGCAATTTGAGAAAGCCTTCCAACCTCGAGTAATGTCAACC 516  
QY 452 ACTAAATTCACCAAGATTTCAAAGGGATTTGACAGATCATGATTTGCCCTTTAGGACTCG 511  
DB 517 TCTGACATTCACCAAGTCTCTGAGGTCACAGACATCATGATATCTTTTGTCAAGGG 576  
QY 512 AGTCAATGTCTGTCTCGCTATTTTGAAGTCCCTTTGGAGTGTCTGGCCATGCTCTT 571  
DB 577 AGATCATCGGACAACTCTCC---TTTGTAGTACCTGGAGGAAATCTTTGCTCATGCTTT 633  
QY 572 TCCTCTGTCTCGGCTCTGGGTGTGACATCATTTTGTAGTGAAGTGAAGAACTGACCAAA 631  
DB 634 TCAACAGGCCAGGATTTGGAGGGGATGCTCAATTTGATGAAGATGAAGAGTGGACCAA 693  
QY 632 GGATGAGCAGGATTTCAACTTGTCTTGTGGCTCTCATGAATTTGGTCAATGCACTGG 691  
DB 694 CAATTTCAAGAGTACAACTTACATCTGTTTGGGCTCATGAATCTGGCCATTTCTCTGG 753  
QY 692 GCTCTCTCACTCAATGATCAACAGCCTTGAATGTTTCCCAAAATATGTCTCCCTGGATCC 751  
DB 754 ACTCTCCCATTTCTACTGATATCGGGGCTTTGATGTACCTTAGCTACACCTTCAGTG--- 809

| Query Match           | 27.4%; | Score                                                            | 445.6;    | DB         | 4;   | Length | 1801; |
|-----------------------|--------|------------------------------------------------------------------|-----------|------------|------|--------|-------|
| Best local similarity | 60.2%; | Pred. No.                                                        | 1.9e-120; |            |      |        |       |
| Matches               | 865;   | Conservative                                                     | 0;        | Mismatches | 529; | Indels | 42;   |
|                       |        |                                                                  |           |            |      |        | Gaps  |
|                       |        |                                                                  |           |            |      |        | 6;    |
| Qy                    | 21     | GGAAATCAAGCGCTTCTGCTTCTGTGTTGTTGTTCTTTATATCAATTTTCTTCGTCGATTTCCC | 80        |            |      |        |       |
| Db                    | 41     | GAATGGAAGTCTTCCAAATCCTACTGTTGCTGTGCGTGGCAGTTTGTCTCAGCCTATCCA     | 100       |            |      |        |       |
| Qy                    | 81     | TTAGTCCG---GATGACGGAAATATGAAGAAATATATGCAACTGCTCAGGCATATCTCAAC    | 137       |            |      |        |       |
| Db                    | 101    | TTGGATGGAGCTCAAGGGGTGAGGACACACGACATGAACCTTGTTCAGAATATCTAGAA      | 160       |            |      |        |       |
| Qy                    | 138    | CAGTTCTACTCTCTCGAAATAGAAAGGGAATCATCTTTGTTCAAAGCAAGAAATAGAGAGTCTC | 197       |            |      |        |       |
| Db                    | 161    | AATCTACTACGACCTCAAAAAGATGTGAAACAGTTTGTTAGGAAAGGACAGCTGGTCTCT     | 220       |            |      |        |       |
| Qy                    | 198    | ATAGATGACAAAATTCGGGAAATGCAAGCAATTTTTTGGATGTGACGTGACTGGAAGAACTG   | 257       |            |      |        |       |
| Db                    | 221    | GTGTTTAAAAAATCCGAGAAATGCAAGAAATTCCTTTGGATTGGAGGTGACGGGGAAGCTG    | 280       |            |      |        |       |
| Qy                    | 258    | GACTCAAAACACCTTCAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGGGCAG       | 317       |            |      |        |       |
| Db                    | 281    | GACTCCGACACTCTGGAGGTGATGCGCAAGCCACAGGTGTGAGTTCCTGATGTGGTCAC      | 340       |            |      |        |       |
| Qy                    | 318    | TATGGGTAC-----ACCTCTCCCTGGGTGGAGAAAATCAACCTCACTACAGAAATAA        | 371       |            |      |        |       |
| Db                    | 341    | TTCAGAACCTTTCTTGSCATCCCGAAGTGAGGAGAAAACCCACCTTACATACAGGATGTG     | 400       |            |      |        |       |
| Qy                    | 372    | AATATACTCCGATATGGACAGCTGCTGTGATGAGGCTATCCAAAGAGGTTTAGAA          | 431       |            |      |        |       |
| Db                    | 401    | AATTTATACACGATTTGCCAAAAGATGCTGTGTGATTTCTGCTGTTGAGAAAGCTCTGAA     | 460       |            |      |        |       |
| Qy                    | 432    | GTGTGAGCAAAAGTCACTCCCACTAAAAATCCACAGATTTCAAAGGGGATGTCAGACATC     | 491       |            |      |        |       |
| Db                    | 461    | GTCTGGGAAGGTGACTCCCACTCACATTTCTCCAGGCTGTATGAAGGAGAGGCTGATATA     | 520       |            |      |        |       |
| Qy                    | 492    | ATGATTCCTTTTAGGACTCGAGTCCATGCTGGGTGCTCGCTATTTTGTATGTCCTCTTG      | 551       |            |      |        |       |
| Db                    | 521    | ATGATCTCTTTTGCAGTTAGAGAACTGGAGACT---TTTACCCTTTTGTATGACCTTGG      | 577       |            |      |        |       |
| Qy                    | 552    | GGAGTGTCTGGCCATGCCTTTCTCTCGTCCCGGCTCGGGTCTGGGTGGTGCACATCATTTTGT  | 611       |            |      |        |       |
| Db                    | 578    | AAATGTTTTGCCCATGCTTATGCCCCCTGGCCAGGGATTAATGAGATGCCCACTTTTGT      | 637       |            |      |        |       |
| Qy                    | 612    | GAGATGAAAACTGGACCAAGGATGGAGCAGGATTCAACTGTTTCTTGTGGCTGCTCAT       | 671       |            |      |        |       |
| Db                    | 638    | GATGATGAACAATGGAACAAAGGATACAAACAGGGACCAATTTATTTCTGTTGCTGCTCAT    | 697       |            |      |        |       |

RESULT 6  
US-09-023-655-1374  
; Sequence 1374, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:



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QY 615 GATGAAACTGGACCAAGGATGGAGGAGGATCAACTTGTCTTGTGGCTGCTCATGAA 674
DB 598 GATGAACTATGGAACAAGGATACACAGGAGCAAAATTTATTTCTGCTGCTGCTCATGAA 657
QY 675 TTTGGTATGATGAGGCTCTCTCACTCCCAATGATCAAAAGAGCTTGAATGCTCCCAAT 734
DB 658 ATTGGCCACTCCCTGGGCTCTTTTCACTCAGCAACACTGAGCTTTGATGATCCCACTC 717
QY 735 TATGCTCCCT---GGATCCAGAAAATPACCACTTTCTCAGGATGATATCAATGGAAATC 791
DB 718 TATCACTCACTCAGACCTGACTCGGTTCCGCTGTCTCAAGATGATATATAATGGCAAT 777
QY 792 CAGTCCATCTATGAGGCTGCTTAAGTACTCTGCTAGCCCAAGGAGGAGGAGGAGGAGG 851
DB 778 CAGTCCCTCTATGAGGCTCCCTGACTCCCTGAGACCCCTGAGTCCCTGAGGAGGAGGAGG 837
QY 852 CATGC-----CTGTGACCTGCTGACTTGTGACTTTTGAAGCTATC 887
DB 838 GTCCCTCCAGAACCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 897
QY 888 ACAACTTTCCGAGAGAGTAAATGTTCTTTAAAGCAGGAGGAGGAGGAGGAGGAGGAGGAG 947
DB 898 AGCACTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 957
QY 948 GATATCAGGATGTTGAGTTGAAATTAATGCTTCAATTTCTGCTGCTGCTGCTGCTGCTGCT 1007
DB 958 AGGAAGCTTGAACCTGGAATTTGATTTGATCTCTTCAATTTTGGCCATCTCTCTCTCAGGC 1017
QY 1008 CTGCAAGCTGCTATGAG---GAACCCAGAGATAAGATTTCTGTTTAAAGATGAAATC 1064
DB 1018 GTGGATGCCGATATGAAATGAGTACTAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1077
QY 1065 TTCTGGATGATCAGAGGATATGCTGTCTGCGAGATTAATCCCAATCCATCCATCATTA 1124
DB 1078 TTCTGGGCACTCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1137
QY 1125 GGTTCCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1184
DB 1138 GGTTCCTCCTCCCAAGCAAAATAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1197
QY 1185 ACCTACTCTTTGTGGGCAATTTGGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1244
DB 1198 ACATATTTCTTTGAGAGCAAAATAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1257
QY 1245 AAAGGATTTCCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1304
DB 1258 CCAGGCTTTCCCAAGCAAAATAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1317
QY 1305 GCTTTCCAGTACAAAGATTTCTTTTTCAGCCGCTGATCAAGCAATTTGAATACAAAC 1364
DB 1318 GTTTTGAAGAAATTTGGGTTCTTTTATTTTCTTACTGGATCTTCAAGTTGGAGTTGAC 1377
QY 1365 ATTAAGCAAGAAATATTACCCGAATCATGAGAACTAATATCTTGGTTTCAATG 1417
DB 1378 CCAATGCAAAAGAGTACACACACTTTGAGAGGATACAGCTGGCTTAATG 1430

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RESULT 8

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US-09-178-002-3
; Sequence 3, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CCG 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2223
; TYPE: DNA
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (72)..(1475)
US-09-178-002-3
Query Match 26.8%; Score 435.6; DB 1; Length 2223;
Best Local Similarity 60.6%; Pred. No. 1.8e-117;
Matches 809; Conservative 0; Mismatches 504; Indels 21; Gaps 5;

QY 99 AATCAAGAAATATGCAACTGGCTCAGGCATATCTCAACCAAGTCTTACTCTCTTGAATA 158
DB 147 AAAGAGAAATAAATAAATACTGTTTCAAGACTTCTCTGGAAGTCTTCACTTACCAAGC 206
QY 159 GAAGGGAATCATCTTGTTCCTCAAGCAAGAAATAGGAGTCTCTAGATGACAAATTCGGAA 218
DB 207 AACCAATCATCTTCAAGCAAGAAATAGGAGTCTCTAGATGACAAATTCGGAA 266
QY 219 ATCAAGCAATTTTGTGATGACAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 278
DB 267 ATGAGCAATTTTGTGATGACAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 326
QY 279 ATGAGCAATTTTGTGATGACAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 332
DB 327 ATGAGCAATTTTGTGATGACAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 386
QY 333 CTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 392
DB 387 CCCAAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 446
QY 393 CGAGTCTGTTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 452
DB 447 GAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 506
QY 453 CTAAATTTTCAACCAAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 512
DB 507 CTCATCTTCAACCAAGTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 566
QY 513 GTCCATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 572
DB 567 GATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 623
QY 573 CTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 632
DB 624 CAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 683
QY 633 GATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 692
DB 684 ACCTCCGAAATTAACCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 743
QY 693 CTCTCTCACTTCAATGATCAACAGCCTTGTGATGTTCCCAATTTATGTTCTCTCTGATCCC 752
DB 744 CTGCTCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 803
QY 753 AGAAATACCACTTTCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 812
DB 804 AGCAACTACTCACTCTCTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 860
QY 813 CCTAAGTACTCTGCTAAGCCAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 872
DB 861 TCAAGCAATCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCACTT 920
QY 873 ACTTTTGAAGCTATCACTTCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 932
DB 921 ACATTTGATGCTATCACTTCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 980
QY 933 TGAGGAGTCTATTAATGATCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 992
DB 981 TGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1040
QY 993 TCTCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1049
DB 1041 TCCCTTCAACTGGTATACAGGCTGCTTATGAAGATTTTGACAGAGGAGGAGGAGGAGGAGGAGGAG 1100

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1050 TTTAAAGATGAAACCTTCTGATGATCAGAGGATATGCTGTCTGCGCAGATTATCCCAA 1109  
1101 TTTAAAGGCAACCAATACCTGGCTCTGAGTGGCTATGATATCTGCAAGGTTATCCCAAG 1160  
1110 TCCATCCATCATAGTGTTCAGGACGCTGTGAAGAAATAGATGAGCGCTGTGTGAT 1169  
1161 GATATATCAAACTATGCTTCCCGCAGCAGGCTCCAGCAATGACGAGCTGTTTCTA- 1219  
1170 AAGACCAAGAAACCTACTTCTTGTGGCATTTGGTGGAGTTTGTGAATG 1229  
1220 -----CAGAAGTAAACATACTTCTTGTAAATGACCAATCTGGAGATATGAAACAA 1274  
1230 ACCAAACCATGACAAAGATTTCCCGCAGAGAGTGTGAACACATTTCTCGAATCAGT 1289  
1275 AGACAATTCATGAGCAGGTTATCCCAAGCATATCAGTGCCTTTCAGGATAGAG 1334  
1290 ATCGGTGTGATGCTGTTCCAGTACAAAGGATTTCTTCTTTTTCAGCGGTGATCAAAG 1349  
1335 AGTAAAGTTGATCAGTGTTCAGCAGCAAGACATTTCTTCCATGCTTTCAGTGGACCAAGA 1394  
1350 CAATTTGAATACAAACATTAAGACAAAGATATTACCGAATCATGAGAACTAATCTTGG 1409  
1395 TATTACGCAATTCATCTTATGCTCAGAGATTACAGAGTTCCAGAGTTCCAAAGAGCAATAATGG 1454  
1410 TTTCAATGCAAGA 1423  
1455 CTTAACTGTAGATA 1468

## RESULT 9

US-09-023-655-1040  
; Sequence 1040, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1040:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2223 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g180617  
; US-09-023-655-1040

Query Match 26.8%; Score 435.6; DB 4; Length 2223;  
Best Local Similarity 60.8%; Pred. No. 1.8e-117;  
Matches 809; Conservative 0; Mismatches 504; Indels 21; Gaps 5;

|    |      |                                                              |      |
|----|------|--------------------------------------------------------------|------|
| QY | 99   | AATGAAGAAATATGCAACTGGCTCAGGCATATCTCAACCAGTCTTACTCTCTTGAATA   | 158  |
| Db | 147  | AAAGAGAAATAACAAAACCTGTTCAAGACTACTCTGGAAGATTCTACCAATTACCAAGC  | 206  |
| QY | 159  | GAAGGAAATCATCTTGTTCAGCAAGATAGGAGTCTCATAGATGACAAAATTTGGGAA    | 218  |
| Db | 207  | AACCATGATCAGTCTACAAGGAAGATGACATAATGTGATCGTTGAAAAGCTTAAAGAA   | 266  |
| QY | 219  | ATGCAAGCATTTTTTGGATTGACAGTGACTGGGAAACTGGACTCAAAACACCTTGAGATC | 278  |
| Db | 267  | ATGACGGATTTTTTGGGTTGATGACGGGAAGCCAATGAGGAAACTCTGGACATG       | 326  |
| QY | 279  | ATGAAGACACCCAGGTGTGGGGTGCCTGATGTGGGCCAGTATGGCTACACCC-----TC  | 332  |
| Db | 327  | ATGAAAAGCGCTCGCTGTGGAGTGCCTGACAGTGGTGGTTTATGTAAACCCAGGAAAC   | 386  |
| QY | 333  | CTGGGTGGAGAAATACAACTCAGTACAGAAATATAAACTATACTCCGGATATGGCA     | 392  |
| Db | 387  | CCCAAGTGGGAACGCCTAACTTGACTACAGGATTCGAAACTATATACCCACAGCTGTCA  | 446  |
| QY | 393  | CGAGCTGCTGTGATGAGGCTATCCAAAGAGGTTTAGAGTGTGGAGCAAGTCACTCCA    | 452  |
| Db | 447  | GAGGCTGAGTAGAAGAGCTATCAAGGATGCCCTTTGAACTCTGGAGTGTGCATCACCT   | 506  |
| QY | 453  | CTAAAATTCACCAAGATTTCAAAGGGGATTGAGAGCATCATGATTCCTTTAGGACTCGA  | 512  |
| Db | 507  | CTCATCTTCACAGGATCTCACAGGAGAGGAGATATCAACATTCCTTTTACCAAGA      | 566  |
| QY | 513  | GTCCATGTTGGTGTCTCTGCTATTTTATGTTGCCCTTGGAGTGTCTGGCAATGCTTT    | 572  |
| Db | 567  | GATCAGGTGACAAATTTCTCA---TTTGATGACCAATGGAATCCTTCTCATGCTTT     | 623  |
| QY | 573  | CCTCTGTTCCGGTCTGGGTGTCACACTCAATTTTGTAGAGATCAAACTGAGCAAG      | 632  |
| Db | 624  | CAGCAGGCAAGGATTTGGAGAGATGCTCAATTTGATGCCGAAGAAACATGGACCAAC    | 683  |
| QY | 633  | GATGAGCAGGATTCAACTGTTTCTTGTGGCTGCTCATGAATTTGGTTCATGCACTGGGG  | 692  |
| Db | 684  | ACCTCCGCAAAATTAACAATTTCTTGTGCTGCTCATGAATTTGGCAATCTTTGGGG     | 743  |
| QY | 693  | CTCTCTCACTCAATGATCAACACAGCTTGTATGTTCCCAAAATATGTTCTCCCTGATCC  | 752  |
| Db | 744  | CTCGTCACTCTCTGACCTGCTGCTTGTATGATATCCCACTATGCTTTTCAAGGAAACC   | 803  |
| QY | 753  | AGAAAATACCACTTTTCTCAGGATGATATCAATGAATCCAGTCCATCTATGAGGCTG    | 812  |
| Db | 804  | AGCACTACTCACTCCCTCAAGATGATCAATGAGCATTCAGGCCATCTATGGA---CTT   | 860  |
| QY | 813  | CCTAAGGTACCTGTAAAGCAAGGAACCACTATACCCCATGCTGTGACCCCTGACTTG    | 872  |
| Db | 861  | TCAAGCAACCTTATCCAACCTACTGGAACAGCACACCAACCCCTGTGACCCCACTTG    | 920  |
| QY | 873  | ACTTTGAGGTATCAAACTTTTCGCAAGAGTAATGTTCTTTTAAAGGAGGACCACTA     | 932  |
| Db | 921  | ACATTTGATGCTATCACCACACTCCGTGGAGAAATACCTTTCTTTTAAAGACAGGTACTC | 980  |
| QY | 933  | TGGAGATCTATTATGATATCAGGATGTTGAGTTGAAATTAATGCTTCACTTCGGCA     | 992  |
| Db | 981  | TGGAGAGGATCCCTCAGCTACAAAGAGTCCAAATGAATTTTCTTCTTATTCCTGSCCA   | 1040 |
| QY | 993  | TCTCTGCCAGCTGATCTGCAAGCTGCATACAGAAA---CCCCAGAGATAAGATTCTGTT  | 1049 |
| Db | 1041 | TCCCTTCCAACTGGTATACAGCTGCTTATGAAGATTTTGACAGAGACCTCATTTTCTTA  | 1100 |



|                                                                   |      |                                                                |      |
|-------------------------------------------------------------------|------|----------------------------------------------------------------|------|
| QY                                                                | 1050 | TTTAAAGATGAAACCTTCTGGATGATCAGAGGATATGCTCTCTGCGAGATTATCCCAA     | 1109 |
| Db                                                                | 1101 |                                                                | 1160 |
| QY                                                                | 1110 | TCCATCATACATATAGTCTTTTCCAGGACGCTGTAAGAAATATAGATGAGCGCTCTGTGAT  | 1169 |
| Db                                                                | 1161 | GATATATCAAACTATGCTTCCAGAGCGTTCACAGCAATGACGAGCTGTTTCTA          | 1219 |
| QY                                                                | 1170 | AAGACCAAGAAACCTACTCTTTTGTGGGCAATTTGGTCTGGAGGTTTGATGAATG        | 1229 |
| Db                                                                | 1220 | -----CAGAAGTAAACATACTCTTTGTTAAATGACCAATCTCGAGATATGATAACAA      | 1274 |
| QY                                                                | 1230 | ACCAACCATGAGCAAGATTTCCCGCAGAGTGTGTAACACTTTCTGGGAATCAGT         | 1289 |
| Db                                                                | 1275 | AGACAATTCTAGGACCGAGGTATCCCAAAAGCATATCAGGTGCTTTCCAGGAATAGAG     | 1334 |
| QY                                                                | 1290 | ATCCGCTCTGATGCTGCTTTCCAGTACAAGGATTTCTTTTTCAGCCGCTGGATCAAG      | 1349 |
| Db                                                                | 1335 | AGTAAAGTTGATGAGTTTCCAGCAAGACATTTCTTCCATGCTTTCAGTGGACCAAGA      | 1394 |
| QY                                                                | 1350 | CAATTTGCAATACAACTAAGACAAAGAAATATTAACCGAATCATGAGAACTAATACTGG    | 1409 |
| Db                                                                | 1395 | TATTACGCAATTTGATCTATTGCTCAGAGAGTTACAGAGTTGCAAGAGGCAATAAATGG    | 1454 |
| QY                                                                | 1410 | TTTCAATGCCAAGA                                                 | 1423 |
| Db                                                                | 1455 | CTTAACTGTAGATA                                                 | 1468 |
| RESULT 10                                                         |      |                                                                |      |
| US-09-178-002-1                                                   |      |                                                                |      |
| ; Sequence 1, Application US/09178002                             |      |                                                                |      |
| ; Patent No. H001973                                              |      |                                                                |      |
| ; GENERAL INFORMATION:                                            |      |                                                                |      |
| ; APPLICANT: Hu, Shou-Ih                                          |      |                                                                |      |
| ; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant |      |                                                                |      |
| ; FILE REFERENCE: CGC 2048                                        |      |                                                                |      |
| ; CURRENT APPLICATION NUMBER: US/09/178,002                       |      |                                                                |      |
| ; CURRENT FILING DATE: 1998-10-22                                 |      |                                                                |      |
| ; NUMBER OF SEQ ID NOS: 9                                         |      |                                                                |      |
| ; SOFTWARE: PatentIn Ver. 2.0                                     |      |                                                                |      |
| ; SEQ ID NO 1                                                     |      |                                                                |      |
| ; LENGTH: 2314                                                    |      |                                                                |      |
| ; TYPE: DNA                                                       |      |                                                                |      |
| ; ORGANISM: Homo sapiens                                          |      |                                                                |      |
| ; FEATURE:                                                        |      |                                                                |      |
| ; NAME/KEY: CDS                                                   |      |                                                                |      |
| ; LOCATION: (232)..(1566)                                         |      |                                                                |      |
| US-09-178-002-1                                                   |      |                                                                |      |
| Query Match 26.1%; Score 425.4; DB 1; Length 2314;                |      |                                                                |      |
| Best Local Similarity 60.6%; Pred. No. 1.8e-114;                  |      |                                                                |      |
| Matches 794; Conservative 0; Mismatches 496; Indels 21; Gaps 5;   |      |                                                                |      |
| QY                                                                | 122  | TCAGGCATATCTCAACAGTTCTACTCTCTTCAAAATAGAGGAATCATCTTGTTCAAAG     | 181  |
| Db                                                                | 261  | TAATGACTACCTGGAAAGTTTCTCAATATCAAGACACAGTATCATGCTACAGGNA        | 320  |
| QY                                                                | 182  | CAAGAATAGGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTGGATTTGAC    | 241  |
| Db                                                                | 321  | GAATGGCACTAATGTGATCGTTGAAAGCTTAAAGAAATGCGAGCATTTTGGGTGAA       | 380  |
| QY                                                                | 242  | AGTGACTGAAACCTGGACTCAACCCCTTGAGTATCATGAGACACCCAGCTGTGGGT       | 301  |
| Db                                                                | 381  | TGTGACGGGGAAGCCAAATGAGGAAACTCTGACATGATGAAAGAGCCCTCGCTGTGGAGT   | 440  |
| QY                                                                | 302  | GCTGATGTGGCCAGTATGGCTTACACCC-----TCCCTGGGTGGAGAAAATACAACCT     | 355  |
| Db                                                                | 441  | GCTGACAGTGTGGTTTATGTTATACCCAGGAACCCCAAGTGGGAACGCATACCTT        | 500  |
| QY                                                                | 356  | CACCTACAGAAATAATAACTATCTCCGGATATGGCACGAGTGTCTGTGATGAGGCTAT     | 415  |
| Db                                                                | 501  | GACCTACAGGATTCGAAACTATATACCCCAACAGCTGTGAGAGGTGAGGTAGAAAGAGCTAT | 560  |
| RESULT 11                                                         |      |                                                                |      |
| US-09-280-116-77                                                  |      |                                                                |      |
| ; Sequence 77, Application US/09280116A                           |      |                                                                |      |

Patent No. 6331427  
GENERAL INFORMATION:  
APPLICANT: Robison, Keith E.  
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs  
FILE REFERENCE: 5800-24, 035800/176965  
CURRENT APPLICATION NUMBER: US/09/280,116A  
CURRENT FILING DATE: 1999-03-26  
NUMBER OF SEQ ID NOS: 268  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 77  
LENGTH: 474  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: matrix metalloproteases  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)..(474)  
OTHER INFORMATION: n = a, t, c or g  
US-09-280-116-77

Query Match 26.0%; Score 423; DB 3; Length 474;  
Best Local Similarity 100.0%; Pred. No. 3.7e-114;  
Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 641 AGGATTCAACTTCTTCTTGTGGCTGCTCATGAATTTGGTTCATGCACTGGGGCTCTCTCA 700  
DB |||||  
QY 701 CTCGAATGATCAACAGCCTTGATGTTCCAAATTAATGTTCTCCCTGGATCCCAAGAAATA 760  
DB |||||  
QY 761 CCACATTTCTCAGGATGATATCAATGGAATCCAGTCCATCTATGAGGTTCTGCTAAGGT 820  
DB |||||  
QY 821 ACCTGCTAAGCCAAAGAACCCACTATACCCATGCTGTGACCTGACTTGACTTTTGA 880  
DB |||||  
QY 881 CGTATFACAACCTTCCGAGAGAGTAATGTTCTTTAAAGGCAGGCACCTATGAGGAT 940  
DB |||||  
QY 941 CTATTATGATATCACGGATGTTGAGTTGAAATTAATGCTTCAATCTGCGCATCTCTGCC 1000  
DB |||||  
QY 1001 AGCTGATCTGCAAGCTGCAATACAGAACCCAGAGATAAGATTCTGTTTTTAAAGATGA 1060  
DB |||||  
QY 1061 AAA 1063  
DB |||||  
QY 471 AAA 473

RESULT 12  
US-08-068-392-1  
Sequence 1, Application US/08068392  
Patent No. 6150152  
GENERAL INFORMATION:  
APPLICANT: Shapiro, Steven M.  
TITLE OF INVENTION: Human Macrophage Metalloprotease  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SM  
STREET: 800 N. Lindbergh Blvd.  
CITY: St. Louis  
STATE: Missouri  
COUNTRY: USA  
ZIP: 63167

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/068,392  
FILING DATE: 19930528  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meyer, Scott J.  
REGISTRATION NUMBER: 25275  
REFERENCE/DOCKET NUMBER: 07-24 (12406)A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (314)694-3117  
TELEFAX: (314)694-5435  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1410 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1410  
US-08-068-392-1  
Query Match 23.9%; Score 389.4; DB 3; Length 1410;  
Best Local Similarity 59.0%; Pred. No. 5.1e-104;  
Matches 786; Conservative 0; Mismatches 526; Indels 21; Gaps 6;  
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DB |||||  
QY 163 GGAATCATCTGTTCAAAGCAAGATA---GGAGTCTCATAGATGACAAAATTCGGGAAA 219  
DB |||||  
QY 220 TGAAGACATTTTGGATTGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 279  
DB |||||  
QY 280 TGAAGACATTTTGGATTGACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 333  
DB |||||  
QY 334 CTGGGTGGAGAAATACAACTCAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 393  
DB |||||  
QY 394 GAGTCTGTGGATGAGGCTATCCAAGAGGTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 453  
DB |||||  
QY 454 TAAATTCACCAAGATTTCAAAGGAGTTGACAGATCATGATTTAGCTTTAGGACTCGAG 513  
DB |||||  
QY 514 TCATGGTTCGGTGTCTCTGCTATTTTGTGAGTCCCTTGGAGTGTCTTGGCCATGCTTTTC 573  
DB |||||  
QY 574 CTCTGGTTCGGGCTCTGGGTGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 633  
DB |||||  
QY 634 ATGAGCAGGATTCAACTTTGTTTCTTGTGGTGTCTGATGAATTTGGTGTATGCACTGGGGC 693  
DB |||||  
QY 694 TCTCTCACTCAATGATCAACAGCCTTGATGTTCCCAAAATTTATGTCCTCCCTGGATCCA 753  
DB |||||

Db 677 TTGGCCATTTAGTATCAAGCTGTAAATGTTCCCACTCAAAATATCTGCACATCA 736  
Qy 754 GAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATCTATGGAGTCTGC 813  
Db 737 ACACATTTGGCTCTCTGCTGATGACATAGTGGCAITCACTCTGTATGGAGACCAA 796  
Qy 814 CTAAGGTACCTGTGAAGCAAA---GGAAACCACTATACCCCATGCTGTGACCTGACT 870  
Db 797 AAGAGAACCACCGTTGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 856  
Qy 871 TGACTTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 930  
Db 857 TGAGTTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 916  
Qy 931 TATGAGGATCTATTATGATATACGAGTGTGAGTTTGAATTAATTTGCTTCTGCTGCT 990  
Db 917 TCTGGCTGAAGTTTCTGAGAGACCAAGACCAAGTGTAAATTAATTTCTTCTTATGGC 976  
Qy 991 CATCTCTGCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1047  
Db 977 CAACCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1036  
Qy 1048 TTTTAAAGATGAAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1107  
Db 1037 TTTTAAAGATGAAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1096  
Qy 1108 AATCCATCCATACATGAGTTTCCAGGAGTGTGAAGAAATAGATGACGCGCTGCTGCT 1167  
Db 1097 AGAGCATACATCTTTTGGTTTCTTAACTTTTGTGAAATAATTTGATGCTGCTGCT 1156  
Qy 1168 ATAAGACCAAGAAACCTACTCTTTTGGGCAATTTGCTGCTGCTGCTGCTGCTGCT 1227  
Db 1157 ACCACGTTTTATAGGACCTACTCTTTTGTAGATAACCGATTTTGGAGGTATGATGAA 1216  
Qy 1228 TGACCCAAACCATGCAAGAGATTCGCGAGAGAGTGTGTAACACTTCTCTGGAATCA 1287  
Db 1217 GGAGACAGATGATGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1276  
Qy 1288 GTATCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1344  
Db 1277 GGCCTAAATTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1336  
Qy 1345 CAAGCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1404  
Db 1337 CTAACCAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1396  
Qy 1405 CTGCTTTCAATG 1417  
Db 1397 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT

RESULT 13  
US-08-396-988-1

; Sequence 1, Application US/08396988  
; Patent No. 6204043  
; GENERAL INFORMATION:  
; APPLICANT: Shapiro, Steven M.  
; TITLE OF INVENTION: Human Macrophage Metalloproteinase  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SM  
; STREET: 800 N. Lindbergh Blvd.  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63167  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/396,988  
; FILING DATE: 01-MAR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/068,392  
; FILING DATE: 28-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyer, Scott J. 25275  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 07-24(12406)A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)694-3117  
; TELEFAX: (314)694-5435  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1410 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1410  
; US-08-396-988-1  
  
Query Match 23.9%; Score 389.4; DB 3; Length 1410;  
Best Local Similarity 59.0%; Pred. No. 5.1e-104; Indels 21; Gaps 6;  
Matches 786; Conservative 0; Mismatches 526;  
  
Qy 103 AAGAAATATGCAACTGGCTCAGGCATATCTCAACCAAGTTCTACTCTCTGAAATAGAG 162  
Db 80 AATATATGCTATTTGGTGAGAGATTTAGAAAAATTTATGGCCTTGAGATAACA 139  
Qy 163 GGAATCATCTTGTTCAGAGCAAGATA---GGAGTCTCATAGATGACAAATTCGGGAAA 219  
Db 140 AACTTCCAGTGACAAAAATGAAATATATAGTGGAAATCTTAATGAAGAAAAATCCAGAAA 199  
Qy 220 TGCAAGCATTTTGGATTGACAGTCACTGCAAACTGGACTCAAAACACCTTGAGATCA 279  
Db 200 TGCAGCACTTCTGGTCTGAAAGTACCGGGCACTGGACACATCTACCTTGGAGATGA 259  
Qy 280 TGAAGACACCCAGGTGTGGGTGCTGATGTGGGCCAGTATGGCTTACACCC-----TCC 333  
Db 260 TGCAGCACTTCTGGTGTGGGTGCTGATGTGGGCCAGTATGGCTTACACCC-----TCC 319  
Qy 334 CTGGTGGAGAAATATACAACTCCTACATGACAAATAATAAATACTACTCGGATATGGCAC 393  
Db 320 CCGTATGGAGAAACATTTATATCACTACGAATCAATTAATTAACACCTGACATGAACC 379  
Qy 394 GAGCTGTGCTGATGAGGCTATCCAAGAAAGTTTGAAGTGTGGAGCAAAAGTCACTCCAC 453  
Db 380 GTGAGATGTTGATCTAGCAATCGGAAGCTTTCCAGATGAGATGATGATGATGATGATGAT 439  
Qy 454 TAAATATCAACAAAGATTTCAGAGGGGATTCAGACATCATGATGCTCTTTAGGATCGAG 513  
Db 440 TGAATTCAGCAAGATTAAACAGGCAATGCTGATGATGATGATGATGATGATGATGATGATGAT 499  
Qy 514 TCCATGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 573  
Db 500 CTCATGGAGACTTCCATGC---TTTGTATGGCAAGGTGGAAATCTTACCCATGCTTTG 556  
Qy 574 CTCCTGTGCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 633  
Db 557 GACCTGGATCTGGCATTGGAGGGATGCACATTCGATGAGGACGAATTTCTGGACTACAC 616  
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Db 617 ATTCAGGAGGACAACTTTGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 676  
Qy 694 TCTCTCACTCCAAATGATCAACAGCCTTGTGTTTCCCAAAATTTATGCTCTCCCTGGATCCCA 753  
Db 677 TTGGCCATTTAGTATCAAGGCTGTAAATGTTTCCCACTCAAAATATCTGCACATCA 736



841 CCCTATACCCCATGCTGCTGACCTGACTTGCTTTGACGCTATCAACACTTTCCGCA 900  
885 CTGAGACCCAGTCAAAATGATCTGCTTTGCTTTGATGAGTCAACATGCTGAG 944  
901 GAGAGTAATGTTCTTTAAAGGAGGACCTATGAGGATCTATATGATATCAGGATG 960  
945 GGGAAATCTTATCTTTAAAGACAGGCACTCTGGCGTAGAACCCAGTGGAAATCCGAGC 1004  
961 TTGAGTTGATTAATGCTTCACTTGGCCATCTCTGCCAGTGAATGCAAGTGCAT 1020  
1005 CTGAATTCATTTGATTTGACATTTGGCCCTCTCTTCTTCCAGGCTTAGATGCTGCT 1064  
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1065 ATGAGGCAATAA CAAGACAGAGTTCTGATTTTAAAGGAAGTCAGTTCTGGGAGTCC 1124  
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1185 CCGTGAAGAGATGATGACGCTGTTTGAAGAGGAGAGAGAGACGTATTCTTTTG 1244  
1198 TGGCAATTTGCTGCTGGAGGTTTGATGAAATGACCCAAACCATGCAAAAGGATTTCCCGC 1257  
1245 TAGGTGACAAATCTGGAGATTTGATGAGACAGACAGCTATGATTAAGGCTTCCGA 1304  
1258 AGAGAGTGGTAAACACTTTCTCGATCAGATATCCGTTGTTGATGCTGCTTTCCAGTACA 1317  
1305 GACTGATAACAGATGACTTCCAGGAATGAGCCACAAAGTTGATGCTGTGTATGATGAT 1364  
1318 AAGGATCTCTTTTTCAGCGCTGATCAAGCAATTTGATCAACAAATTAAGACAAGA 1377  
1365 TTGGGTTTTTATTTCTCTGTGATCATCAGATTCGAGTTGACCCCAATGCGAGGA 1424  
1378 ATATTACCGGAATCATGAGAACTAATCTTGGTTTCAATGCAAAAGAACCA 1427  
1425 CGGTGACACACACTGAAGAGCAACAGCTGGCTTTGCTGATTAACA 1474

## RESULT 15

US-08-645-865-12  
; Sequence 12, Application US/08645865  
; Patent No. 5654406

## GENERAL INFORMATION:

; APPLICANT: RAZIUDIN  
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN  
; TITLE OF INVENTION: NEOPlastic DISEASE  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NEEDLE & ROSENBERG PC  
; STREET: 127 Peachtree Street, Suite 1200  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: usa  
; ZIP: 30303

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/645,865

; FILING DATE: 14 MAY 1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: PERRYMAN, DAVID G

; REGISTRATION NUMBER: 33,438

; REFERENCE/DOCKET NUMBER: 1414.608

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 404-688-0770

; TELEFAX: 404-688-9880  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1717 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-645-865-12

Query Match 23.3%; Score 379.2; DB 1; Length 1717;

Best Local Similarity 57.7%; Pred. No. 5.7e-101;  
Matches 791; Conservative 0; Mismatches 543; Indels 36; Gaps 5;

QY 91 TGACGGAAATGAAGAAATATGCAACTGGCTCAGGATATCTCAACAGTCTTACTCTC 150  
Db 108 TGACACAGACCACTCAACCATGGATCTTGTCTAGCAATACCTAGAAAAATACTACA 167  
QY 151 TTGAAATAGAGGGAATCATCTTCTTCAAGCAAGATAGAGTCTCTATAGATGACAAA 210  
Db 168 TTGAAAAAATGAGAAAAAATTTTCAAAAGAAAAAGACAGTAGTCTCTGTCTCAAAAA 227  
QY 211 TTCGGGAATGCAAGCAATTTTTCGATTGACAGTCTGGAAGAACTGGACTCAACACCC 270  
Db 228 TTGAAGAAATGCAAGATTCCTTGGCTTGGAGATGACAGGGAAGCTGAGCTCGAACCTG 287  
QY 271 TTGAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGCCAGTATGGCTACACCC 330  
Db 288 TGGAGATGATGACAAAGCCCGGTGTGGTGTCCCGAGCTTGGTGGCTTCAGTACCTTC 347  
QY 331 -----TCCCTGGGTGGAGAAAAATACAACTCACTACAGAAATATAAACTATATCTCGG 384  
Db 348 CAGGTTCAACCAATGGAGAAAAACACATCTCTACAGGATTTGAAATATATACACTGG 407  
QY 385 ATATGGCAGAGCTGCTGTGGATGAGCTATCCAGAGGATTTAGAGTGTGGAGCAAG 444  
Db 408 ATTACCAAGAGAGAGTGTGGATTTCTGCCATTGAGAGAGCTTTGAAGTCTGGAGGAGG 467  
QY 445 TCACCTCACTAAAAATTCACCAAGATTTCAAGGGGATTTGACAGATCATGATTTGCTTTA 504  
Db 468 TGACCCCACTCACATTTCCAGGATCTTGAAGAGAGGCTGACATATGATCTCTTTG 527  
QY 505 GGACTCGAGTCCATGTCGGGTGCTCGCTATTTTGTATGTCCTTGGGAGTGTCTGGCC 564  
Db 528 CAGTTGGAGAAATGAGAGACTTTTACCC---TTTTGTAGAGTGGGACAGAGCTTGGCTC 584  
QY 565 ATGCTTTCTCTCTGCTCGGCTGCTGGGTGTGACACTCAATTTTGATGAGATGAAAACT 624  
Db 585 ATGCTTACCCACCTGGCCCTGGATTTATGAGAGATGCTCACTTCGATGATGATGAGAA 644  
QY 625 GGACCAAGGATGAGACAGGATTTCAACTTTTGTGGCTGCTCATGAATTTGTCATG 684  
Db 645 GGTCACTGGGACCTCAGGGACCAATTTATTTCTGTTGCTGCGCATGAACTTGTCTACT 704  
QY 685 CACTGGGGCTCTCTCACTTCCAAATGATCAAAAGCCTTGTATGTTTCCCAAAATTA---TGTCT 741  
Db 705 CCCTGGGTCTCTTTCACTCAAAACAAAGAAATCTCTGATGATGACCCAGCTCTACAGTTCT 764  
QY 742 CCCTGGATCCCAAGAAATACCCACTTCTCAGGATGATATCAATGGATCCAGTCCATCT 801  
Db 765 CCAGAGCAAGCAACATTCGCTTCTCAGGATGATATAGAGGCAATTCATCCCTGT 824  
QY 802 ATGGAGGTC-----TGCCCTAAGGTACCTGTCTAAGCCAAAGGAAC 840  
Db 825 ATGGAGCCCGCCCTCTCTGTGATGCCACAGTGGTTCCTGTGCTCTGTCTCTCAAAAC 884  
QY 841 CCATATACCCCATGCTCTGACCCCTGACCTTGAATTTTGAAGCTATCAACATTTCCGCA 900  
Db 885 CTGAGACCCAGTCAAAATGATCTCTGCTTTGTCTTTGATGCACTACCTGCTGAGAG 944  
QY 901 GAGAAATGATGTTCTTTAAAGCAGGACCTATGAGGATCTATTTATGATATCAAGGATG 960  
Db 945 GGGAAATCTCTATTCTTTAAAGACAGGCACTTCTGGCGTAGAACCCAGTGGAAATCCGAGC 1004

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QY 961 TTGAGTTTGAATTAATGCTTCATCTGCGCATCTCTGCCAGCTGATCTGCAAGCTGCAT 1020
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1005 CTGAATTCATTTGATTTTTCAGCATTTTGCCCTCTCTCTTCCTTCAGCTTAGATGCTGCT 1064
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1021 ACGAG---AACCCGAGAGATAAGATTCTGGTTTTTAAAGATGAAAACTTCTGGATGATCA 1077
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1065 ATGAGGCAAAATACCAAGACAGATTCATGATTTTAAAGGAAGTCAGTTCTGGGAGTCC 1124
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1078 GAGGATATGCTCTCTTGCCAGATTAATCCAAATCCATCCATACATTAAGTTTTCAGGAC 1137
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1125 GAGGAAATGAAGTCCCAAGCAGGTTACCCAAAGAGGATCCACACTCTTTGGCTTTCTCCCA 1184
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1138 GTGTGAAGAAATAGATGAGCCGCTCTGTGATAAGACCAAGAAAACTTACTTCTTTG 1197
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1185 CCGTGAAGGAAGATTGATGAGCTGTTTTTGAAGAGAGAGAGACGATATTTCTTTG 1244
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1198 TGGGCATTTTGGTGTGGAGGTTTGATGAAATGACCCAAACCATGGACAAAGGATTCCTCGC 1257
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1245 TAGGTGACAAATACTGGAGATTTGATGACAAAGACAGCTTATGGATAAAGGCTTCCCGA 1304
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1258 AGAGAGTGGTAATAACACTTCTCTGGAATCAGTATCCGTTGATGCTGCTTTCCAGTACA 1317
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1305 GACTGATAACAGATGACTTCCAGGAATTGAGCCCAAGTTGATGCTGTGTACATGCTAT 1364
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1318 AAGGATTTCTTTTTCAGCCGTTGGATCAAGCAATTTGAATACACATTAAGACAAAGA 1377
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1365 TTGGGTTTTTTTATTTCTCTGTGGATCATCAAGTTGAGTTGACCCCAATGCCAGGA 1424
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1378 ATATTACCCGAATCATGAGAACTAATPACTTGGTTTCAATGCAAGAAACCA 1427
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1425 CCGTGACACACACACTGAAGAGCAACAGCTGGCTGTTGTGCTGATTATCA 1474
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Job time : 162 secs



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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 15, 2004, 21:08:48 ; Search time 136 Seconds  
(without alignments)  
2681.137 Million cell updates/sec

Title: US-10-729-807-10

Perfect score: 2763

Sequence: 1 MKRLLLCLFFITFSSAPFL.....SLSLFFIGIVHLKNTSIYQ 513

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOC=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued\_Patents\_NA:\*  
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2: /cgn2.6/prodata/1/ina/5B COMB.seq:\*  
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5: /cgn2.6/prodata/1/ina/PCUTUS COMB.seq:\*  
6: /cgn2.6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID              | Description       |
|------------|--------|-------------|--------|--------------------|-------------------|
| 1          | 2763   | 100.0       | 1845   | US-09-862-631-1    | Sequence 1, Appli |
| 2          | 2752   | 99.6        | 1647   | US-10-140-002-191  | Sequence 191, App |
| 3          | 2455   | 88.9        | 1687   | US-09-280-116-78   | Sequence 78, Appl |
| 4          | 1254   | 45.4        | 1434   | US-09-023-655-1174 | Sequence 1174, Ap |
| 5          | 1250   | 45.2        | 1801   | US-09-023-655-1374 | Sequence 1374, Ap |
| 6          | 1198.5 | 43.4        | 1717   | US-08-229-515A-12  | Sequence 12, Appl |
| 7          | 1198.5 | 43.4        | 1717   | US-08-645-865-12   | Sequence 12, Appl |
| 8          | 1161.5 | 42.0        | 1970   | US-09-023-655-1264 | Sequence 1264, Ap |
| 9          | 1161   | 42.0        | 2223   | US-09-178-002-3    | Sequence 3, Appli |
| 10         | 1161   | 42.0        | 2223   | US-09-023-655-1040 | Sequence 1040, Ap |
| 11         | 1153.5 | 41.7        | 1981   | US-09-484-970B-62  | Sequence 62, Appl |
| 12         | 1133   | 41.0        | 1410   | US-08-068-392-1    | Sequence 1, Appli |

|    |        |      |      |   |                    |                   |
|----|--------|------|------|---|--------------------|-------------------|
| 13 | 1133   | 41.0 | 1410 | 3 | US-08-396-988-1    | Sequence 1, Appli |
| 14 | 1132   | 41.0 | 1521 | 4 | US-08-994-689C-18  | Sequence 18, Appl |
| 15 | 1132   | 41.0 | 2792 | 4 | US-08-994-689C-8   | Sequence 8, Appli |
| 16 | 1127   | 40.8 | 2314 | 1 | US-09-178-002-1    | Sequence 1, Appli |
| 17 | 1033.5 | 37.4 | 1160 | 3 | US-07-780-973-15   | Sequence 15, Appl |
| 18 | 786.5  | 28.5 | 474  | 3 | US-09-280-116-77   | Sequence 77, Appl |
| 19 | 769.5  | 27.9 | 2123 | 3 | US-09-194-468A-29  | Sequence 29, Appl |
| 20 | 718    | 26.0 | 1923 | 3 | US-09-294-841-1    | Sequence 1, Appli |
| 21 | 715.5  | 25.9 | 3530 | 3 | US-08-704-711A-10  | Sequence 10, Appl |
| 22 | 715.5  | 25.9 | 3530 | 3 | US-09-521-220-10   | Sequence 10, Appl |
| 23 | 713.5  | 25.8 | 2116 | 3 | US-09-000-041A-1   | Sequence 1, Appli |
| 24 | 713.5  | 25.8 | 2116 | 4 | US-09-734-002-1    | Sequence 1, Appli |
| 25 | 713    | 25.8 | 3403 | 3 | US-08-448-489-2    | Sequence 2, Appli |
| 26 | 713    | 25.8 | 3437 | 3 | US-08-704-711A-9   | Sequence 9, Appli |
| 27 | 713    | 25.8 | 3437 | 3 | US-09-521-220-9    | Sequence 9, Appli |
| 28 | 713    | 25.8 | 3437 | 4 | US-09-919-497-34   | Sequence 34, Appl |
| 29 | 672    | 24.3 | 3456 | 3 | US-08-704-711A-8   | Sequence 8, Appli |
| 30 | 672    | 24.3 | 3456 | 3 | US-09-521-220-8    | Sequence 8, Appli |
| 31 | 600    | 21.7 | 825  | 3 | US-08-896-062-1    | Sequence 1, Appli |
| 32 | 597    | 21.6 | 2335 | 4 | US-09-799-451-346  | Sequence 346, App |
| 33 | 594.5  | 21.5 | 837  | 1 | US-08-371-082-1    | Sequence 1, Appli |
| 34 | 594.5  | 21.5 | 1078 | 3 | US-09-492-543-28   | Sequence 28, Appl |
| 35 | 594.5  | 21.5 | 1078 | 3 | US-09-492-543-29   | Sequence 29, Appl |
| 36 | 594.5  | 21.5 | 1078 | 4 | US-09-023-655-1368 | Sequence 1368, Ap |
| 37 | 594    | 21.5 | 2334 | 1 | US-08-457-304A-33  | Sequence 33, Appl |
| 38 | 594    | 21.5 | 2334 | 1 | US-08-456-701A-33  | Sequence 33, Appl |
| 39 | 594    | 21.5 | 2334 | 4 | US-08-684-932A-33  | Sequence 33, Appl |
| 40 | 594    | 21.5 | 2334 | 4 | US-09-023-655-996  | Sequence 996, App |
| 41 | 590    | 21.4 | 2260 | 1 | US-07-794-393-3    | Sequence 3, Appli |
| 42 | 590    | 21.4 | 2260 | 1 | US-08-001-711-3    | Sequence 3, Appli |
| 43 | 580    | 21.0 | 2247 | 4 | US-09-023-655-1410 | Sequence 1410, Ap |
| 44 | 580    | 21.0 | 2256 | 1 | US-07-794-393-1    | Sequence 1, Appli |
| 45 | 580    | 21.0 | 2256 | 1 | US-08-001-711-1    | Sequence 1, Appli |

#### ALIGNMENTS

RESULT 1

US-09-862-631-1  
; Sequence 1, Application US/09862631  
; Patent No. 6734005  
; GENERAL INFORMATION:  
; APPLICANT: Holmgren, Erik  
; APPLICANT: Kihlen, Mats  
; APPLICANT: Wood, Tim  
; APPLICANT: Ekblom, Jonas  
; TITLE OF INVENTION: No. 6734005el Matrix Metalloproteinases  
; FILE REFERENCE: 00014regus  
; CURRENT APPLICATION NUMBER: US/09/862,631  
; CURRENT FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: 206119  
; PRIOR FILING DATE: 2000-05-22  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 1845  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-862-631-1

Alignment Scores:  
Pred. No.: 0  
Score: 2763.00  
Length: 1845  
Matches: 513  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Conservative: 0  
Query Match: 100.00%  
Mismatches: 0  
DB: 4  
Indels: 0  
Gaps: 0

US-10-729-807-10 (1-513) x US-09-862-631-1 (1-1845)

QY 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheLeuThrPheSerSerAlaPheProLeu 20

DB 24 ATGAAGCGCTTCGCTTCCTGTTGTTCTTATACATTTCTTCGATTCCTCCCTTA 83

|    |      |                                                              |      |
|----|------|--------------------------------------------------------------|------|
| Qy | 21   | ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe | 40   |
| Db | 84   | GTCCGGATGACGGAATAAGAAAAATATGCAACTGGCTCAGGCATATCTCAACCACTTC   | 143  |
| Qy | 41   | TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp | 60   |
| Db | 144  | TACTCTCTTGAATAGAAAGGAATCTCTTGTTCAAAGCAAGAAATAGAGTCTCATAGAT   | 203  |
| Qy | 61   | AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer | 80   |
| Db | 204  | GACAAAATTCGGGAATTCGAAGCATTTTGGATTGACAGTGACTGGAAAACCTGACTCA   | 263  |
| Qy | 81   | AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly | 100  |
| Db | 264  | AACACCTTCAGATCATGAACACACCCAGGTGTGGGTGCTGATGTGGGCGAGTATGGC    | 323  |
| Qy | 101  | TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro | 120  |
| Db | 324  | TACACCTTCCTCGGTGGAGAAATACACCTCCTACAGTAATAAATACTATCTCCG       | 383  |
| Qy | 121  | AspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys | 140  |
| Db | 384  | GATATGGCAGCAGCTGCTGTGGATGAGGCTATCCAAAGAAGTTTAGAAGTGTGGAGCAA  | 443  |
| Qy | 141  | ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe | 160  |
| Db | 444  | GTCACTCCACTAAAATTCACCAAGATTTCAAAGGGGATTCAGACATCATGATTCCTTT   | 503  |
| Qy | 161  | ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly | 180  |
| Db | 504  | AGGACTCGAGTCCATGGTGGTGCTCCTCGCTATTTTGAATGCTCCCTGGGAGTGTGGC   | 563  |
| Qy | 181  | HisAlaPheProProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn | 200  |
| Db | 564  | CATGCTTCTCTCTGCTCGGGTCTGGTGTGACCTCATTTTGTATGAGGATGAAAC       | 623  |
| Qy | 201  | TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis | 220  |
| Db | 624  | TGGACCAAGATGGAGCAGGATTCAACTTGTTCCTGTGGCTGCTCATGAATTTGGTCAT   | 683  |
| Qy | 221  | AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer | 240  |
| Db | 684  | GCATGGGGCTCTCTCATCTCAATGATCAACAGCCTTGATGTTCCTCAAAATATGCTCC   | 743  |
| Qy | 241  | LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr    | 260  |
| Db | 744  | CTGGATCCAGAAATACCCACTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT    | 803  |
| Qy | 261  | GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp | 280  |
| Db | 804  | GGAGGTCTGCCTAAGGTACTCTAAGCCAAAGGAACCCACTATACCCCATGCCCTGTGAC  | 863  |
| Qy | 281  | ProaspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly | 300  |
| Db | 864  | CCTGACTTGACTTTTGAGCTATCAACACTTCCGAGAGAGTAATGTTCTTTAAAGGC     | 923  |
| Qy | 301  | ArgHisLeuTyrArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer | 320  |
| Db | 924  | AGGCACCTATGGAGGATCTATTATGATATCAGGATGTGAGTTTGAATTAATTCCTTCA   | 983  |
| Qy | 321  | PheThrProSerLeuProAlaAspLeuGlnAlaIaTyrGluAsnProArgAspLysIle  | 340  |
| Db | 984  | TTCTGGCCATCTCTGCCACTGATCTGCAAGCTGCATACGAAACCCAGAGATAGATT     | 1043 |
| Qy | 341  | LeuValPheLysAspGluAsnPheTyrMetIleArgGlyTyrAlaValLeuProAspTyr | 360  |
| Db | 1044 | CTGGTTTTTAAGATGAAGAAACTTCTGGATGATCAGAGGATATGCTCTCTGCGAGATTAT | 1103 |
| Qy | 361  | ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaIaVal  | 380  |
| Db | 1104 | CCCAAAATCCATCATATAGTTTTCAGGACGTTGTGAAGAAAAATAGATGACGCGTC     | 1163 |

|    |      |                                                                |      |
|----|------|----------------------------------------------------------------|------|
| Qy | 381  | CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTyrArgPheAsp   | 400  |
| Db | 1164 | TGTGATAAGACCAACAGAAAAACCTACTTCTTTGTGGCAATTTGGTCTGGAGGTTTGT     | 1223 |
| Qy | 401  | GluMetThrGlnThrMetAspLysGlyPheProGlnArgValLysHisPheProGly      | 420  |
| Db | 1224 | GAATGACCCCAACCATGGACAAAGGATTCCTCCGAGAGAGTGGTAAACACACTTTCTCTGGA | 1283 |
| Qy | 421  | IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArgGly      | 440  |
| Db | 1284 | ATCAGTATCCGTGTGATGCTGCTTTCCAGTACAAAGATTCCTCTTTTTCAGCCGTGGA     | 1343 |
| Qy | 441  | SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn   | 460  |
| Db | 1344 | TCAAAGCAATTTGAATACACATTAACAAAGAAATATTACCCGAATCATGAGAACTAAT     | 1403 |
| Qy | 461  | ThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu   | 480  |
| Db | 1404 | ACTTGGTTTCAATGCAAAAGAACCAAGAACTCTCTCATTTGTTTGTATATCAACAGGAA    | 1463 |
| Qy | 481  | LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe   | 500  |
| Db | 1464 | AAACACATTCAGGAGGCATTAAGATATTGTATCATAGAGTTTAAGCTTCTTTATTTT      | 1523 |
| Qy | 501  | GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln                        | 513  |
| Db | 1524 | GGTATTGTTTCATTTTGTCTGAAAAACACATCTATTATCAAA                     | 1562 |

RESULT 2

US-10-140-002-191

; Sequence 191, Application US/10140002

; Patent No. 6725730

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330RIC59

; CURRENT APPLICATION NUMBER: US/10/140,002

; CURRENT FILING DATE: 2002-05-06

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 191

; LENGTH: 1647

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-140-002-191

Alignment Scores:

Pred. No.: 0

Score: 2752.00

Percent Similarity: 99.81%

Best Local Similarity: 99.81%

Query Match: 99.60%

DB: 4

Length: 1647

Matches: 512

Conservative: 0

Mismatches: 1

Indels: 0

Gaps: 0

US-10-729-807-10 (1-513) x US-10-140-002-191 (1-1647)

QY 1 MetLysArgLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeu 20  
 DB 24 ATGAAGCGCTTCTGCTTCTGTTTGTCTTTATAACATTTTCTCTGCAATTTCCCTTA 83  
 QY 21 ValArgMetThrGluAsnGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPhe 40  
 DB 84 GTCCCGGATGACCGAAATGAGAAATATGCAACTGGCTCAGGCATATCTCAACAGATTC 143  
 QY 41 TyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAsp 60  
 DB 144 TACTCTCTTGAATAGAGGGAATCATCTGTTCAAAGCAAGAAATAGGAGTCTCATAGAT 203  
 QY 61 AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer 80  
 DB 204 GACAAATTCGGAAATGCAAGCAATTTTGGATTGACAGTGACTGGAAAACCTGCACTCA 263  
 QY 81 AsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGly 100  
 DB 264 AACACCTTGAGATCATGAAGACACCCAGGTGTGGGTGCTGATGTGGCCAGTATGCG 323  
 QY 101 TyrThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrPro 120  
 DB 324 TACACCTTCCCTGGGTGGAGAAATACACCTCACTACAGAAATATAAATATATCTCG 383  
 QY 121 AspMetAlaArgAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLys 140  
 DB 384 GATATGGCAGCGCTGCTGTGATGAGGCTATCCAAAGAGGTTTAGAAGTGTGGAGCAAA 443  
 QY 141 ValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPhe 160  
 DB 444 GTCACTCCACTAAATTCACCAAGATTTCAAAGGGGATTCAGACATCATGATTCCTTT 503  
 QY 161 ArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGly 180  
 DB 504 AGGACTCGAGTCCATGGTGGGTGCTCTCGCTATTTTGGTGGTCCCTTGGGAGTGTCTGGC 563  
 QY 181 HisAlaPheProGlyProGlyLeuGlyAspThrHisPheAspGluAspGluAsn 200  
 DB 564 CATGCTTTTCTCTCTGCTCGGCTCTGGGTGGTGACATCTATTTTGTAGAGATGAAAC 623  
 QY 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaHisGluPheGlyHis 220  
 DB 624 TGGACCAAGATGGAGCAGGATTCAACTTGTCTGTGGTCTCATGAATTTGGTCTAT 683  
 QY 221 AlalaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240  
 DB 684 GCATGGGGCTCTCTCACTCAATGATCAACAGCCCTTGATGTTCCTCAAAATATATCTCC 743  
 QY 241 LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr 260  
 DB 744 CTGGATCCAGAAATATCCACTTCTCAGGATGATATCAATGGAATCCAGTCCATCTAT 803  
 QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280  
 DB 804 GGAGGTCTGCTTAAGGTACCTGCTAAGCAAGAAACCCACTATATACCCCATGCTGTGAC 863  
 QY 281 ProAspLeuThrPheAspAlaIleThrPheArgArgGluValMetPhePheLysGly 300  
 DB 864 CTGACTTGACTTTTGACGCTATCACTTCCGACAGAGTAAATGTCTTTAAAGGC 923  
 QY 301 ArgHisLeuTyrArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320  
 DB 924 AGGCACCTATGGAGATCTATATGATATCAGGATGTTGAGTTTCAATTAATTTGCTTCA 983  
 QY 321 PheTyrProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnProArgAspLysIle 340  
 DB 984 TTCTGGCCATCTCTCCAGCTGATCTGCAAGCTGCATACAGAAACCCAGAGATAAGATT 1043  
 QY 341 LeuValPheLysAspGluAsnPheTyrMetIleArgGlyTyrAlaValLeuProAspTyr 360  
 DB 1044 CTGGTTTTAAAGATGAAGAACTTCTGGATGATCAGAGGATATGCTGTTCGCAATTAT 1103  
 QY 361 ProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaVal 380

DB 1104 CCCAANTCCATCATCATAGTTTTCAGAGCGTGTGAAGAAATAGATGCAGCCGTC 1163  
 QY 381 CysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTyrPheArgPheAsp 400  
 DB 1164 TGTGATAAGACCAACAGAAAAACCTACTTCTTTGTGGGCATTTGGTCTCGAGGTTTGAT 1223  
 QY 401 GluMetThrGlnThrMetAspLysGlyPheProGlnArgValValIleHisPheProGly 420  
 DB 1224 GAAATGACCCCAACCATGGACAAGGATTCGCGCAGAGAGTGGTAAACACATTTCTCTGA 1283  
 QY 421 IleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePhePheSerArgGly 440  
 DB 1284 ATCAGTATCCGTTGTGATGCTGCTTTCCAGTACAAGAGATCTCTTTTTCAGCCGTGA 1343  
 QY 441 SerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsn 460  
 DB 1344 TCAAGCAATTTGAATACAAATTAAGACAAAGAAATATTACCGAATCATGAGAACTAAT 1403  
 QY 461 ThrTyrPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLysGlu 480  
 DB 1404 ACTTGGTTTCAATGCAAGAACCAAGAACTCTCTATTTGGTTTGTATATCAACAGGAA 1463  
 QY 481 LysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIlePhe 500  
 DB 1464 AAAGCACATTCAGAGGCGCATTAAGATATTGTATCATAGAGTTTAAGCTTGTATTATTT 1523  
 QY 501 GlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513  
 DB 1524 GGTATTGTATCTTCTGAAAAACACTTCTATTTATCA 1562

## RESULT 3

US-09-280-116-78/c  
 ; Sequence 78, Application US/09280116A  
 ; Patent No. 6331427  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robison, Keith E.  
 ; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs  
 ; FILE REFERENCE: 5800-24, 035800/176965  
 ; CURRENT APPLICATION NUMBER: US/09/280,116A  
 ; CURRENT FILING DATE: 1999-03-26  
 ; NUMBER OF SEQ ID NOS: 268  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 78  
 ; LENGTH: 1687  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; OTHER INFORMATION: matrix metalloproteases  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(1687)  
 ; OTHER INFORMATION: n = a, t, c or g  
 US-09-280-116-78

Alignment Scores:  
 Pred. No.: 3.83e-288 Length: 1687  
 Score: 2455.00 Matches: 454  
 Percent Similarity: 99.78% Conservative: 0  
 Best Local Similarity: 99.78% Mismatches: 0  
 Query Match: 88.85% Indels: 1  
 DB: 3 Gaps: 0

US-10-729-807-10 (1-513) x US-09-280-116-78 (1-1687)

QY 60 AspAspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAsp 79  
 DB 1675 GATGACAAATTCGGGAATTCGAAGCATTTTGGATTGACAGTGACTGGAATACTGAC 1616  
 QY 80 SerAsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGlnTyr 99  
 DB 1615 TCAACACCCCTTGAGATCATGAGACACCCAGGTTGGGGTGCCTGATGTGGCCAGTAT 1556

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QY 100 GlyTyrThrIeuProGlyTrpArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThr 119
Db 1555 GGCTACACCTCCCTGGGTGGAGAAATACAACTCACCTACAGAAATATAAACTATACT 1496
QY 120 ProAspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTrpSer 139
Db 1495 CCGGATATGGCAGAGCTGCTGTGGATGAGGCTATCCAAGAAGTTTAGAAGTGTGGAGC 1436
QY 140 LysValThrProLysLysPheThrLysIleSerLysGlyIleAlaIleMetIleAla 159
Db 1435 AAAGTCACCTCCACTAAAATTCACCAAGATTTCAAAGGGGATTCAGACATCATGATGCC 1376
QY 160 PheArgThrArgValHisGlyArgCysProArgTyrPheAspGlyProLysGlyValLeu 179
Db 1375 TTTAGGACTCGAGTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1316
QY 180 GlyHisAlaPheProGlyProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGlu 199
Db 1315 GGCATGCTCTTCTCTGCTCGGGTCTGGGTGGTGCACACTCATTTTATGAGGATGAA 1256
QY 200 AsnTrpThrLysAspGlyAlaGlyPheAsnLeuPheValAlaHisGluPheGly 219
Db 1255 AACTGGACCAAGAGTGGAGCAGGATTCAACTTGTCTTGTGGTGTCTCATGAATTTGGT 1196
QY 220 HisAlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrVal 239
Db 1195 CATGCACTGGGGCTCTCTCACTCAATGATCAACACGCTTGATGTTCCCAATATATGTC 1136
QY 240 SerLeuAspProArgLysTrpProLeuSerGlnAspAspIleAsnGlyIleGlnSerIle 259
Db 1135 TCCCTGGATCCAGAAAATACCCACTTTCTCAGGATGATATCAATGGAATCCAGTCCATC 1076
QY 260 TyrGlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCys 279
Db 1075 TATGGAGTCTGCTGAGTACCTGCTTAAGCCAAAGGAACCCACTATACCCCATGCTGT 1016
QY 280 AspProAspLeuThrPheAspAlaIleThrPheArgArgGluValMetPhePheLys 299
Db 1015 GACCTGACTGACTTTTGACGCTATCACAACTTTCGCGAGAGAGTAATGTTCTTTAAA 956
QY 300 GlyArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAla 319
Db 955 GGCAGGCACCTATGAGGATCTATTATGATATACGAGATGTGAGTTGATTAATGCT 896
QY 320 SerPheTrpProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnProArgAspLys 339
Db 895 TCATTCTGGCCATCTCTGCCAGCTGATCTGCAAGCTCATACGAGAACCCAGAGATAAG 836
QY 340 IleLeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAsp 359
Db 835 ATCTGTTGTTTAAAGATGAAAACCTCTCGGATGATCAGGATATGCTGCTGCCAGAT 776
QY 360 TyrProLysSerIleHisThrLeuGlyPheProGly-ArgValLysLysIleAspAlaAl 379
Db 775 TATCCCAATCCATCCATACATATTAGTGTTCAGGACCGTGTGAAGAAAATAGATGCAGC 716
QY 379 aValCysAspLysThrThrArgLysThrTyrPhePheValGlyIleTrpCysTrpArgPh 399
Db 715 CGTCTGTGTAAGACCAACAAAGAAACCTACTCTTTGTGGGCATTTTGGTGTGGAGTT 656
QY 399 eAspGluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPhePr 419
Db 655 TGATGAATGACCCAAACCATGGCAAGAGATTCGCGAGAGAGTGGTAAACACTTTCC 596
QY 419 oGlyIleSerIleArgValAspAlaIlePheGlnTyrLysGlyPhePhePheSerAr 439
Db 595 TGGAAATCAGTATCCGTGTGATGCTGCTTCCAGTACAAAGGATTCCTCTTTTTCAGCGC 536
QY 439 gGlySerLysGlnPheGlnTyrAsnIleLysThrIysAsnIleThrArgIleMetArgTh 459
Db 535 TGGATCAAAGCAATTTGAATACAAATTAAGACAAAGAAATATTACCGAATCATGAGAAC 476
QY 459 rAsnThrTrpPheGlnCysLysGluProLysAsnSerSerPheGlyPheAspIleAsnLys 479
```

```
Db 475 TAATACTTGGTTTCAATGCAAGAACCAAGAACTCCTCATTTGGTTTTCATATCAACA 416
QY 479 sGluLysAlaHisSerGlyGlyIleLysIleLeuTyrHisLysSerLeuSerLeuPheIl 499
Db 415 GGAAGAACGACATTCAGGAGGCATAAAGATATTGTATCATATAAGAGTTTAAGCTTGT 356
QY 499 ePheGlyIleValHisLeuLeuLysAsnThrSerIleTyrGln 513
Db 355 TTTTGTATTGTTTCAATTTGCTGTAACAACTTCTATTATCA 313

RESULT 4
US-09-023-655-1174
; Sequence 1174, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1174:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1434 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g188618
; US-09-023-655-1174

Alignment Scores:
Pred. No.: 3,4e-142 Length: 1434
Score: 1254.00 Matches: 247
Percent Similarity: 66.04% Conservative: 70
Best Local Similarity: 51.46% Mismatches: 145
Query Match: 45.39% Indels: 18
DB: 4 Gaps: 9

US-10-729-807-10 (1-513) x US-09-023-655-1174 (1-1434)
QY 1 MetLysArgLeuLeuLeuLeuCysLeuPhePheIleThrPheSerSerAlaPheProLeu 20
Db 1 ATGAAGAGTCTCTCCAATCTACTGTTGCGTGGCAGCTTGTGCTCAGCCTATCCATTG 60
```

|    |      |                                                               |                                   |           |    |
|----|------|---------------------------------------------------------------|-----------------------------------|-----------|----|
| Qy | 21   | ValArgMetThrGluAsnGluGlu---                                   | AsnMetGlnLeuAlaGlnAlaTyrl         | LeuAsnGln | 39 |
| Db | 61   | GATGGAGCTGCAGGGGTGAGCACCAGCATGAACTTGTTCAGAAATATCTGAA          | AAC                               | 120       |    |
| Qy | 40   | PheTyrSerLeuGluIleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeu     | Ile                               | 59        |    |
| Db | 121  | TACTACGACCTCGAAAAAGATGTGAAACAGTTGTITAGGAGAAAGACAGTGGTCTCTGT   | 180                               |           |    |
| Qy | 60   | AspAspIysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeu     | Asp                               | 79        |    |
| Db | 181  | GTTTAAAAAATCCCGAGAAATCGAGAAGTTCCTGTGATTGGAGGTACGCGGGGAAGTGGAC | 240                               |           |    |
| Qy | 80   | SerAsnThrLeuGluIleMetIysThrProArgCysGlyValProAspValGlyGlnTyr  | 99                                |           |    |
| Db | 241  | TCCGACACTCTGGAGGTGATGCGCAAGCCAGGTCTGGAGTTCCTGACGTTGGTCACTTC   | 300                               |           |    |
| Qy | 100  | GlyTyrThrLeuProGly-----                                       | TrpArgLysTyrAsnLeuThrTyrArgIleIle | 116       |    |
| Db | 301  | ---AGAACCTTTCTCTGGCATCCCGAAGTGTGGAGAAACCCACCTTACATACAGGATTGTG | 357                               |           |    |
| Qy | 117  | AsnTyrThrProAspMetAlaArgAlaAlaValAspGluAlaIleGlnGlnGlyLeuGlu  | 136                               |           |    |
| Db | 358  | AATTATACACAGATTGCCAAAGATGCTGTGTGATTCTGCTGTGTGAGAAAGCTCTGAA    | 417                               |           |    |
| Qy | 137  | ValTrpSerIysValThrProLeuLysPheThrIysIleSerLysGlyIleAlaAsp     | Ile                               | 156       |    |
| Db | 418  | GTCTGGGAAGAGGTACTCCACTCACATTTCTCCAGGCTGTATGAAGGAGAGCTGATATA   | 477                               |           |    |
| Qy | 157  | MetIleAlaPheArgThrArgValHisGlyArg---                          | CysProArgTyrPheAspGlyPro          | 175       |    |
| Db | 478  | ATGATCTCTTTTGGCATTAGAGAACATGGAGACTTTTACCCT-----               | TTTGATGGACCT                      | 531       |    |
| Qy | 176  | LeuGlyValLeuGlyHisAlaPheProGlyProGlyLeuGlyValAspThrHisPhe     | 195                               |           |    |
| Db | 532  | GGAAATGTTTTGGCCATGCTCTATGCCCTGGCCAGGGATTAA                    | TGGAGATGCCACATT                   | 591       |    |
| Qy | 196  | AspGluAspGluAsnTrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAla     | Ala                               | 215       |    |
| Db | 592  | GATGATGAACAATGGACAAAGGATACACAGGGACCAATTTATTTCTCGTTGCTGCT      | 651                               |           |    |
| Qy | 216  | HisGluPheGlyHisAlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPhe  | 235                               |           |    |
| Db | 652  | CATGAATTTGGCCACTCCCTGGTCTCTTTCACTCAGCCACACTGAAGCTTTGATGATC    | 711                               |           |    |
| Qy | 236  | ProAsnTyrValSerLeu---AspProArgLysTyrProLeuSerGlnAspAspIleAsn  | 254                               |           |    |
| Db | 712  | CCACTCTATCACTCACTCACAGACCTGACTCGGTTCCGCTGTCTCAAGATGATATAAT    | 771                               |           |    |
| Qy | 255  | GlyIleGlnSerIleTyrGly-----                                    | GlyLeuProLysValProAla             | 268       |    |
| Db | 772  | GGCATTCAGTCCCTATATGACCTCCCGCTGACTCCCGCTGAGACCCCTCGTACCCACG    | 831                               |           |    |
| Qy | 269  | Lys-----ProLysGluProThrIleProHisAlaCysAspProAspLeuThrPheAsp   | 286                               |           |    |
| Db | 832  | GAACCTGTCCCTCCAGAACCTGGGACGCGCAGCCAACTGTGATCTGTCTGTCTCTTGAT   | 891                               |           |    |
| Qy | 287  | AlaIleThrThrPheArgArgGluValMetPhePheLysGlyArgHisLeuTrpArgIle  | 306                               |           |    |
| Db | 892  | GCTGTACGACTCTGAGGGGAGAAATCCTGATCTTTAAAGACAGGCACTTTTGGCGCAA    | 951                               |           |    |
| Qy | 307  | TyrTyrAspIleThrAspValGluPheGluLeuIleAlaSerPheTrpProSerLeuPro  | 326                               |           |    |
| Db | 952  | TCCCTCAGGAAGCTTGAACCTGAATTGCATTGTATCTCTTCATTTTGGCCACTCTTCCT   | 1011                              |           |    |
| Qy | 327  | AlaAspLeuGlnAlaAlaTyrlGlu---                                  | AsnProArgAspIysIleLeuValPheLysAsp | 345       |    |
| Db | 1012 | TCAGGCTGGATGCGCATATGAAGTTACTAGCAAGGACCTCGTTTTTCATTTTAAAGGA    | 1071                              |           |    |
| Qy | 346  | GluAsnPheTrpMetIleArgGlyTyralaValLeuProAspTyrProLysSerIleHis  | 365                               |           |    |
| Db | 1072 | AATCAATTCCTGGGCCATCAGAGGAAATGAGGTACGAGCTGGATACCAAGGAGGATCCAC  | 1131                              |           |    |

## RESULT 5

US-09-023-655-1374  
; Sequence 1374, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Sellhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1374:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1801 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: G36632  
US-09-023-655-1374

|                     |           |               |
|---------------------|-----------|---------------|
| Alignment Scores:   |           |               |
| Pred. No.:          | 1.51e-141 | Length:       |
| Score:              | 1250.00   | Matches:      |
| Percent Similarity: | 66.04%    | Conservative: |
|                     |           | 71            |



|                   |           |          |      |
|-------------------|-----------|----------|------|
| Alignment Scores: | 2.56e-135 | Length:  | 1717 |
| Pred. No.:        | 1198.50   | Matches: | 243  |
| Score:            |           |          |      |

; TOPOLOGY: linear





|                        |        |             |     |
|------------------------|--------|-------------|-----|
| Best Local Similarity: | 48.31% | Mismatches: | 157 |
| Query Match:           | 42.02% | Indels:     | 6   |
| DB:                    | 1      | Gaps:       | 8   |

US-10-729-807-10 (1-513) x US-09-178-002-3 (1-2223)

|    |      |                                                                 |      |
|----|------|-----------------------------------------------------------------|------|
| Qy | 1    | MetLysArgLeuLeuLeuLeuCysLeuPhePheThrPheSerSerAlaPheProLeu       | 20   |
| Db | 81   | CTGAAGACGCTTCATTTCTGCTCTTACTCCATGTGCAGATTCCAAGGCCCTTCTCT---     | 137  |
| Qy | 21   | ValArgMetThrGluAsnGluGluAsnMetGlnLeuAlaGlnAlaIleThrLeuAsnGlnPhe | 40   |
| Db | 138  | -----GTATCTTCTTAAGAAGAAATAACAATAAAGCTGTCAGGACTACCTCGAAAAGTTC    | 191  |
| Qy | 41   | TyrSerLeuGluLeuGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuLeuAsp    | 60   |
| Db | 192  | TACCAATTTACCAAGCACCATGATCATGCTFACAAGGAAGAAATGGCCACTAATGTGATCGTT | 251  |
| Qy | 61   | AspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSer    | 80   |
| Db | 252  | GAAGAAGCTTAAGAAGAAATGCAGCGAATTTTTGGGGTGCAATGTGACGGGGAAGCAAATGAG | 311  |
| Qy | 81   | AsnThrLeuGluLeuMetLysThrProArgCysGlyValProAspValGlyGlnTyrlGly   | 100  |
| Db | 312  | GAAACTCTGGACATGATGAATAAACCCCTGCGTGTGGAGTGCTGACAGTGGT-----GGT    | 365  |
| Qy | 101  | TyrThrLeu-----ProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIle           | 116  |
| Db | 366  | TTTATGTTAAACCCACGAGAAACCCCAGTGGGAACGCCTAACTTGACTACAGGATTCGA     | 425  |
| Qy | 117  | AsnTyrThrProAspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGlu    | 136  |
| Db | 426  | AACATATACCCACAGCTGTGCAGAGCGCTGAGAGAGCTATATCAAGGATGCTTTGAA       | 485  |
| Qy | 137  | ValTrpSerLysValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIle    | 156  |
| Db | 486  | CTTCGGAGTGTGGCATCACCTCTCATCTTACCAGGATCTCAGGAGAGGCGAGATATC       | 545  |
| Qy | 157  | MetIleAlaPheArgThrArgValHisGly---ArgCysProArgTyrPheAspGlyPro    | 175  |
| Db | 546  | AACATTGCTTTTACCAAGAGATCACGGTGACAATTTCTCCA-----TTTGATGACCC       | 599  |
| Qy | 176  | LeuGlyValLeuGlyHisAlaPheProProGlyProGlyLeuGlyAspThrHisPhe       | 195  |
| Db | 600  | AATGGAATCTCTGTCTCATGCTCTTTTCAGCAGCCAGGATATTGGAGAGATGCTCATTTT    | 659  |
| Qy | 196  | AspGluAspGluAsnTTPThrLysAspGlyValaglyPheAsnLeuPheLeuValAlaAla   | 215  |
| Db | 660  | GATGCCGAAGAAACATGACCAACACCTCCGCAATTAACAACITGTTCTTGTTGCTGCT      | 719  |
| Qy | 216  | HisGluPheGlyHisAlaLeuGlyLysSerHisSerAsnAspGlnThrAlaLeuMetPhe    | 235  |
| Db | 720  | CATGNAITTTGGCCATTCTTTGGGGCTGCTCACTCCCTTGACCCCTGGTGGCTTGATGAT    | 779  |
| Qy | 236  | ProAsnTyrValSerLeuAspProArgLysTyrProLeuSerGlnAspAlleAsnGly      | 255  |
| Db | 780  | CCCAACTATGCTTTTCAGGAAACACCAACTACTCACTCCCTCAAGATGCATCGATGGC      | 839  |
| Qy | 256  | IleGlnSerIleTyrGlyLeuProLysValProAlaLysProLysGluProThrIle       | 275  |
| Db | 840  | ATTCAGGCCATCTAT--GGACTTTCAGCAACCCCTATCCAACTCTGGCAAGCAACGACA     | 896  |
| Qy | 276  | ProHisAlaCysAspProAspLeuThrPheAspAlaIleThrThrPheArgTgGluVal     | 295  |
| Db | 897  | CCCAACCCCTGTGACCCAGTTTGACATTTGATGCTATCACCACTCCCGTGGAGAAATA      | 956  |
| Qy | 296  | MetPhePheLysGlyArgHisLeuTyrPargIleTyrTyrAspIleThrAspValGluPhe   | 315  |
| Db | 957  | CTTTCTTTTAAAGACAGGTACTTCTGGAGAAGGCATCCTCAAGTACAAAAAGATCGAAATG   | 1016 |
| Qy | 316  | GluLeuIleAlaSerPheTyrProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsn    | 335  |
| Db | 1017 | AATTTTATTTCTTACTTGGCCATCCCTTCCAACTGGTATCAGCGCTGGATGAAGAT        | 1076 |





Db 104 CTGCTGCTGTTCTGGGGTGTGTCTCAGCTTCCAGGACCTCTAGAAACACAA--- 160  
QY 27 GluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPheTyrSerLeuGluLeuGlu 46  
Db 161 GAGCAAGATGTGGACTTAGCTCAGAAATACCTCGAAATAATCTACCAACCTGGAAGATGAT 220  
QY 47 GlyAsnHisLeuValGlnSerLysAsnArgSerLeuLeuAspLysIleArgGluMet 66  
Db 221 GGGAGGCAAGTTGAAAGCGGGAATACTGGCCCGTGGTTGAAATTTGAAGCAATG 280  
QY 67 GlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSerAsnThrLeuGluLeuMet 86  
Db 281 CAGGAATTTCTTGGGCTGAAAGTGAATCGGAAACACAGATGCTCAAAACCTCGAAGGTGATG 340  
QY 87 LysThrProArgCysGlyValProAspValGlyGlnTyrGlyTyrThr-----LeuPro 104  
Db 341 AAGCAGCCAGATGTGGAGTGTGATGTGGTCAAGTTTCTCCTCAGCGGGGAGACCCCT 400  
QY 105 GlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrProAspMetAlaArg 124  
Db 401 CCTGGGAGCAACACATCTGACATGACAGATGAAATTAACGCCAGATTGGCAAGA 460  
QY 125 AlaAlaValAspGluAlaIleGlnGlyLeuGluValTyrSerLysValThrProLeu 144  
Db 461 GCAGATGTGACCATGCCATTCAGAAAGCCTTCCAACTCTGGAGTAATGTCAACCTCTG 520  
QY 145 LysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPheArgThrArgVal 164  
Db 521 ACATTCACCAAGGTCTCTGAGGTCAGGAGTCAAGCAGCATCATGATATCTTTT---GTCAGGGA 577  
QY 165 HisGlyArgCysProArgTyrPheAspGlyProLeuGlyValLeuGlyHisAlaPhePro 184  
Db 578 GATCATCGGAGCAACTCTCTTTTGTATGAGACCTGGAGGAAATCTTGCTCATGCTTTTCAA 637  
QY 185 ProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsnTrpThrLysAsp 204  
Db 638 CCAGGCCAGGTTATGGAGGGATGCTCATTTTGTATGAGATGAAAGTGGACCAACAT 697  
QY 205 GlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGlyPheGlyHisAlaLeuGlyLeu 224  
Db 698 TTCAGAGATACAACTATCATCGTGTGGGGTCTATGAATCGGCCATTTCTCTTGACTC 757  
QY 225 SerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrVal---SerLeuAspPro 243  
Db 758 TCCATCTACTGATATCGGGCTTTGTATGATGACCTTAGCTACACCTTCAGTGGTGTAT 817  
QY 244 ArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyrGlyGlyLeu 263  
Db 818 CAG-----CTAGCTCAGGATGACATTCATGATGATGATGATGATGATGATGATGAT 865  
QY 264 ProLysValProAlaLysProLysGluProThrIleProHisAlaCysAspProAspLeu 283  
Db 866 TCCAAATTCCTGTCAGGCCATCGGCCCAACAAACCCCAAGCGGTGACAGTAAGCTA 925  
QY 284 ThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGlyArgHisLeu 303  
Db 926 ACCTTTGATGCTATACTACGATTCGGGGAAGTGTCTTTTAAAGACAGATTCCTAC 985  
QY 304 TrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSerPheTrpPro 323  
Db 986 ATCGGCACAAATCCCTTCTACCGGGAAGTTGAGCTCAATTTCTGTTTTCTGGCCA 1045  
QY 324 SerLeuProAlaAspLeuGlnAlaTyrGlu---AsnProArgAspLysIleLeuVal 342  
Db 1046 CAACTGCCAAATCGGCTTGAAGCTGTCTTACGAATTTGCCGACAGATGAAGTCCGGTTT 1105  
QY 343 PheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAspTyrProLys 362  
Db 1106 TTCARAGGAATTAAGTACTGGCTGTTTCGGGACAGAAATGTCTACACGATACCCCAAG 1165  
QY 363 SerIleHis---ThrLeuGlyPheProGlyArgValLysIleAspAlaValCys 381  
Db 1166 GACATCTACAGCTCCTTTGGCTTCCCTAGAACTGTGAAGCATATCGATGCTGCTCTTCT 1225

QY 382 AspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTyrArgPheAspGlu 401  
Db 1286 GAGGAAACACCTGGAAACACCTCTCTTTGTTGTAACAATACTGGAGGTATGATGAA 1285  
QY 402 MetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPheProGlyIle 421  
Db 1286 TATAAACGATCTATGATCCAGGTTATCCCAAAATGATAGCACATGACTTCTCTGGAAT 1345  
QY 422 SerIleArgValAspAlaPheGlnTyrLysGlyPhePhePhePheSerArgGlySer 441  
Db 1346 GCCCAACAAGTTGATGCAAGTTTTCATGAAAGATGATTTCTATTTCTTCATGGAACA 1405  
QY 442 LysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThrAsnThr 461  
Db 1406 AGCAATACAAATTTGATCCTTAAACGAGAGAAATTTGACTCTCCAGAAAGTAATAGC 1465  
QY 462 TrpPheGlnCysLysGlu 467  
Db 1466 TGGTTCACTGCAGGAAA 1483

RESULT 12  
US-08-068-392-1  
; Sequence 1, Application US/08068392  
; Patent No. 6150152  
; GENERAL INFORMATION:  
; APPLICANT: Shaparo, Steven M.  
; TITLE OF INVENTION: Human Macrophage Metalloproteinase  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Scott J. Meyer, Monsanto Co., A3SM  
; STREET: 800 N. Lindbergh Blvd.  
; CITY: St. Louis  
; STATE: Missouri  
; COUNTRY: USA  
; ZIP: 63167  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/068,392  
; FILING DATE: 19930528  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meyer, Scott J.  
; REGISTRATION NUMBER: 25275  
; REFERENCE/DOCKET NUMBER: 07-24 (12406) A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (314)694-3117  
; TELEFAX: (314)694-5435  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1410 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..1410  
US-08-068-392-1

Alignment Scores:  
Pred. No.: 1,72e-127 Length: 1410  
Score: 1133.00 Matches: 229  
Percent Similarity: 64.56% Conservative: 77  
Best Local Similarity: 48.31% Mismatches: 152  
Query Match: 41.01% Indels: 16  
DB: 3 Gaps: 10

US-10-729-807-10 (1-513) x US-08-068-392-1 (1-1410)



Percent Similarity: 64.56% Conservative: 77  
Best Local Similarity: 48.31% Mismatches: 152  
Query Match: 48.01% Indels: 16  
DB: 3 Gaps: 10

US-10-729-807-10 (1-513) x US-08-396-988-1 (1-1410)

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QY 3 ArgLeuLeuLeuLeuLeuLeuPhePheIleThrPheSerSerAlaPheProLeuValArg 22
DB 4 AAGTTTCTTAAATACCTGCTCTGCGAGGCACCTCTTGGAGCTCTTCCCTTGAACAGC 63
QY 23 MetThrGluAsnGluGluAsnMetGlnLeu--AlaGlnAlaIleThrLeuAsnGlnPheTyr 41
DB 64 TCTACAGCCTGGAAAAAATAATATGCTATTGTGTGAGAGATACCTTAGAAAAATTTAT 123
QY 42 SerLeuGluIleGluGlyAsnHisLeuValGlnSerIleAsnArg-----SerLeu 58
DB 124 GGCCTTGTAGATA-----AACAACTTCCAGTGACAAAAAATGAAATATATAGTGAACCTTA 177
QY 59 IleAspAspLysIleArgGluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeu 78
DB 178 ATGAGGAAAAAATCCAGAAATGACGACTTCTTGGGTCTGAAAGTGACCGGCGCACTG 237
QY 79 AspSerAsnThrLeuGluIleMetLysThrProArgCysGlyValProAspValGlyGln 98
DB 238 GACACATCTACCTCGAGATGATGACGCGACCTCGATGTGGAGTCCCGATGTCCATCAT 297
QY 99 TyrGlyTyrThrLeuProGly-----TyrArgLysTyrAsnLeuThrTyrArgIle 115
DB 298 TTC--AGGAAATGCCAGGGGGCCCGTATGAGGAAACATTATATACCTACAGAAATC 354
QY 116 IleAsnTyrThrProAspMetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeu 135
DB 355 AATAATTACACCTGACATGACCGTGAGGATGTTGACTACGCAATCCGGAAGCTTTC 414
QY 136 GluValTyrSerLysValThrProLeuLysPheThrLysIleSerLysGlyIleAlaAsp 155
DB 415 CAAGTATGAGTAAATGTTACCCCTTTGAAATTCAGCAAGATTAAACACAGCATGGCTGAC 474
QY 156 IleMetIleAlaPheArgThrArgValHisGlyArgCysProArgTyrPheAspGlyPro 175
DB 475 ATTTGGTGGTTTTCGCCGTGGAGCTCATGGAGACTTC---CATGCTTTTGATGCCAAA 531
QY 176 LeuGlyValLeuGlyHisAlaPheProGlyProGlyLeuGlyValAspThrHisPhe 195
DB 532 GTGGATCTGAGCCATGCTTTGGACCTGGATCTGGCATTTGGAGGGATGCACATTTTC 591
QY 196 AspGluAspGluAsnTrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAla 215
DB 592 GATGAGGACGAATCTGGACTACATCTCAGGAGGCACAACTTGTTCCTCACTGCTGTT 651
QY 216 HisGluPheGlyHisAlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPhe 235
DB 652 CACGAGATTGGCCATCTCTTAGTCTTGGCCATCTTAGTGATCCAAAGGCTGTAATGTTTC 711
QY 236 ProAsnTyrValSerLeuAspProArgLysTyrProLeuSerGlnAspIleAsnGly 255
DB 712 CCCACTACAATATGTCAGATCAACACATTTTCGCTCTCTGCTGATGACATACGTGTC 771
QY 256 IleGlnSerIleTyrGlyLeuProLysValProAlaLysProLysGluPro----- 273
DB 772 ATTGAGTCCCTGTATGGAGAC--CCAAAAGAGAACCAACGCTTGGCAAAATCCTGACAA 828
QY 274 ThrIleProHisAlaCysAspProAspLeuThrPheAspAlaIleThrThrPheArgArg 293
DB 829 TCAGAACCGAGCTCTCTGTGACCCCAATTTGATTTTGTGCTGCTACCTACCGTGGGAAAT 888
QY 294 GluValMetPhePheLysGlyArgHisLeuTyrPheGlyIleTyrTyrAspIleThrAspVal 313
DB 889 AAGATCTTTTCTTCAAGACAGGTTCTTCTGCTGAGGTTTCTGAGAGACCAAGACC 948
QY 314 GluPheGluIleAlaSerPheTrpProSerLeuProAlaAspLeuGlnAlaIleTyr 333
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DB 949 AGTGTTAATTAATTTCTTCTTATGGCCCAACTTATGCCATCTGGCATTTGAAGCTGCTTAT 1008
QY 334 Glu---AsnProArgAspLysIleLeuValPheLysAspGluAsnPheTrpMetIleArg 352
DB 1009 GAAATTTGAAGCCAGAAATCAAGTTTCTTTTAAAGATGACAAATACTGGTTAATTAGC 1068
QY 353 GlyTyrAlaValLeuProAspTyrProLysSerIleHisThrLeuGlyPheProGlyArg 372
DB 1069 AATTTAAGCAGGAGCAAAATATCCCAAGAGCATACATCTTTGGTTTTCTCAACTTT 1128
QY 373 ValLysLysIleAspAlaAlaValCysAspLysThrThrArgLysThrTyrPhePheVal 392
DB 1129 GTGAAAAAATTTGATGACGCTGTTTAAACCCAGCTTTTATAGGACCTACTTCTTTGTA 1188
QY 393 GlyIleTyrCysTrpArgPheAspGluMetThrGlnThrMetAspLysGlyPheProGln 412
DB 1189 GATAACCAAGTATTTGGAGGTATGATGAAGAGGACACAGATGATGACCTGTTATCCCAA 1248
QY 413 ArgValValLysHisPheProGlyIleSerIleArgValAspAlaAlaPheGlnTyrLys 432
DB 1249 CTGATTACCAAGAACTTCCAGGAATCGGCCCTAAATTTGATGCAGTCTTCTATTCTAAA 1308
QY 433 Gly---PhePhePhePheSerArgLysSerLysGlnPheGluTyrAsnIleLysThrLys 451
DB 1309 AACAAATACTACTATTCTTCCAGGATCTAACCAATTTGAATATGACTTCTCTACTCCAA 1368
QY 452 AsnIleThrArgIleMetArgThrAsnThrTrpPheGlnCys 465
DB 1369 CGTATCACCAAAACACTGAAAGCAATAGCTGGTTGGTTGT 1410
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## RESULT 14

US-08-994-689C-18  
Sequence 18, Application US/08994689C  
Patent No. 6613958  
GENERAL INFORMATION:  
APPLICANT: Neuhold, Lisa  
APPLICANT: Killar, Loran  
TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR  
TITLE OF INVENTION: DEGENERATIVE DISEASES OF CARTILAGE  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby & Darby PC  
STREET: 805 Third Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/994,689C  
FILING DATE: 1997-12-19  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Green, Reza  
REGISTRATION NUMBER: 38,475  
REFERENCE/DOCKET NUMBER: 0630/0D532  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX: 212-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1521 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

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; MOLECULE TYPE: cDNA
US-08-994-689C-18

Alignment Scores:
Pred. No.: 2,58e-127 Length: 1521
Score: 1132.00 Matches: 221
Percent Similarity: 63.45% Conservative: 62
Best Local Similarity: 49.55% Mismatches: 151
Query Match: 40.97% Indels: 12
DB: 4 Gaps: 8

US-10-729-807-10 (1-513) x US-08-994-689C-18 (1-1521)

Qy 26 AsnGluGluAsnMetGlnLeuAlaAlaValThrLeuAsnGlnPheTyr---SerLeuGlu 44
Db 98 TCTGAGGAAGACCTCCAGCTTTGCGAGCGCTACCTGAGATCATATACCTACCAAT 157
Qy 45 IleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAspAspLysIleArg 64
Db 158 CTCGGGGA-----ATCCTGAAGGAGNATGCAGCAAGCTCCATGACTGAGAGGCTCGA 211
Qy 65 GluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSerAsnThrLeuGlu 84
Db 212 GAAATGCACTCTTCTTCGGCTTAGAGGTGACTGCGCAAACTTGACGATAACACCTTAGAT 271
Qy 85 IleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGlyTyr----- 101
Db 272 GTCATGAAAGCCAGATCGGGGTGTCTGATGGTGGAATACAAATGTTTCCCTCGA 331
Qy 102 ThrLeuProGlyTrpArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrProAsp 121
Db 332 ACTCTTAA--TGCTCAAAATGAATTAACCTACAGATTGGAATTACACCCCTGAT 388
Qy 122 MetAlaArgAlaAlaValAspGluAlaIleGlnGlyLeuGluValTrpSerLysVal 141
Db 389 ATGACTCATTTCTGAAGTCGAAAGGCAATTCAAAAAGCCCTTCAAAAGTTTGGTCGGATGA 448
Qy 142 ThrProLysPheThrLysIleSerLysGlyLeuAlaAlaPheIleMetIleAlaPheArg 161
Db 449 ACTCTCTGAATTTTACAGATTTTACAGATGGCAATGCTGACATGATCTCTTTTGGGA 508
Qy 162 ThrArgValHisGlyArg--CysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
Db 509 ATTAAGGAGCATGGCGACTTCTACCCA-----TTGATGGGCCCTCTGGCTGCTGCT 562
Qy 181 HisAlaPheProGlyProGlyLeuGlyAspThrHisPheAspGluAspGluAsn 200
Db 563 CATGCTTTTCTCTCGGCCCAATATTATGGAGGAGATGCCCAATTTTGATGATGATGATGA 622
Qy 201 TrpThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
Db 623 TGGCAAGTAGTTTCAAGGCTTACAACTGTCTTGTGCTGCGCATGAGTTCGGCCAC 682
Qy 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
Db 683 TCCATTAGTCTTGACCACTCCAGGACCTCGAGCACTCATGTTTCTCTATCTACACCTAC 742
Qy 241 LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr 260
Db 743 ACCGGCAAAAGCCACTTTATCTCTGATGACGATGTACAAAGGATCCAGTCTCTCTAT 802
Qy 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
Db 803 GGTCCAGGAGATGAAGACCCC---AACCTTAACATCCAAAACGCGCAGCAAAATGTGAC 859
Qy 281 ProAspLeuThrPheAspAlaIleThrThrPheArgArgGluValMetPhePheLysGly 300
Db 860 CTTCTTATCCCTTGATGCCATTACCACTCTCCGAGGAGAAACATGATCTTTAAAGAC 919
Qy 301 ArgHisLeuTrpArgIleTyrTyrAspIleThrAspValGluPheGluLeuIleAlaSer 320
Db 920 AGATTCTCTCGCGCTGTCATCCTCAGCAGGTGTGATGGGAGTGTCTTTTAAACGAATCA 979

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Qy 321 PheTrpProSerLeuProAlaAspLeuGluAlaAlaTyrGluAsnPro---ArgAspLys 339
Db 980 TTTTGGCCAGAACTTCCCAACCGTATTGATGCTGCATATGACACCTTCTCATGACCTC 1039
Qy 340 IleLeuValPheLysAspGluAsnPheTrpMetIleArgGlyTyrAlaValLeuProAsp 359
Db 1040 ATCTTCATCTTCAGAGGTAGAAAATTTTGGCTCTTAATGGTTATGACATCTCGAAGGT 1099
Qy 360 TyrProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAla 379
Db 1100 TATCCCAAAAAATATCTGAACCTGGGTCTTCCAAAAGAAAGTAAAGAGATAGTGACGT 1159
Qy 380 ValCysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTyrArgPhe 399
Db 1160 GTTCACCTTTGAGGATACAGCAGACCTCTCTGTCTCAGAAACACGAGTCTGGAGATAT 1219
Qy 400 AspGluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPhePro 419
Db 1220 GATGATACTAACCATAATTATGATAAAGACTATCCGAGACTAATAGAAGAAGACTTCCCA 1279
Qy 420 GlyIleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArg 439
Db 1280 GGAATTCGTGATAAAGTAGATGCTGTCTATGAGAAAATGGTTATATCTATTTTCAAC 1339
Qy 440 GlySerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThr 459
Db 1340 GGACCCATACAGTTTGATATACAGCATCTGGAGTAACCGTATTTGTCGGTCTATGCCAGCA 1399
Qy 460 AsnThrTrpPheGlnCys 465
Db 1400 AATTCACATTTTGTGGTGT 1417

RESULT 15
US-08-994-689C-8
; Sequence 8, Application US/08994689C
; Patent No. 6613958
; GENERAL INFORMATION:
; APPLICANT: Neuhold, Lisa
; APELLICANT: Killar, Loran
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR
; DEGENERATIVE DISEASES OF CARTILAGE
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ FOR Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,689C
; FILING DATE: 1997-12-19
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 0630/0D532
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2792 base pairs
; TYPE: nucleic acid

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STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-994-689C-8

## Alignment Scores:

Pred. No.: 6,91e-127 Length: 2792  
Score: 1132.00 Matches: 221  
Percent Similarity: 63.45% Conservative: 62  
Best Local Similarity: 49.55% Mismatches: 151  
Query Match: 40.97% Indels: 12  
DB: 4 Gaps: 8

US-10-729-807-10 (1-513) x US-08-994-689C-8 (1-2792)

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QY 26 AsnGluGluAsnMetGlnLeuAlaGlnAlaTyrLeuAsnGlnPheTyr---SerLeuGlu 44
DB 595 TCTGAGGAAGACCTCCAGTTTGCAGAGCGCTACCTGAGATCATACTACCAAT 654
QY 45 IleGluGlyAsnHisLeuValGlnSerLysAsnArgSerLeuIleAspAspLysIleArg 64
DB 655 CTCGGCGGA-----ATCTGAAGAGAGANTGCAGCAAGCTCCATGACTGAGAGGCTCCGA 708
QY 65 GluMetGlnAlaPhePheGlyLeuThrValThrGlyLysLeuAspSerAsnThrLeuGlu 84
DB 709 GAAATGCAGCTCTTCTTCGGCTTAGAGGTGACTGGCAAACTTGACGATACACCTTAGAT 768
QY 85 IleMetLysThrProArgCysGlyValProAspValGlyGlnTyrGlyTyr----- 101
DB 769 GTCATGAAAGCAAGATGCGGGGTTGTCGATGTGGGTGAATACAAATGTTTCCCTCGA 828
QY 102 ThrLeuProGlyTyrArgLysTyrAsnLeuThrTyrArgIleIleAsnTyrThrProAsp 121
DB 829 ACTCTTAAA---TGGTCCAAATGAATTTAACTCAGAAATGTGGAATACACCCCTGAT 885
QY 122 MetAlaArgAlaAlaValAspGluAlaIleGlnGluGlyLeuGluValTyrSerLysVal 141
DB 886 ATGACTCATCTCGAAGTCGAAGGCAATTCAMAAAGCCCTCAAGATTGGTCCGATGA 945
QY 142 ThrProLeuLysPheThrLysIleSerLysGlyIleAlaAspIleMetIleAlaPheArg 161
DB 946 ACTCCTCTGAATTTTACCAGACTTCACGATGGCAATTTGCTGACATCATGATCTCTTTTGA 1005
QY 162 ThrArgValHisGlyArg---CysProArgTyrPheAspGlyProLeuGlyValLeuGly 180
DB 1006 ATTAGGACCATGGGACTTCTACCCA-----TTTGATGGGCCCTCTGGCCTCTGGCT 1059
QY 181 HisAlaPheProGlyProGlyLeuGlyGlyAspThrHisPheAspGluAspGluAsn 200
DB 1060 CATGCTTTTCTCTCTGGGCCAAATATGAGGAGATGCCCATTTTGATGATGATGATAACC 1119
QY 201 ThrThrLysAspGlyAlaGlyPheAsnLeuPheLeuValAlaAlaHisGluPheGlyHis 220
DB 1120 TGGACAAGPAGTTCCAAAGGCTACAACTTTGTTTCTGTGCTGGCGATGAGTTCGGCCAC 1179
QY 221 AlaLeuGlyLeuSerHisSerAsnAspGlnThrAlaLeuMetPheProAsnTyrValSer 240
DB 1180 TCCTTAGGCTTTGACCACTCCAGGACCTCGAGCACTCATGTTTCTCTATCTACACCTAC 1239
QY 241 LeuAspProArgLysTyrProLeuSerGlnAspIleAsnGlyIleGlnSerIleTyr 260
DB 1240 ACCGGCAAAAGCCACTTTATGCTTCTGATGACGATGTACAAGGGATCCAGTCTCTCTAT 1299
QY 261 GlyGlyLeuProLysValProAlaLysProLysGluProThrIleProHisAlaCysAsp 280
DB 1300 GGTCCAGGAGATGAGACACCC---AACCTTAAACATCCAAAACCGCCAGACAAATGTGAC 1356
QY 281 ProAspLeuThrPheAspAlaIleThrPheArgArgGluValMetPhePheLysGly 300
DB 1357 CTTCTCTATCCTTGTAGCCATTACCACTCTCCGAGGAGAAACAAATGATCTTTAAAGAC 1416
QY 301 ArgHisLeuThrArgIleTyrTyrAspIleThrAspValGluPheGluIleAlaSer 320
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DB 1417 AGATTCTTCTGGCGCTGCTCATCTCAGCAGGTTGATGCGGAGCTGTTTTTAACGAATCA 1476
QY 321 PheTyrProSerLeuProAlaAspLeuGlnAlaIleTyrGluAsnPro---ArgAspLys 339
DB 1477 TTTTGGCCAGAACTTCCCAACCGTATTGATGCTGATATGAGCACCCTTCTCATGACCTC 1536
QY 340 IleLeuValPheLysAspGluAsnPheTyrMetIleArgGlyTyrAlaValLeuProAsp 359
DB 1537 ATCTTCATCTTCAGAGGTAGAAAAATTTGGGCTCTTAATGGTTATGACATCTTGGAGGT 1596
QY 360 TyrProLysSerIleHisThrLeuGlyPheProGlyArgValLysLysIleAspAlaAla 379
DB 1597 TATCCCAAAAAATATCTGAACTGGGTCTTCCAAAAAGAGTTAAGAAGATAAGTGCAGCT 1656
QY 380 ValCysAspLysThrThrArgLysThrTyrPhePheValGlyIleTyrCysTyrArgPhe 399
DB 1657 GTTCACTTTGAGGATACAGCAAGACTCTCTCTGTTCTCAGAAAAACCGGTCTGGAGATAT 1716
QY 400 AspGluMetThrGlnThrMetAspLysGlyPheProGlnArgValValLysHisPhePro 419
DB 1717 GATGATACCTAACCATATATGATTAAGACTATCCGAGACTAATAGAAGAGACTTCCCA 1776
QY 420 GlyIleSerIleArgValAspAlaAlaPheGlnTyrLysGlyPhePhePheSerArg 439
DB 1777 GCAATTTGGTGATAAAGTAGATGCTGCTATGAGAAAAATGGTTATATCTATTTTCAAC 1836
QY 440 GlySerLysGlnPheGluTyrAsnIleLysThrLysAsnIleThrArgIleMetArgThr 459
DB 1837 GGACCCCATACAGTTTGAATACAGCATCTGGAGTAACCGTATTGTTGCGCTCATGCCAGCA 1896
QY 460 AsnThrTyrPheGlnCys 465
DB 1897 AATTCCATTTTGTGGTGT 1914
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Search completed: November 16, 2004, 00:33:30

Job time : 169 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 15, 2004, 20:53:31 ; Search time 28 Seconds  
(without alignments)  
1215.041 Million cell updates/sec

Title: US-10-729-807-10

Perfect score: 2763

Sequence: 1 MKRLLLCLEFFITSSAPPL.....SLSLFIFGIVHLLKNTSIQ 513

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Match | Length | DB | ID                | Description       |
|------------|--------|-------|--------|----|-------------------|-------------------|
| 1          | 2763   | 100.0 | 513    | 4  | US-09-862-631-4   | Sequence 4, Appli |
| 2          | 2752   | 99.6  | 513    | 4  | US-10-140-002-192 | Sequence 192, App |
| 3          | 1254   | 45.4  | 477    | 3  | US-08-704-711A-20 | Sequence 20, Appl |
| 4          | 1254   | 45.4  | 477    | 3  | US-08-281-313-1   | Sequence 9, Appli |
| 5          | 1254   | 45.4  | 477    | 3  | US-09-521-220-20  | Sequence 20, Appl |
| 6          | 1250   | 45.2  | 477    | 3  | US-08-448-489-15  | Sequence 15, Appl |
| 7          | 1250   | 45.2  | 477    | 3  | US-09-391-104-21  | Sequence 21, Appl |
| 8          | 1234   | 44.7  | 476    | 3  | US-08-704-711A-21 | Sequence 21, Appl |
| 9          | 1234   | 44.7  | 476    | 3  | US-08-448-489-14  | Sequence 14, Appl |
| 10         | 1234   | 44.7  | 476    | 3  | US-09-521-220-21  | Sequence 21, Appl |
| 11         | 1234   | 44.7  | 476    | 3  | US-09-391-104-22  | Sequence 22, Appl |
| 12         | 1161.5 | 42.0  | 469    | 3  | US-09-391-104-23  | Sequence 23, Appl |
| 13         | 1161   | 42.0  | 467    | 1  | US-09-178-002-4   | Sequence 4, Appli |
| 14         | 1161   | 42.0  | 467    | 3  | US-09-391-104-24  | Sequence 24, Appl |
| 15         | 1161   | 42.0  | 468    | 3  | US-08-448-489-13  | Sequence 13, Appl |
| 16         | 1157.5 | 41.9  | 469    | 3  | US-08-448-489-12  | Sequence 12, Appl |
| 17         | 1150.5 | 41.6  | 469    | 3  | US-08-704-711A-16 | Sequence 16, Appl |
| 18         | 1150.5 | 41.6  | 469    | 3  | US-09-521-220-16  | Sequence 16, Appl |
| 19         | 1146.5 | 41.5  | 466    | 3  | US-08-704-711A-17 | Sequence 17, Appl |
| 20         | 1146.5 | 41.5  | 466    | 3  | US-09-521-220-17  | Sequence 17, Appl |
| 21         | 1141   | 41.0  | 471    | 3  | US-09-391-104-25  | Sequence 25, Appl |
| 22         | 1133   | 41.0  | 470    | 3  | US-08-068-392-2   | Sequence 2, Appli |
| 23         | 1133   | 41.0  | 470    | 3  | US-08-396-988-2   | Sequence 2, Appli |
| 24         | 1133   | 41.0  | 470    | 3  | US-08-391-104-26  | Sequence 26, Appl |
| 25         | 1132   | 41.0  | 471    | 4  | US-08-994-689C-1  | Sequence 1, Appli |
| 26         | 1125   | 40.7  | 471    | 4  | US-08-994-689C-21 | Sequence 21, Appl |
| 27         | 1120.5 | 40.6  | 444    | 1  | US-09-178-002-2   | Sequence 2, Appli |

28 1016.5 36.8 462 3 US-08-068-392-3 Sequence 3, Appli  
29 1016.5 36.8 462 3 US-08-396-988-3 Sequence 3, Appli  
30 797 28.8 660 3 US-09-391-104-19 Sequence 19, Appl  
31 797 28.8 660 4 US-09-917-254-89 Sequence 89, Appl  
32 796 28.8 660 3 US-08-704-711A-18 Sequence 18, Appl  
33 796 28.8 660 3 US-09-521-220-18 Sequence 18, Appl  
34 788 28.5 631 3 US-08-448-489-17 Sequence 17, Appl  
35 769.5 27.9 563 4 US-09-194-468A-30 Sequence 30, Appl  
36 716 25.9 532 3 US-09-294-841-2 Sequence 2, Appli  
37 715.5 25.9 669 3 US-08-704-711A-3 Sequence 3, Appli  
38 715.5 25.9 669 3 US-09-521-220-3 Sequence 3, Appli  
39 715.5 25.9 669 3 US-09-391-104-29 Sequence 29, Appl  
40 713.5 25.8 607 3 US-09-000-041A-2 Sequence 2, Appli  
41 713.5 25.8 607 3 US-09-211-704A-10 Sequence 10, Appl  
42 713.5 25.8 607 4 US-09-734-002-2 Sequence 2, Appli  
43 713 25.8 582 3 US-08-704-711A-2 Sequence 2, Appli  
44 713 25.8 582 3 US-08-448-489-1 Sequence 1, Appli  
45 713 25.8 582 3 US-09-211-704A-9 Sequence 9, Appli

#### ALIGNMENTS

RESULT 1  
US-09-862-631-4  
; Sequence 4, Application US/09862631  
; Patent No. 6734005  
; GENERAL INFORMATION:  
; APPLICANT: Holmgren, Erik  
; APPLICANT: Kihlen, Mats  
; APPLICANT: Wood, Tim  
; APPLICANT: Ekblom, Jonas  
; TITLE OF INVENTION: No. 6734005el Matrix Metalloproteinases  
; FILE REFERENCE: 00014regus  
; CURRENT APPLICATION NUMBER: US/09/862,631  
; PRIOR FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: 206119  
; PRIOR FILING DATE: 2000-05-22  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 4  
; LENGTH: 513  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-862-631-4

Query Match 100.0%; Score 2763; DB 4; Length 513;  
Best Local Similarity 100.0%; Pred. No. 1e-285;  
Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKRLLLCLEFFITSSAPPLVVRMTENEENMOLQAAYLNQFYSLETEGHNHVSQKNRSLID 60  
DB 1 MKRLLLCLEFFITSSAPPLVVRMTENEENMOLQAAYLNQFYSLETEGHNHVSQKNRSLID 60  
QY 61 DKIREMQAFGLTVTGKLDNSTLEIMKTPRCGVPDVGQGYTLPCGRKYNLTIRIINTP 120  
DB 61 DKIREMQAFGLTVTGKLDNSTLEIMKTPRCGVPDVGQGYTLPCGRKYNLTIRIINTP 120  
QY 121 DMARAAVDEALQEGLEVMSKVTPLKFTKISKGIADIMIAFTRVHGRCPRYFDGPGVLG 180  
DB 121 DMARAAVDEALQEGLEVMSKVTPLKFTKISKGIADIMIAFTRVHGRCPRYFDGPGVLG 180  
QY 181 HAPPPGGLGDTDFDENWTKDAGFNFLVAHFEFGHALGSHNSDQALMPFNVS 240  
DB 181 HAPPPGGLGDTDFDENWTKDAGFNFLVAHFEFGHALGSHNSDQALMPFNVS 240  
QY 241 LDPRKYPLOSDDINGIQSIYGLPKVPKPKPTIPHACDPLDFTDAITTRRERVMFPKG 300  
DB 241 LDPRKYPLOSDDINGIQSIYGLPKVPKPKPTIPHACDPLDFTDAITTRRERVMFPKG 300  
QY 301 RHLNRIYDITDVEFELIASFWPSLPADLOAAENPRDKILVFKDENFWMIRGVAVLDPY 360  
DB 301 RHLNRIYDITDVEFELIASFWPSLPADLOAAENPRDKILVFKDENFWMIRGVAVLDPY 360



QY 361 PKSIHTLGPGRVKKIDAAVCDKTRKTYFFVGIWCRFDEMOTQMDKGPQVVKHFP 420  
 DB 361 PKSIHTLGPGRVKKIDAAVCDKTRKTYFFVGIWCRFDEMOTQMDKGPQVVKHFP 420  
 QY 421 ISIRVDAAFQYKGFSSRSGSKQFEYNKTKNITRIMRTNTWFOCKEPKNSFGFDINKE 480  
 DB 421 ISIRVDAAFQYKGFSSRSGSKQFEYNKTKNITRIMRTNTWFOCKEPKNSFGFDINKE 480  
 QY 481 KAHSGGKILYHKSLSLFIFGIHVHLLKNTSIYQ 513  
 DB 481 KAHSGGKILYHKSLSLFIFGIHVHLLKNTSIYQ 513

## RESULT 2

US-10-140-002-192  
 ; Sequence 192, Application US/10140002  
 ; Patent No. 6725730

## GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeForge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: F3330R1C59  
 ; CURRENT APPLICATION NUMBER: US/10/140,002  
 ; CURRENT FILING DATE: 2002-05-06  
 ; Prior Application removed - See Palm or File Wrapper  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 192  
 ; LENGTH: 513  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-140-002-192

Query Match 99.6%; Score 2752; DB 4; Length 513;  
 Best Local Similarity 99.8%; Pred. No. 1.6e-284;  
 Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLCLEFFITSSAPFLVRMTENENMQLAQYLNQFYSLRIGNHLVQSKNRSLLD 60  
 DB 1 MKRLLLCLEFFITSSAPFLVRMTENENMQLAQYLNQFYSLRIGNHLVQSKNRSLLD 60  
 QY 61 DKIREMQAFLTLVTGKLDNTLEIMKTPRCGVPDVGQYVTLPGWRKYNLTIRIINYP 120  
 DB 61 DKIREMQAFLTLVTGKLDNTLEIMKTPRCGVPDVGQYVTLPGWRKYNLTIRIINYP 120  
 QY 121 DMARAAVDEALQEGLEWVSKYTPKFTKISGIADIATAPETRVHGRCPRYFDGPGVLG 180  
 DB 121 DMARAAVDEALQEGLEWVSKYTPKFTKISGIADIATAPETRVHGRCPRYFDGPGVLG 180  
 QY 181 HAPPPGGLGDTDFDENWTKDAGFNFLVAHAHFEGHALGSHSNDQTALMFPNYS 240  
 DB 181 HAPPPGGLGDTDFDENWTKDAGFNFLVAHAHFEGHALGSHSNDQTALMFPNYS 240  
 QY 241 LDPKPYLSQDDINGIQSIYGLGPKVPKPKPEPIPHACDPLDFDAITTFRRVMPFKG 300  
 DB 241 LDPKPYLSQDDINGIQSIYGLGPKVPKPKPEPIPHACDPLDFDAITTFRRVMPFKG 300

QY 301 RHLWRYYIDTVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGVAVLDPY 360  
 DB 301 RHLWRYYIDTVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGVAVLDPY 360  
 QY 361 PKSIHTLGPGRVKKIDAAVCDKTRKTYFFVGIWCRFDEMOTQMDKGPQVVKHFP 420  
 DB 361 PKSIHTLGPGRVKKIDAAVCDKTRKTYFFVGIWCRFDEMOTQMDKGPQVVKHFP 420  
 QY 421 ISIRVDAAFQYKGFSSRSGSKQFEYNKTKNITRIMRTNTWFOCKEPKNSFGFDINKE 480  
 DB 421 ISIRVDAAFQYKGFSSRSGSKQFEYNKTKNITRIMRTNTWFOCKEPKNSFGFDINKE 480  
 QY 481 KAHSGGKILYHKSLSLFIFGIHVHLLKNTSIYQ 513  
 DB 481 KAHSGGKILYHKSLSLFIFGIHVHLLKNTSIYQ 513

## RESULT 3

US-08-704-711A-20  
 ; Sequence 20, Application US/08704711A  
 ; Patent No. 6114159

## GENERAL INFORMATION:

; APPLICANT: WILL, Horst  
 ; APPLICANT: HINZMANN, Bernd  
 ; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
 ; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE  
 ; NUMBER OF SEQUENCES: 22  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: 3000 K Street, N.W., Suite 500  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA: US/08/704,711A  
 ; APPLICATION NUMBER: US/08/704,711A  
 ; FILING DATE: 20-NOV-1996  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: WO PCT/DE95/00357  
 ; FILING DATE: 17-MAR-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: DE 4438838.1  
 ; FILING DATE: 21-OCT-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: DE 4409663.1  
 ; FILING DATE: 17-MAR-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: GRANADOS, Patricia D.  
 ; REGISTRATION NUMBER: 33,683  
 ; REFERENCE/DOCKET NUMBER: 26083/124  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; TELEX: 904136  
 ; INFORMATION FOR SEQ ID NO: 20:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 477 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 US-08-704-711A-20

## Query Match

45.4%; Score 1254; DB 3; Length 477;

Best Local Similarity 51.5%; Pred. No. 9.9e-125;

Matches 247; Conservative 70; Mismatches 145; Indels 18; Gaps 9;

QY

1 MKRLLLCLEFFITSSAPFLVRMTENEE-NMQLAQYLNQFYSLRIGNHLVQSKNRSLLI 59

1 MKSLPILLLCVAVCSAYPLDGAAGDTSNNLVQKYLENYDLEKDVQKQFVRKDSGPV 60  
60 DDKIREMOAFLGLTVTGKLDSTLEIMKTIPRCGVDPVQGYGTYLPG---WRKYNLYTRII 116  
61 VKKIREMOKFLGLEVTGKLDSTLEVMRKPRCGVPDVGHF-RTFPGIPKWRKTHLYTRIV 119  
117 NYTPDMARAAVDEAQEGLEVWVKVTLKFTKISGIADIAMIAPRTRVHGRCPRY-FDGP 175  
120 NYTPDLPKDAVSAYEKALKWEEVITPLTFSKLYEGEADIMISFAVREHG--DFTPFDPG 177  
176 LGVLGHAFPPGGLGGDTHFEDENWTKDGAGFNLFVAAEHFGHALGSHNSDQATLMF 235  
178 GNVLAHAYAPGPGINGDAHFDDEQWTKDOTTGNTLFLVAHEIGHISGLGFSHANTEALMY 237  
236 PNYVSL-PPRKVPLSQDDINGIQSYG-----GLPKVPK--PKEPTIPHACDPLDFTD 286  
238 PLYHSLTDLTRFLSQDDINGIQSYGPPDPSPETPLVPTPEVPPGPTPANCDFPALSFD 297  
287 ALTTPRREVMRFKGRHLRIYVDITDVERFELIASWPISLPADLOAAVE-NPRDKILVFKD 345  
298 AVSTLURGILFDRHFRKSRKURKEPELHLISSFWPSLPDGAAYEVTSKDLVFIKRG 357  
346 ENFMIRGYAVLPDYPKSIHTLGFPGRVKKIDAAVCDKTRTKTYFFVGIGWCRFDEMFTQ 405  
358 NOFWAIRGNEVRAGYPRGHTLGFPPPTVRKIDAAISDKENKTYFFVEDKYWRFDKENS 417  
406 MDKGPQVRVHFGPGISIRVDAAFOYKGGFFFSRSGSKFQFENIKYNTIRIMRTNWFQC 465  
418 MBPGFPKQIAEDFPFGIDSKIDAVFEFGFFFTGSSQLEFDPNAKVTHTLKSNWLNLC 477

## RESULT 4

US-08-281-313-1  
Sequence 9, Application US/09368169  
Patent No. 6284511  
GENERAL INFORMATION:  
APPLICANT: Tetsuya INAKA et al.  
TITLE OF INVENTION: HEAT-STABLE PROLYENDOPREPTIDASE  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.  
STREET: 2033 K Street, N.W., Suite 800  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/368,169  
FILING DATE: August 5, 1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/750,816  
FILING DATE: January 8, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee Cheng  
REGISTRATION NUMBER: 40,949  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-721-8200  
TELEFAX: 202-721-8250  
TELEX:  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acid residues  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: Protein  
ORIGINAL SOURCE:  
ORGANISM: Flavobacterium meningosepticum  
ORGANISM: Met Lys Tyr Asn Lys Leu Ser Val Ala Val Ala Phe Ala Phe Ala Ala Val 15  
ORGANISM: 1 5 10  
Sequence 1, Application US/08281313  
Patent No. 6284513  
GENERAL INFORMATION:  
APPLICANT: Ye, Qi-Zhuang  
APPLICANT: Johnson, Linda L.  
APPLICANT: Hupe, Donald J.  
APPLICANT: Baragi, Vijaykumar  
TITLE OF INVENTION: Process for the Production of  
TITLE OF INVENTION: Stromelysin Catalytic Domain Protein  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Warner-Lambert Company  
STREET: 2800 Plymouth Rd.  
CITY: Ann Arbor  
STATE: MI  
COUNTRY: US  
ZIP: 48105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/281,313  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/012,705  
FILING DATE: 03-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Timney, Francis J.  
REGISTRATION NUMBER: 33,069  
REFERENCE/DOCKET NUMBER: 4415-01-PJT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 313 996-7295  
TELEFAX: 313 996-1553  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 477 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 100..273  
OTHER INFORMATION: /note= "Mature stromelysin  
OTHER INFORMATION: catalytic domain protein"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..17  
OTHER INFORMATION: /note= "Signal peptide"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 18..99  
OTHER INFORMATION: /note= "Propeptide"  
US-08-281-313-1

Query Match 45.4%; Score 1254; DB 3; Length 477;  
Best Local Similarity 51.5%; Pred. No. 9.9e-125;  
Matches 247; Conservative 70; Mismatches 145; Indels 18; Gaps 9;

Qy 1 MKRLLLLCLPFITFSSAPPLVMTENEENMQLAQAYLNQFYSLEIGNHLVQSKNRSLLI 59  
Db 1 MKSLPILLLCVAVCSAYPLDGAAGDTSNNLVQKYLENYDLEKDVQKQFVRKDSGPV 60  
Qy 60 DDKIREMOAFLGLTVTGKLDSTLEIMKTIPRCGVDPVQGYGTYLPG---WRKYNLYTRII 116

Db 61 VKKIREMOKFLGLEVTGKLDSDTLEVMKPRCGVPDVGHF--RTFPGIPKWRKTHLTYRIV 119  
QY 117 NYTPDMARAADVAEBAIQEGLEVMKSVTPKFTKISKIGIADIIMIAFRTRVHGRCPRY--FDGP 175  
Db 120 NYTPDLPKDAVDSAVEKALKVWEVTPLTAFSRLYEGEADIMISFAVREHG--DFYFPDGP 177  
QY 176 LGVILGHAFPPGGLGSDTHFEDENWTKDAGNLFVAHAEFGHALGSHSNDQTALMF 235  
Db 178 GNVLAHAYAPGPGINGDAHFDDDEQWTKDTGTGNLFVAHAEIGHSLGLFHSANTALMY 237  
QY 236 PNYVSL--DPRKYPLSQDDINGIOSIYG-----GLPKVPKAK--PKEPTIPHACDPDLTFD 286  
Db 238 PLYHSLTDLTRFLSQDDINGIOSLYGPPDPSPETPLVPTPEPVPPEPGTPANCDPALSF 297  
QY 287 AITTFRRVWFFKGRHLWRIYDITDVEPELIASFVWPSLPADLOAAVE--NPRDKILVFKD 345  
Db 298 AVSTLAGEILIFKDRHFWKSLRKLPELHLISSFWPSLPSGVDAAYEVTSKDLVFIK 357  
QY 346 ENFMWIRGVAVLPDYPKSIHTLGFGRVKKIDAAVCDKTRTKTYFFVGIWCFWDEMTOT 405  
Db 358 NQFWAIRGNEVRAGYPRGIHTLGFPTVRKIDAAISDKENKTYFFVEDKYWRFDEKRN 417  
QY 406 MDKGFPPQVAVKHPGGSIRVDAAFQYKGFPPFSRSGSKQFEYNIKTNITRIMTNTWFOC 465  
Db 418 MEGFPFKQIAEDFPDGIDSKIDAVFEBFGFFYFTGSSQLFEDPNNAKVTHTLKSNSWLNC 477

RESULT 5

US-09-521-220-20  
; Sequence 20, Application US/09521220  
; Patent No. 6395348  
; GENERAL INFORMATION:  
; APPLICANT: WILLI, Horst  
; HINZMANN, Bernd  
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
; METALLOPROTEASES, THEIR PRODUCTION AND USE  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/521,220  
; FILING DATE: 08-Mar-2000  
; CLASSIFICATION: <Unknown>  
; 21-OCT-1994  
; 17-MAR-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/704,711  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: DE 4438838.1  
; FILING DATE: 21-OCT-1994  
; APPLICATION NUMBER: DE 4409663.1  
; FILING DATE: 17-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRANADOS, Patricia D.  
; REGISTRATION NUMBER: 33,683  
; REFERENCE/DOCKET NUMBER: 26083/124  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 477 amino acids

; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-09-521-220-20  
Query Match 45.4%; Score 1254; DB 3; Length 477;  
Best Local Similarity 51.5%; Pred. No. 9.9e-125; Indels 18; Gaps 9;  
Matches 247; Conservative 70; Mismatches 145;  
QY 1 MKRLLLCLLFFITFSSAFPLVRMTENEE--NMQLAQAYLNOFYSLIEGHNHLVQSKNRSLI 59  
Db 1 MKSLPILLLLCVAVCSAYPLDGAARGEDTSMNLVQKYLENYXDLEKDVQKQFVRKDKSGPV 60  
QY 60 DKIRMQAFAFGTLVTGKLDSENTLEIMKTGRCVGPVQYGYTLPG---WRKNLNYRII 116  
Db 61 VKKIREMOKFLGLEVTGKLDSDTLEVMKPRCGVPDVGHF--RTFPGIPKWRKTHLTYRIV 119  
QY 117 NYTPDMARAADVAEBAIQEGLEVMKSVTPKFTKISKIGIADIIMIAFRTRVHGRCPRY--FDGP 175  
Db 120 NYTPDLPKDAVDSAVEKALKVWEVTPLTAFSRLYEGEADIMISFAVREHG--DFYFPDGP 177  
QY 176 LGVILGHAFPPGGLGSDTHFEDENWTKDAGNLFVAHAEFGHALGSHSNDQTALMF 235  
Db 178 GNVLAHAYAPGPGINGDAHFDDDEQWTKDTGTGNLFVAHAEIGHSLGLFHSANTALMY 237  
QY 236 PNYVSL--DPRKYPLSQDDINGIOSIYG-----GLPKVPKAK--PKEPTIPHACDPDLTFD 286  
Db 238 PLYHSLTDLTRFLSQDDINGIOSLYGPPDPSPETPLVPTPEPVPPEPGTPANCDPALSF 297  
QY 287 AITTFRRVWFFKGRHLWRIYDITDVEPELIASFVWPSLPADLOAAVE--NPRDKILVFKD 345  
Db 298 AVSTLAGEILIFKDRHFWKSLRKLPELHLISSFWPSLPSGVDAAYEVTSKDLVFIK 357  
QY 346 ENFMWIRGVAVLPDYPKSIHTLGFGRVKKIDAAVCDKTRTKTYFFVGIWCFWDEMTOT 405  
Db 358 NQFWAIRGNEVRAGYPRGIHTLGFPTVRKIDAAISDKENKTYFFVEDKYWRFDEKRN 417  
QY 406 MDKGFPPQVAVKHPGGSIRVDAAFQYKGFPPFSRSGSKQFEYNIKTNITRIMTNTWFOC 465  
Db 418 MEGFPFKQIAEDFPDGIDSKIDAVFEBFGFFYFTGSSQLFEDPNNAKVTHTLKSNSWLNC 477

RESULT 6

US-08-448-489-15  
; Sequence 15, Application US/08448489  
; Patent No. 6184022  
; GENERAL INFORMATION:  
; APPLICANT: SEIKI, Motoharu  
; APPLICANT: SATO, Hiroshi  
; APPLICANT: SHINAGAWA, Akira  
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR  
; FILE REFERENCE: 55-290P  
; CURRENT APPLICATION NUMBER: US/08/448,489  
; CURRENT FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 477  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Known Member of  
; OTHER INFORMATION: Matrix Metalloproteinase Family  
US-08-448-489-15

Query Match 45.2%; Score 1250; DB 3; Length 477;  
Best Local Similarity 51.2%; Pred. No. 2.6e-124;  
Matches 246; Conservative 71; Mismatches 145; Indels 18; Gaps 9;  
QY 1 MKRLLLCLLFFITFSSAFPLVRMTENEE--NMQLAQAYLNOFYSLIEGHNHLVQSKNRSLI 59  
Db 1 MKSLPILLLLCVAVCSAYPLDGAARGEDTSMNLVQKYLENYXDLEKDVQKQFVRKDKSGPV 60



QY 4 LLLLCLEFFITSSAPPLVMTENE-NMOLAQALNOFYSLEIEGHLVQSKNSLDDK 62  
Db 7 LVLLCL---PVC SAYPLSGAAKEEDSNKDLAQOYLEKYNNLEKDVQKF-RRKDSNLIVKK 62  
QY 63 IREMOAFGLTWTGKLDNTLEIMKTPRCGPDVGOYGY--TLPGWRKYNLTTRIINYTP 120  
Db 63 IQOMQKFLGLEVTGKLDNTLEIMKTPRCGPDVGOYGY--TLPGWRKYNLTTRIINYTP 122  
QY 121 DMARAAVDAIEQGLEWVSKVTPKFTKISKGIADIMIAFTRVHGRCPRYFDGPGVLG 180  
Db 123 DLPRADVDAIEKALKVWEVETPLTFSRLYEGEADIMISFAVKEHGF-YSFDPGHSLSLA 181  
QY 181 HAPFPGLGDDTHFEDENWTKDAGFNLFLVAHEFGHALGSLSHNSDQALMFPNYVS 240  
Db 182 HAYPFGPLGYDTHFEDDDKWTEDASGTNLFVAHEFGHALGSLSHNSDQALMFPNYVS 241  
QY 241 L-DPRKYPUSQDDINGIOSIYGLPKVPAKPKPT-----IPHACDPLTFDAITTF 291  
Db 242 FTLEAQFRLSQDDVNGIQSLYGPDPASTEPLVPTKSPGSEMPAKCDPALSFDAISTL 301  
QY 292 RREVMFFKGRHLWRIYDITDVEFELIASFWPSLPADLQAAVE-NPRDKILVFKDENFWM 350  
Db 302 RGEYLFKDRYFWRSHWNPEPEFHLISAFWPSLYDAAYEVNSRDVTFIKGNEFWA 361  
QY 351 IRGYAVLPDYPKSIHTLGFPGVKKIDAAVCDKTKTKTYFFVGIWCRFDEMOTQMDKGF 410  
Db 362 IRGNEVQAGYPRGIHTLGFPPTRKIDAAVSDKTKTYFFFAADKYWRFDENSQSMEOGF 421  
QY 411 PORVVKHFGPISIRVDAAFQYKGFPPFSRGSQKFEYNIKTNTIRMTNTWFOC 465  
Db 422 PRLIADDFGVEPKVDALQAFGFFYFFSGSSQFEDPNARMVTHILKNSWLHC 476

## RESULT 9

US-08-448-489-14  
; Sequence 14, Application US/08448489  
; Patent No. 6184022  
; GENERAL INFORMATION:  
; APPLICANT: SEIKI, Motoharu  
; APPLICANT: SATO, Hiroshi  
; APPLICANT: SHINAGAWA, Akira  
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR  
; FILE REFERENCE: 55-230P  
; CURRENT APPLICATION NUMBER: US/08/448,489  
; CURRENT FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 14  
; LENGTH: 476  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Known Member of  
; OTHER INFORMATION: Matrix Metalloproteinase Family  
US-08-448-489-14

Query Match 44.7%; Score 1234; DB 3; Length 476;  
Best Local Similarity 51.4%; Pred. No. 1.3e-122;  
Matches 244; Conservative 77; Mismatches 136; Indels 18; Gaps 8;

QY 4 LLLLCLEFFITSSAPPLVMTENE-NMOLAQALNOFYSLEIEGHLVQSKNSLDDK 62  
Db 7 LVLLCL---PVC SAYPLSGAAKEEDSNKDLAQOYLEKYNNLEKDVQKF-RRKDSNLIVKK 62  
QY 63 IREMOAFGLTWTGKLDNTLEIMKTPRCGPDVGOYGY--TLPGWRKYNLTTRIINYTP 120  
Db 63 IQOMQKFLGLEVTGKLDNTLEIMKTPRCGPDVGOYGY--TLPGWRKYNLTTRIINYTP 122  
QY 121 DMARAAVDAIEQGLEWVSKVTPKFTKISKGIADIMIAFTRVHGRCPRYFDGPGVLG 180  
Db 123 DLPRADVDAIEKALKVWEVETPLTFSRLYEGEADIMISFAVKEHGF-YSFDPGHSLSLA 181

QY 181 HAPFPGLGDDTHFEDENWTKDAGFNLFLVAHEFGHALGSLSHNSDQALMFPNYVS 240  
Db 182 HAYPFGPLGYDTHFEDDDKWTEDASGTNLFVAHEFGHALGSLSHNSDQALMFPNYVS 241  
QY 241 L-DPRKYPUSQDDINGIOSIYGLPKVPAKPKPT-----IPHACDPLTFDAITTF 291  
Db 242 FTLEAQFRLSQDDVNGIQSLYGPDPASTEPLVPTKSPGSEMPAKCDPALSFDAISTL 301  
QY 292 RREVMFFKGRHLWRIYDITDVEFELIASFWPSLPADLQAAVE-NPRDKILVFKDENFWM 350  
Db 302 RGEYLFKDRYFWRSHWNPEPEFHLISAFWPSLYDAAYEVNSRDVTFIKGNEFWA 361  
QY 351 IRGYAVLPDYPKSIHTLGFPGVKKIDAAVCDKTKTKTYFFVGIWCRFDEMOTQMDKGF 410  
Db 362 IRGNEVQAGYPRGIHTLGFPPTRKIDAAVSDKTKTYFFFAADKYWRFDENSQSMEOGF 421  
QY 411 PORVVKHFGPISIRVDAAFQYKGFPPFSRGSQKFEYNIKTNTIRMTNTWFOC 465  
Db 422 PRLIADDFGVEPKVDALQAFGFFYFFSGSSQFEDPNARMVTHILKNSWLHC 476

## RESULT 10

US-09-521-220-21  
; Sequence 21, Application US/09521220  
; Patent No. 6399348  
; GENERAL INFORMATION:  
; APPLICANT: WILL, Horst  
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Coley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/521,220  
; FILING DATE: 08-Mar-2000  
; CLASSIFICATION: <Unknown>  
; 21-OCT-1994  
; 17-MAR-1994

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/704,711  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: DE 4438838.1  
; FILING DATE: 21-OCT-1994  
; APPLICATION NUMBER: DE 4409663.1  
; FILING DATE: 17-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRANADOS, Patricia D.  
; REGISTRATION NUMBER: 33,683  
; REFERENCE/DOCKET NUMBER: 26083/124  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 672-5300  
; TELEFAX: (202) 672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 476 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:  
US-09-521-220-21





Db 245 DVQ---LAQDDIDIGIQAIY-GRSQNPVQPIGPQTPKACDSKLTDFDAITIRGEVMEFFKDR 300  
QY 302 HLMRIYYDITDVEFELIASFWSLPADLQAAVE-NRPDKILVPKDFNFWMIRGYAVLPDY 360  
Db 301 FYMRTNFFYPEVLENFISVFWPLPGLNGLEAAVEFADRDVEVRFPKNGKYWAVQSQNVLHG 360  
QY 361 PKSIH-TLGPGRVKKIDAAVCDKTRTKYFFVGIWCFDFDENTQMDKGFPPORVVKHFP 419  
Db 361 PKDIYSFGFPRTVKHIDALSENTGKTYFFVANKYRYDEVKRSMDFGYPKMIADHP 420  
QY 420 GISIRVDAAFQYKGFFFSRGSKQFEYNKTKNITRMTNTWFOCKE 467  
Db 421 GIGHKVDVEMKDGFFYFHGTQYKFDKPKTRILTLQKANSWFNCRK 468

## RESULT 13

US-09-178-002-4  
; Sequence 4, Application US/09178002  
; Patent No. H001973  
; GENERAL INFORMATION:  
; APPLICANT: Hu, Shou-Ih  
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant  
; FILE REFERENCE: CGC 2048  
; CURRENT APPLICATION NUMBER: US/09/178,002  
; CURRENT FILING DATE: 1998-10-22  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 467  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-178-002-4

Query Match 42.0%; Score 1161; DB 1; Length 467;  
Best Local Similarity 48.3%; Pred. No. 8e-115;  
Matches 228; Conservative 71; Mismatches 157; Indels 16; Gaps 8;

QY 1 MKRELLLLCLFFITFSSAFFLVMTENEENWLAQAALNQLFYSLEIEGNHLVQSKNLSLID 60  
Db 4 LKTLFPLLLHVOISKAFF---VSSKEKNTKVQDYLEKPYQLPSNQYOSTRKNGTNVIV 60  
QY 61 DKIREMAQFFGLTVTGKLDNSTLEIMKTPRCGVPDVGQYGYTL-----PGWRKYNLTYYRII 116  
Db 61 EKLKEMQRFGLNVTGKPNEEITLDMKKPCRCGVPDSG--GFMLTPCNPXKWTNLTYYRIR 118  
QY 117 NTPDMARAADVEAIOEGLEVSKVTPKFTKISKIADIIMIAFRTRVIG-RCPRYFDGP 175  
Db 119 NTPQLSEAEVERAIKDAFELMSVASPLIFTRISQGEADINIAFYQRDHGDNPS--FDGP 176  
QY 176 LGVLGHAFPPGGLGDDTHFDEENWTKDAGFNLFVAAREFGHALGSHSNDQTALMF 235  
Db 177 NGLIAHAFOPGOGIGGDAHFDAEETWNTSANYNLFVAAREFGHSLGLAHSSDPGALMY 236  
QY 236 PNVVSLDPRKYPPLSQDDINGIQSIYGLPKVPKAPKEPTIPHACDPLDFAITTTFRREV 295  
Db 237 PNYAFRETSNYSLPQDDIDIGIQAIY-GLSSNPQTGPSTPKPCDPSLFDAITTLRGEI 295  
QY 296 MFKGRLHRIYYDITDVEFELIASFWPSLPADLQAAAYEN-PRDKILVPKDFNFWMIRGY 354  
Db 296 LFFKDRYFRRHPQLQRVEMNFIISLFWPSLPTGIAAYEDFDRDLIFLFGNQYWALS 355  
QY 355 AVLDPYKPSIHTLGPGRVKKIDAAVCDKTRTKTYFFVGIWCFDFDENTQMDKGFPPORV 414  
Db 356 DILQGYPKDISNYGFFSSVQAIIDAAVYRS--KTYFFVNDQFWRYDNQRFMEPGYPKSI 413  
QY 415 VKHFGISIRVDAAFQYKGFFFSRGSKQFEYNKTKNITRMTNTWFOCK 466  
Db 414 SGAFPGIESKVDVAFQOEHHFHFVSGPRYVAFDLIAQRTVRVARGNKWLNCR 465

## RESULT 14

US-09-391-104-24  
; Sequence 24, Application US/09391104

; Patent No. 6399371  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Falduto, Michael T.  
; APPLICANT: Magnuson, Scott R.  
; APPLICANT: Morgan, Douglas W.  
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,  
; TITLE OF INVENTION: OF USING SAME  
; FILE REFERENCE: 6073.US.PI  
; CURRENT APPLICATION NUMBER: US/09/391,104  
; CURRENT FILING DATE: 1999-09-07  
; PRIOR APPLICATION NUMBER: US 08/814,394  
; PRIOR FILING DATE: 1997-03-11  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 24  
; LENGTH: 467  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-391-104-24

Query Match 42.0%; Score 1161; DB 3; Length 467;  
Best Local Similarity 48.3%; Pred. No. 8e-115;  
Matches 228; Conservative 71; Mismatches 157; Indels 16; Gaps 8;

QY 1 MKRELLLLCLFFITFSSAFFLVMTENEENWLAQAALNQLFYSLEIEGNHLVQSKNLSLID 60  
Db 4 LKTLFPLLLHVOISKAFF---VSSKEKNTKVQDYLEKPYQLPSNQYOSTRKNGTNVIV 60  
QY 61 DKIREMAQFFGLTVTGKLDNSTLEIMKTPRCGVPDVGQYGYTL-----PGWRKYNLTYYRII 116  
Db 61 EKLKEMQRFGLNVTGKPNEEITLDMKKPCRCGVPDSG--GFMLTPCNPXKWTNLTYYRIR 118  
QY 117 NTPDMARAADVEAIOEGLEVSKVTPKFTKISKIADIIMIAFRTRVIG-RCPRYFDGP 175  
Db 119 NTPQLSEAEVERAIKDAFELMSVASPLIFTRISQGEADINIAFYQRDHGDNPS--FDGP 176  
QY 176 LGVLGHAFPPGGLGDDTHFDEENWTKDAGFNLFVAAREFGHALGSHSNDQTALMF 235  
Db 177 NGLIAHAFOPGOGIGGDAHFDAEETWNTSANYNLFVAAREFGHSLGLAHSSDPGALMY 236  
QY 236 PNVVSLDPRKYPPLSQDDINGIQSIYGLPKVPKAPKEPTIPHACDPLDFAITTTFRREV 295  
Db 237 PNYAFRETSNYSLPQDDIDIGIQAIY-GLSSNPQTGPSTPKPCDPSLFDAITTLRGEI 295  
QY 296 MFKGRLHRIYYDITDVEFELIASFWPSLPADLQAAAYEN-PRDKILVPKDFNFWMIRGY 354  
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QY 355 AVLDPYKPSIHTLGPGRVKKIDAAVCDKTRTKTYFFVGIWCFDFDENTQMDKGFPPORV 414  
Db 356 DILQGYPKDISNYGFFSSVQAIIDAAVYRS--KTYFFVNDQFWRYDNQRFMEPGYPKSI 413  
QY 415 VKHFGISIRVDAAFQYKGFFFSRGSKQFEYNKTKNITRMTNTWFOCK 466  
Db 414 SGAFPGIESKVDVAFQOEHHFHFVSGPRYVAFDLIAQRTVRVARGNKWLNCR 465

## RESULT 15

US-08-448-489-13  
; Sequence 13, Application US/08448489  
; Patent No. 6184022  
; GENERAL INFORMATION:  
; APPLICANT: SEIKI, Motoharu  
; APPLICANT: SATO, Hiroshi  
; APPLICANT: SHINAGAWA, Akira  
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR  
; FILE REFERENCE: 55-290P  
; CURRENT APPLICATION NUMBER: US/08/448,489  
; CURRENT FILING DATE: 1995-06-07  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: Patent In Ver. 2.0

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; SEQ ID NO 13
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: X = UNKNOWN
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-13

Query Match      42.0%; Score 1161; DB 3; Length 468;
Best Local Similarity 48.3%; Pred. No. 8.1e-115;
Matches 228; Conservative 71; Mismatches 157; Indels 16; Gaps 8;

QY 1 MKRLLLCLGFTTFSAPFLVMTNEENMQAQLNQFISLETEGHNHVLQSKNRSLLD 60
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QY 61 DKIREMQAFFGLTVTGKLDNSTLEIMKTPRCGVPDVGQGYTL---PGWRKYNTYRII 116
Db 61 EKLKMQRFGLNVTGKNEETLDMKPRCGVPDSG--GFMLTPGNPKWERTNLTYYIR 118

QY 117 NYTPDMARAANDVAIQEGLEVMKVTPLKFTKISKGIADIMIAFRTRVHG-RCPRYFDGP 175
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QY 176 LGVLGHAFPPGPGCLGDDTHFDEENWTGAGFNLFLVAAHEFGHALGSHSNDOTALMF 235
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QY 236 PNYVSLDPKPYLSODDINGIQSIYGLPKVPKPKPTIPHACDPDLTDAITTFREBV 295
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QY 296 MFFKGRHLWRIYYDITDVEFELIASFWPSLPADLQAAYEN-PRDKILVFKDENFWMIRGY 354
Db 296 LFFKDRYFWRHRPQLQRVEMNFISLFWPSLPTGIQAAYEDFDRDLIFLFKGNQYWALSGY 355

QY 355 AVLDPYPKSIHTLGPGRVKKIDAAVCCKTRKTYFFVGICWRPEDEMTQTMDKGFPORV 414
Db 356 DILQGYPKDINSYGFPSVQAIDAAVFYRS--KTYFFVNDQFWRYDNQRFMEPGYPKSI 413

QY 415 VKHPPGISIRVDAAFQYKGFPPFSRGSKOFEYNIKTKNITRIMRTNTWFOCK 466
Db 414 SGAPFGIESKVDVAFQEHFFHVSFGPRIYAPDLIAQRVTRVARGNKWLNCR 465
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Job time : 29 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 15, 2004, 13:11:05 ; Search time 1645 Seconds  
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5341.888 Million cell updates/sec

Title: US-10-729-807-28

Perfect score: 1627

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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11: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID | Description       |
|------------|--------|-------------|--------|-------|-------------------|
| 1          | 1627   | 100.0       | 1627   | 17    | US-10-729-807-28  |
| 2          | 1627   | 100.0       | 1647   | 10    | US-09-862-631-1   |
| 3          | 1625.4 | 99.9        | 1647   | 14    | US-10-028-072-191 |
| 4          | 1625.4 | 99.9        | 1647   | 14    | US-10-140-808-191 |
| 5          | 1625.4 | 99.9        | 1647   | 14    | US-10-121-049-191 |
| 6          | 1625.4 | 99.9        | 1647   | 14    | US-10-123-262-191 |
| 7          | 1625.4 | 99.9        | 1647   | 14    | US-10-140-470-191 |
| 8          | 1625.4 | 99.9        | 1647   | 14    | US-10-175-746-191 |
| 9          | 1625.4 | 99.9        | 1647   | 14    | US-10-176-918-191 |
| 10         | 1625.4 | 99.9        | 1647   | 14    | US-10-176-921-191 |
| 11         | 1625.4 | 99.9        | 1647   | 14    | US-10-137-865-191 |
| 12         | 1625.4 | 99.9        | 1647   | 14    | US-10-140-474-191 |

|    |        |      |      |    |                    |                   |
|----|--------|------|------|----|--------------------|-------------------|
| 13 | 1625.4 | 99.9 | 1647 | 14 | US-10-142-431-191  | Sequence 191, App |
| 14 | 1625.4 | 99.9 | 1647 | 14 | US-10-143-114-191  | Sequence 191, App |
| 15 | 1625.4 | 99.9 | 1647 | 14 | US-10-140-002-191  | Sequence 191, App |
| 16 | 1625.4 | 99.9 | 1647 | 14 | US-10-142-419-191  | Sequence 191, App |
| 17 | 1625.4 | 99.9 | 1647 | 14 | US-10-123-262-191  | Sequence 191, App |
| 18 | 1625.4 | 99.9 | 1647 | 14 | US-10-142-423-191  | Sequence 191, App |
| 19 | 1625.4 | 99.9 | 1647 | 14 | US-10-121-050-191  | Sequence 191, App |
| 20 | 1625.4 | 99.9 | 1647 | 14 | US-10-141-755-191  | Sequence 191, App |
| 21 | 1625.4 | 99.9 | 1647 | 14 | US-10-143-032-191  | Sequence 191, App |
| 22 | 1625.4 | 99.9 | 1647 | 14 | US-10-123-108-191  | Sequence 191, App |
| 23 | 1625.4 | 99.9 | 1647 | 14 | US-10-123-236-191  | Sequence 191, App |
| 24 | 1625.4 | 99.9 | 1647 | 14 | US-10-123-261-191  | Sequence 191, App |
| 25 | 1625.4 | 99.9 | 1647 | 14 | US-10-140-921-191  | Sequence 191, App |
| 26 | 1625.4 | 99.9 | 1647 | 14 | US-10-140-928-191  | Sequence 191, App |
| 27 | 1625.4 | 99.9 | 1647 | 14 | US-10-121-045-191  | Sequence 191, App |
| 28 | 1625.4 | 99.9 | 1647 | 14 | US-10-123-292-191  | Sequence 191, App |
| 29 | 1625.4 | 99.9 | 1647 | 14 | US-10-123-903-191  | Sequence 191, App |
| 30 | 1625.4 | 99.9 | 1647 | 14 | US-10-127-825A-191 | Sequence 191, App |
| 31 | 1625.4 | 99.9 | 1647 | 14 | US-10-124-819-191  | Sequence 191, App |
| 32 | 1625.4 | 99.9 | 1647 | 14 | US-10-124-822-191  | Sequence 191, App |
| 33 | 1625.4 | 99.9 | 1647 | 14 | US-10-140-925-191  | Sequence 191, App |
| 34 | 1625.4 | 99.9 | 1647 | 14 | US-10-160-498-191  | Sequence 191, App |
| 35 | 1625.4 | 99.9 | 1647 | 14 | US-10-124-824-191  | Sequence 191, App |
| 36 | 1625.4 | 99.9 | 1647 | 14 | US-10-127-825A-191 | Sequence 191, App |
| 37 | 1625.4 | 99.9 | 1647 | 14 | US-10-127-829A-191 | Sequence 191, App |
| 38 | 1625.4 | 99.9 | 1647 | 14 | US-10-127-835A-191 | Sequence 191, App |
| 39 | 1625.4 | 99.9 | 1647 | 14 | US-10-127-839A-191 | Sequence 191, App |
| 40 | 1625.4 | 99.9 | 1647 | 14 | US-10-128-693A-191 | Sequence 191, App |
| 41 | 1625.4 | 99.9 | 1647 | 14 | US-10-131-813A-191 | Sequence 191, App |
| 42 | 1625.4 | 99.9 | 1647 | 14 | US-10-131-818A-191 | Sequence 191, App |
| 43 | 1625.4 | 99.9 | 1647 | 14 | US-10-131-823A-191 | Sequence 191, App |
| 44 | 1625.4 | 99.9 | 1647 | 14 | US-10-131-824A-191 | Sequence 191, App |
| 45 | 1625.4 | 99.9 | 1647 | 14 | US-10-131-830A-191 | Sequence 191, App |

#### ALIGNMENTS

RESULT 1  
US-10-729-807-28  
; Sequence 28, Application US/10729807  
; Publication No. US20040132158A1  
; GENERAL INFORMATION:  
; APPLICANT: SANDMAN, Olga; HILLMAN, Jennifer L.  
; APPLICANT: TANG, Y. Tom; LAL, Preeti G.  
; APPLICANT: YUE, Henry; AZIMZAI, Yalda  
; APPLICANT: BAUGHN, Mariah R.; LU, Dyoung Aina M.  
; TITLE OF INVENTION: HUMAN PEPTIDASES  
; FILE REFERENCE: PF-0651-1 DIV  
; CURRENT APPLICATION NUMBER: US/10/729,807  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: US 09/889,238  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: PCT/US00/00641  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: US 60/172,247  
; PRIOR FILING DATE: 1999-01-11  
; PRIOR APPLICATION NUMBER: US 60/132,253  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US 60/136,653  
; PRIOR FILING DATE: 1999-05-27  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PERL Program  
; SEQ ID NO 28  
; LENGTH: 1627  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: 3772696CB1  
US-10-729-807-28

Query Match

100.0%; Score 1627; DB 17; Length 1627;

|    |      |                                                                  |              |              |            |    |        |    |      |    |
|----|------|------------------------------------------------------------------|--------------|--------------|------------|----|--------|----|------|----|
|    |      | Best Local Similarity                                            | 100.0%;      | Pred. No. 0; | Mismatches | 0; | Indels | 0; | Gaps | 0; |
|    |      | Matches 1627;                                                    | Conservative | 0;           |            |    |        |    |      |    |
| QY | 1    | GCTTCAGCTGAAGAAAGAGAGAGAAATCAAGCGCCTTCTGCTTCTGCTTCTGCTTCTTTTATAA | 60           |              |            |    |        |    |      |    |
| DB | 1    | GCTTCAGCTGAAGAAAGAGAGAGAAATCAAGCGCCTTCTGCTTCTGCTTCTGCTTCTTTTATAA | 60           |              |            |    |        |    |      |    |
| QY | 61   | CAITTTCTTCTGCAATTCCTTCTAGTCCGGATGACGGAATGAAGAAATATGCAACTGG       | 120          |              |            |    |        |    |      |    |
| DB | 61   | CAITTTCTTCTGCAATTCCTTCTAGTCCGGATGACGGAATGAAGAAATATGCAACTGG       | 120          |              |            |    |        |    |      |    |
| QY | 121  | CTCAGGCAATCTCAACCACTTCTACTCTTCTGAAATAGAGGAATCATCTTGTTCAAA        | 180          |              |            |    |        |    |      |    |
| DB | 121  | CTCAGGCAATCTCAACCACTTCTACTCTTCTGAAATAGAGGAATCATCTTGTTCAAA        | 180          |              |            |    |        |    |      |    |
| QY | 181  | GCAAGAAATAGAGCTCTCATAGATGACAAAATTCGGGAAATGCAAGCAATTTTTGGATGA     | 240          |              |            |    |        |    |      |    |
| DB | 181  | GCAAGAAATAGAGCTCTCATAGATGACAAAATTCGGGAAATGCAAGCAATTTTTGGATGA     | 240          |              |            |    |        |    |      |    |
| QY | 241  | CAGTGACTGAAATCTGCACTCAAAACCTTGAGATCATGAACACCCAGGTGTGGG           | 300          |              |            |    |        |    |      |    |
| DB | 241  | CAGTGACTGAAATCTGCACTCAAAACCTTGAGATCATGAACACCCAGGTGTGGG           | 300          |              |            |    |        |    |      |    |
| QY | 301  | TGCTGATGTGGGCGAGTATGGCTACACCTCCCTGGTGGAGAAATACAACTCACCT          | 360          |              |            |    |        |    |      |    |
| DB | 301  | TGCTGATGTGGGCGAGTATGGCTACACCTCCCTGGTGGAGAAATACAACTCACCT          | 360          |              |            |    |        |    |      |    |
| QY | 361  | ACAGAAATATAATCTATCTCCGATATGACAGAGCTGTGTGGATGAGGCTATCAAG          | 420          |              |            |    |        |    |      |    |
| DB | 361  | ACAGAAATATAATCTATCTCCGATATGACAGAGCTGTGTGGATGAGGCTATCAAG          | 420          |              |            |    |        |    |      |    |
| QY | 421  | AAGGTTTAGAGTGTGGAGCAAAAGTCACTCACTAAATTCACCAAGATTTCAAAGGGA        | 480          |              |            |    |        |    |      |    |
| DB | 421  | AAGGTTTAGAGTGTGGAGCAAAAGTCACTCACTAAATTCACCAAGATTTCAAAGGGA        | 480          |              |            |    |        |    |      |    |
| QY | 481  | TTGAGACATCATGATGCTTCTAGGCTTCTAGGCTTCTAGGCTTCTAGGCTTCTAGGCT       | 540          |              |            |    |        |    |      |    |
| DB | 481  | TTGAGACATCATGATGCTTCTAGGCTTCTAGGCTTCTAGGCTTCTAGGCTTCTAGGCT       | 540          |              |            |    |        |    |      |    |
| QY | 541  | ATGCTCCCTTGGGAGTGTGGCCATGCTTCTCTCTGGTCCGGTCTGGGTGTGACA           | 600          |              |            |    |        |    |      |    |
| DB | 541  | ATGCTCCCTTGGGAGTGTGGCCATGCTTCTCTCTGGTCCGGTCTGGGTGTGACA           | 600          |              |            |    |        |    |      |    |
| QY | 601  | CTCAATTTGAGAGATGAATACTGCAAGGATGGAGGAGGATTCACATTTCTTCTG           | 660          |              |            |    |        |    |      |    |
| DB | 601  | CTCAATTTGAGAGATGAATACTGCAAGGATGGAGGAGGATTCACATTTCTTCTG           | 660          |              |            |    |        |    |      |    |
| QY | 661  | TGGCTGCTCATGAATTTGTCTCATGCTGGGCTCTCTCACTCCCAATGATCAACAGCT        | 720          |              |            |    |        |    |      |    |
| DB | 661  | TGGCTGCTCATGAATTTGTCTCATGCTGGGCTCTCTCACTCCCAATGATCAACAGCT        | 720          |              |            |    |        |    |      |    |
| QY | 721  | TGATGTTCCCAATATGTTCTCCCTGGATGCCAATAATACCACTTCTCAGGATGATA         | 780          |              |            |    |        |    |      |    |
| DB | 721  | TGATGTTCCCAATATGTTCTCCCTGGATGCCAATAATACCACTTCTCAGGATGATA         | 780          |              |            |    |        |    |      |    |
| QY | 781  | TCAATGGAATCAGTCCATCTATGAGGCTTCTGCTTAAAGTCTGCTAGGCAAGGAAC         | 840          |              |            |    |        |    |      |    |
| DB | 781  | TCAATGGAATCAGTCCATCTATGAGGCTTCTGCTTAAAGTCTGCTAGGCAAGGAAC         | 840          |              |            |    |        |    |      |    |
| QY | 841  | CCACTATACCCCATGCTGTGACCCCTGACTTCTGACTTTTGACGCTATCAACCTTCCGCA     | 900          |              |            |    |        |    |      |    |
| DB | 841  | CCACTATACCCCATGCTGTGACCCCTGACTTCTGACTTTTGACGCTATCAACCTTCCGCA     | 900          |              |            |    |        |    |      |    |
| QY | 901  | GAGAAGTAATGTTCTTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG          | 960          |              |            |    |        |    |      |    |
| DB | 901  | GAGAAGTAATGTTCTTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG          | 960          |              |            |    |        |    |      |    |
| QY | 961  | TTGAGTTTGAATTAATGCTTCTCTGCGCATCTGCGCATCTGCGCATCTGCGCATCTG        | 1020         |              |            |    |        |    |      |    |
| DB | 961  | TTGAGTTTGAATTAATGCTTCTCTGCGCATCTGCGCATCTGCGCATCTGCGCATCTG        | 1020         |              |            |    |        |    |      |    |
| QY | 1021 | ACGAGAACCCAGAGATAGATTTCTGGTTTAAAGATGAAATCTTCTGATCATCAGAG         | 1080         |              |            |    |        |    |      |    |

|    |      |                                                                |      |  |  |  |  |  |  |  |
|----|------|----------------------------------------------------------------|------|--|--|--|--|--|--|--|
| DB | 1021 | ACGAGAACCCAGAGATAGATTTCTGGTTTAAAGATGAAATCTTCTGATCATCAGAG       | 1080 |  |  |  |  |  |  |  |
| QY | 1081 | GATATCTGCTGCTGCGAGATATCCCAATCCATCCATACATTAAGTTTCCAGGACGTG      | 1140 |  |  |  |  |  |  |  |
| DB | 1081 | GATATCTGCTGCTGCGAGATATCCCAATCCATCCATACATTAAGTTTCCAGGACGTG      | 1140 |  |  |  |  |  |  |  |
| QY | 1141 | TGAAGAAAATAGATGAGCGCTGCTGTGAAGAACCAAGAAAACCTACTTCTTTGTGG       | 1200 |  |  |  |  |  |  |  |
| DB | 1141 | TGAAGAAAATAGATGAGCGCTGCTGTGAAGAACCAAGAAAACCTACTTCTTTGTGG       | 1200 |  |  |  |  |  |  |  |
| QY | 1201 | GCATTTGGTCTGGAGTTTGGATGAATGACCCCAACCAAGGATTCGCGCAGA            | 1260 |  |  |  |  |  |  |  |
| DB | 1201 | GCATTTGGTCTGGAGTTTGGATGAATGACCCCAACCAAGGATTCGCGCAGA            | 1260 |  |  |  |  |  |  |  |
| QY | 1261 | GAGTGTGAAACACTTTCTCGGAATCAGTATCCGTTGTGATGCTTCCAGTACAAAG        | 1320 |  |  |  |  |  |  |  |
| DB | 1261 | GAGTGTGAAACACTTTCTCGGAATCAGTATCCGTTGTGATGCTTCCAGTACAAAG        | 1320 |  |  |  |  |  |  |  |
| QY | 1321 | GATTTCTTTTTCAGCGCTGGATCAAGCAATTTGAATCAACATTAAGCAAGAATA         | 1380 |  |  |  |  |  |  |  |
| DB | 1321 | GATTTCTTTTTCAGCGCTGGATCAAGCAATTTGAATCAACATTAAGCAAGAATA         | 1380 |  |  |  |  |  |  |  |
| QY | 1381 | TTACCCGAATCATGAGAACTAATCTGTTTCAATGCAAGAACCAAGAACTCTCTCAT       | 1440 |  |  |  |  |  |  |  |
| DB | 1381 | TTACCCGAATCATGAGAACTAATCTGTTTCAATGCAAGAACCAAGAACTCTCTCAT       | 1440 |  |  |  |  |  |  |  |
| QY | 1441 | TTGTTTGTGATATCAACAGGAAAGACATTCAGAGGAGCAATTAAGATATGATCATTA      | 1500 |  |  |  |  |  |  |  |
| DB | 1441 | TTGTTTGTGATATCAACAGGAAAGACATTCAGAGGAGCAATTAAGATATGATCATTA      | 1500 |  |  |  |  |  |  |  |
| QY | 1501 | AGAGTTTAAAGCTTTTATTTTGGTATTTGTTCAATTTGCTGAAAGACATTTATTC        | 1560 |  |  |  |  |  |  |  |
| DB | 1501 | AGAGTTTAAAGCTTTTATTTTGGTATTTGTTCAATTTGCTGAAAGACATTTATTC        | 1560 |  |  |  |  |  |  |  |
| QY | 1561 | AATTAATTCATAGACCTTAATAAATCAACCTCAACAGGCTTTTAAATATAAATTCGCTTCAA | 1620 |  |  |  |  |  |  |  |
| DB | 1561 | AATTAATTCATAGACCTTAATAAATCAACCTCAACAGGCTTTTAAATATAAATTCGCTTCAA | 1620 |  |  |  |  |  |  |  |
| QY | 1621 | AATAGAA 1627                                                   |      |  |  |  |  |  |  |  |
| DB | 1621 | AATAGAA 1627                                                   |      |  |  |  |  |  |  |  |

RESULT 2  
US-09-862-631-1  
; Sequence 1, Application US/09862631  
; Publication No US20030032164A1  
; GENERAL INFORMATION:  
; APPLICANT: Holmgren, Erik  
; APPLICANT: Kihlen, Mats  
; APPLICANT: Wood, Tim  
; APPLICANT: Ekblom, Jonas  
; TITLE OF INVENTION: No. US20030032164A1el Matrix Metalloproteinases  
; FILE REFERENCE: 00014regUS  
; CURRENT APPLICATION NUMBER: US/09/862,631  
; PRIOR FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: 206119  
; PRIOR FILING DATE: 2000-05-22  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 1845  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-862-631-1

Query Match 100.0%; Score 1627; DB 10; Length 1845;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1627; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GCTTCAGCTGAAGAAAGAGAGGAAATCAAGCGCCTTCTGCTTCTGCTTCTTTATAA 60  
DB 1 GCTTCAGCTGAAGAAAGAGAGGAAATCAAGCGCCTTCTGCTTCTGCTTCTTTATAA 60

QY 61 CATTTTCTTGTGATTTCCCTTAGTCCGGATGACGGAATGAAGAAATATCAACTGG 120  
Db 61 CATTTTCTTGTGATTTCCCTTAGTCCGGATGACGGAATGAAGAAATATCAACTGG 120  
QY 121 CTCAGCATATCTCAACAGTCTTCTACTCTCTTGAATAGAGGGAATCATCTTTTCAAA 180  
Db 121 CTCAGCATATCTCAACAGTCTTCTACTCTCTTGAATAGAGGGAATCATCTTTTCAAA 180  
QY 181 GCAAGATAGGAGTCTCATAGATGACAAATTCGGGAATGCAAGCAATTTTGGATTGA 240  
Db 181 GCAAGATAGGAGTCTCATAGATGACAAATTCGGGAATGCAAGCAATTTTGGATTGA 240  
QY 241 CAGTGACTGGAATACTGGAATCAAAACACCTTTGAGATCATGAAGACACCCAGTGTGGG 300  
Db 241 CAGTGACTGGAATACTGGAATCAAAACACCTTTGAGATCATGAAGACACCCAGTGTGGG 300  
QY 301 TGCCTGATGTGGGCGAGTATGCTACACCTCCCTGGGTGGAGAAATCAACCTCACCT 360  
Db 301 TGCCTGATGTGGGCGAGTATGCTACACCTCCCTGGGTGGAGAAATCAACCTCACCT 360  
QY 361 ACAGATAATAAATATATCTCCGATATGCGATGACGAGCTCTGATGAGGCTATCCAG 420  
Db 361 ACAGATAATAAATATATCTCCGATATGCGATGACGAGCTCTGATGAGGCTATCCAG 420  
QY 421 AAGGTTTGAAGTGTGGAGAAAGTCACTCCACTAAATTCACCAAGATTTCAAAGGGA 480  
Db 421 AAGGTTTGAAGTGTGGAGAAAGTCACTCCACTAAATTCACCAAGATTTCAAAGGGA 480  
QY 481 TTGAGAGATCATGATGCTTTAGGATCGAGTCCATGCTGCTGCTGCTGCTGCTGCTGCT 540  
Db 481 TTGAGAGATCATGATGCTTTAGGATCGAGTCCATGCTGCTGCTGCTGCTGCTGCTGCT 540  
QY 541 ATGGTCCCTTGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
Db 541 ATGGTCCCTTGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
QY 601 CTCATTTTGTAGGATGAAATCTGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 660  
Db 601 CTCATTTTGTAGGATGAAATCTGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGG 660  
QY 661 TGGCTGCTCATGATTTGGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
Db 661 TGGCTGCTCATGATTTGGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
QY 721 TGATGTTCCCAATATATCTTCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
Db 721 TGATGTTCCCAATATATCTTCCCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
QY 781 TCAATGGAATCCAGTCCATCTATGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
Db 781 TCAATGGAATCCAGTCCATCTATGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
QY 841 CCACTATACCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
Db 841 CCACTATACCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900  
QY 901 GAGAAGTAAATGCTTTTAAAGGAGGACCTATGAGGATCTATGATGATGATGATGATGATG 960  
Db 901 GAGAAGTAAATGCTTTTAAAGGAGGACCTATGAGGATCTATGATGATGATGATGATGATG 960  
QY 961 TTGAGTTGAATTAATGCTTCAATCTGCGCATCTCTGCGCATCTCTGCGCATCTCTGCGCATCT 1020  
Db 961 TTGAGTTGAATTAATGCTTCAATCTGCGCATCTCTGCGCATCTCTGCGCATCTCTGCGCATCT 1020  
QY 1021 ACAGAACCCAGAGATGAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
Db 1021 ACAGAACCCAGAGATGAAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
QY 1081 GATATGCTGCTTCCAGATATATCCCAATCCATCCATCATATAGGTTTCCAGAGCTG 1140  
Db 1081 GATATGCTGCTTCCAGATATATCCCAATCCATCCATCATATAGGTTTCCAGAGCTG 1140

QY 1141 TGAAGAAATAGATGACGCGCTGTGTATAGACCAAGAAACCACTACTTCTTTGTGG 1200  
Db 1141 TGAAGAAATAGATGACGCGCTGTGTATAGACCAAGAAACCACTACTTCTTTGTGG 1200  
QY 1201 GCATTTGGTGTGAGGTTTGTATGAATGACCCAAACCAAGGATTCGCCGAGA 1260  
Db 1201 GCATTTGGTGTGAGGTTTGTATGAATGACCCAAACCAAGGATTCGCCGAGA 1260  
QY 1261 GAGTGTGTAACACATTTCTCGGATCAGTATCGTGTGATGCTGCTTCCAGTACAAAG 1320  
Db 1261 GAGTGTGTAACACATTTCTCGGATCAGTATCGTGTGATGCTGCTTCCAGTACAAAG 1320  
QY 1321 GATCTCTTTTTCAGCCGTGATCAAGCAATTTGAATACCAATTAAGACAAAGATA 1380  
Db 1321 GATCTCTTTTTCAGCCGTGATCAAGCAATTTGAATACCAATTAAGACAAAGATA 1380  
QY 1381 TTACCCGAATCATGAGAACTAATATCTTGGTTTCAATGCAAGAACCCAAAGAACTCTCAT 1440  
Db 1381 TTACCCGAATCATGAGAACTAATATCTTGGTTTCAATGCAAGAACCCAAAGAACTCTCAT 1440  
QY 1441 TTGGTTTGTATATCAAGGAAAGACATTCAGGAGGCATAAAGATATTTGTATCAT 1500  
Db 1441 TTGGTTTGTATATCAAGGAAAGACATTCAGGAGGCATAAAGATATTTGTATCAT 1500  
QY 1501 AGAGTTTAAAGCTTGTATTTTGGTATTTGTTTCAATTTGCTGAAACACCTTCTATTATC 1560  
Db 1501 AGAGTTTAAAGCTTGTATTTTGGTATTTGTTTCAATTTGCTGAAACACCTTCTATTATC 1560  
QY 1561 AATAAATTCATAGACCTTAAATATAACCTCAACAGGTCTTTTAAATATAAATCTGCTTCAA 1620  
Db 1561 AATAAATTCATAGACCTTAAATATAACCTCAACAGGTCTTTTAAATATAAATCTGCTTCAA 1620  
QY 1621 AATAGAA 1627  
Db 1621 AATAGAA 1627

## RESULT 3

US-10-028-072-191  
; Sequence 191, Application US/10028072  
; Publication No. US20030004311A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang  
; TITLE OF INVENTION:  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/028,072  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26  
; PRIOR APPLICATION NUMBER: 60/059113  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059115  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059117  
; PRIOR FILING DATE: 1997-09-17



|    |                                     |    |                                     |
|----|-------------------------------------|----|-------------------------------------|
| 1  | PRIOR APPLICATION NUMBER: 60/059122 | 1  | PRIOR FILING DATE: 1998-02-04       |
| 2  | PRIOR FILING DATE: 1997-09-17       | 2  | PRIOR APPLICATION NUMBER: 60/074086 |
| 3  | PRIOR APPLICATION NUMBER: 60/059184 | 3  | PRIOR FILING DATE: 1998-02-09       |
| 4  | PRIOR FILING DATE: 1997-09-17       | 4  | PRIOR APPLICATION NUMBER: 60/074092 |
| 5  | PRIOR APPLICATION NUMBER: 60/059263 | 5  | PRIOR FILING DATE: 1998-02-09       |
| 6  | PRIOR FILING DATE: 1997-09-18       | 6  | PRIOR APPLICATION NUMBER: 60/077791 |
| 7  | PRIOR APPLICATION NUMBER: 60/059352 | 7  | PRIOR FILING DATE: 1998-03-12       |
| 8  | PRIOR FILING DATE: 1997-09-19       | 8  | PRIOR APPLICATION NUMBER: 60/078910 |
| 9  | PRIOR APPLICATION NUMBER: 60/059588 | 9  | PRIOR FILING DATE: 1998-03-20       |
| 10 | PRIOR FILING DATE: 1997-09-19       | 10 | PRIOR APPLICATION NUMBER: 60/079294 |
| 11 | PRIOR APPLICATION NUMBER: 60/059836 | 11 | PRIOR FILING DATE: 1998-03-25       |
| 12 | PRIOR FILING DATE: 1997-09-24       | 12 | PRIOR APPLICATION NUMBER: 60/079663 |
| 13 | PRIOR APPLICATION NUMBER: 60/062250 | 13 | PRIOR FILING DATE: 1998-02-27       |
| 14 | PRIOR FILING DATE: 1997-10-17       | 14 | PRIOR APPLICATION NUMBER: 60/079728 |
| 15 | PRIOR APPLICATION NUMBER: 60/062285 | 15 | PRIOR FILING DATE: 1998-03-27       |
| 16 | PRIOR FILING DATE: 1997-10-17       | 16 | PRIOR APPLICATION NUMBER: 60/080165 |
| 17 | PRIOR APPLICATION NUMBER: 60/062814 | 17 | PRIOR FILING DATE: 1998-03-31       |
| 18 | PRIOR FILING DATE: 1997-10-24       | 18 | PRIOR APPLICATION NUMBER: 60/081203 |
| 19 | PRIOR APPLICATION NUMBER: 60/062816 | 19 | PRIOR FILING DATE: 1998-04-09       |
| 20 | PRIOR FILING DATE: 1997-10-24       | 20 | PRIOR APPLICATION NUMBER: 60/081229 |
| 21 | PRIOR APPLICATION NUMBER: 60/063045 | 21 | PRIOR FILING DATE: 1998-04-09       |
| 22 | PRIOR FILING DATE: 1997-10-24       | 22 | PRIOR APPLICATION NUMBER: 60/081695 |
| 23 | PRIOR APPLICATION NUMBER: 60/063082 | 23 | PRIOR FILING DATE: 1998-04-14       |
| 24 | PRIOR FILING DATE: 1997-10-31       | 24 | PRIOR APPLICATION NUMBER: 60/081817 |
| 25 | PRIOR APPLICATION NUMBER: 60/063127 | 25 | PRIOR FILING DATE: 1998-04-15       |
| 26 | PRIOR FILING DATE: 1997-10-24       | 26 | PRIOR APPLICATION NUMBER: 60/081818 |
| 27 | PRIOR APPLICATION NUMBER: 60/063327 | 27 | PRIOR FILING DATE: 1998-04-15       |
| 28 | PRIOR FILING DATE: 1997-10-27       | 28 | PRIOR APPLICATION NUMBER: 60/082999 |
| 29 | PRIOR APPLICATION NUMBER: 60/063329 | 29 | PRIOR FILING DATE: 1998-04-24       |
| 30 | PRIOR FILING DATE: 1997-10-27       | 30 | PRIOR APPLICATION NUMBER: 60/083322 |
| 31 | PRIOR APPLICATION NUMBER: 60/063550 | 31 | PRIOR FILING DATE: 1998-04-28       |
| 32 | PRIOR FILING DATE: 1997-10-28       | 32 | PRIOR APPLICATION NUMBER: 60/083545 |
| 33 | PRIOR APPLICATION NUMBER: 60/063561 | 33 | PRIOR FILING DATE: 1998-04-29       |
| 34 | PRIOR FILING DATE: 1997-10-28       | 34 | PRIOR APPLICATION NUMBER: 60/084600 |
| 35 | PRIOR APPLICATION NUMBER: 60/063704 | 35 | PRIOR FILING DATE: 1998-05-07       |
| 36 | PRIOR FILING DATE: 1997-10-29       | 36 | PRIOR APPLICATION NUMBER: 60/084627 |
| 37 | PRIOR APPLICATION NUMBER: 60/063733 | 37 | PRIOR FILING DATE: 1998-05-07       |
| 38 | PRIOR FILING DATE: 1997-10-29       | 38 | PRIOR APPLICATION NUMBER: 60/084637 |
| 39 | PRIOR APPLICATION NUMBER: 60/063735 | 39 | PRIOR FILING DATE: 1998-05-07       |
| 40 | PRIOR FILING DATE: 1997-10-29       | 40 | PRIOR APPLICATION NUMBER: 60/085149 |
| 41 | PRIOR APPLICATION NUMBER: 60/063738 | 41 | PRIOR FILING DATE: 1998-05-12       |
| 42 | PRIOR FILING DATE: 1997-10-29       | 42 | PRIOR APPLICATION NUMBER: 60/085323 |
| 43 | PRIOR APPLICATION NUMBER: 60/063755 | 43 | PRIOR FILING DATE: 1998-05-13       |
| 44 | PRIOR FILING DATE: 1997-10-17       | 44 | PRIOR APPLICATION NUMBER: 60/085338 |
| 45 | PRIOR APPLICATION NUMBER: 60/064248 | 45 | PRIOR FILING DATE: 1998-05-13       |
| 46 | PRIOR FILING DATE: 1997-11-03       | 46 | PRIOR APPLICATION NUMBER: 60/085339 |
| 47 | PRIOR APPLICATION NUMBER: 60/064809 | 47 | PRIOR FILING DATE: 1998-05-13       |
| 48 | PRIOR FILING DATE: 1997-11-07       | 48 | PRIOR APPLICATION NUMBER: 60/085579 |
| 49 | PRIOR APPLICATION NUMBER: 60/065186 | 49 | PRIOR FILING DATE: 1998-05-15       |
| 50 | PRIOR FILING DATE: 1997-11-12       | 50 | PRIOR APPLICATION NUMBER: 60/085697 |
| 51 | PRIOR APPLICATION NUMBER: 60/065846 | 51 | PRIOR FILING DATE: 1998-05-15       |
| 52 | PRIOR FILING DATE: 1997-11-17       | 52 | PRIOR APPLICATION NUMBER: 60/085704 |
| 53 | PRIOR APPLICATION NUMBER: 60/066364 | 53 | PRIOR FILING DATE: 1998-05-15       |
| 54 | PRIOR FILING DATE: 1997-11-21       | 54 | PRIOR APPLICATION NUMBER: 60/086414 |
| 55 | PRIOR APPLICATION NUMBER: 60/066453 | 55 | PRIOR FILING DATE: 1998-05-22       |
| 56 | PRIOR FILING DATE: 1997-11-24       | 56 | PRIOR APPLICATION NUMBER: 60/086430 |
| 57 | PRIOR APPLICATION NUMBER: 60/066511 | 57 | PRIOR FILING DATE: 1998-05-22       |
| 58 | PRIOR FILING DATE: 1997-11-24       | 58 | PRIOR APPLICATION NUMBER: 60/087106 |
| 59 | PRIOR APPLICATION NUMBER: 60/066770 | 59 | PRIOR FILING DATE: 1998-05-28       |
| 60 | PRIOR FILING DATE: 1997-11-24       | 60 | PRIOR APPLICATION NUMBER: 60/088026 |
| 61 | PRIOR APPLICATION NUMBER: 60/069212 | 61 | PRIOR FILING DATE: 1998-06-04       |
| 62 | PRIOR FILING DATE: 1997-12-11       | 62 | PRIOR APPLICATION NUMBER: 60/088730 |
| 63 | PRIOR APPLICATION NUMBER: 60/069278 | 63 | PRIOR FILING DATE: 1998-06-10       |
| 64 | PRIOR FILING DATE: 1997-12-11       | 64 | PRIOR APPLICATION NUMBER: 60/088741 |
| 65 | PRIOR APPLICATION NUMBER: 60/069334 | 65 | PRIOR FILING DATE: 1998-06-10       |
| 66 | PRIOR FILING DATE: 1997-12-11       | 66 | PRIOR APPLICATION NUMBER: 60/088810 |
| 67 | PRIOR APPLICATION NUMBER: 60/069694 | 67 | PRIOR FILING DATE: 1998-06-10       |
| 68 | PRIOR FILING DATE: 1997-12-16       | 68 | PRIOR APPLICATION NUMBER: 60/088858 |
| 69 | PRIOR APPLICATION NUMBER: 60/072320 | 6  |                                     |

; PRIOR APPLICATION NUMBER: 60/089907  
 ; PRIOR FILING DATE: 1998-06-18  
 ; PRIOR APPLICATION NUMBER: 60/089947  
 ; PRIOR FILING DATE: 1998-06-19  
 ; PRIOR APPLICATION NUMBER: 60/090349  
 ; PRIOR FILING DATE: 1998-06-23  
 ; PRIOR APPLICATION NUMBER: 60/090429  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: 60/090445  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: 60/090538  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: 60/090863  
 ; PRIOR FILING DATE: 1998-06-26  
 ; PRIOR APPLICATION NUMBER: 60/091360  
 ; PRIOR FILING DATE: 1998-07-01  
 ; PRIOR APPLICATION NUMBER: 60/091519  
 ; PRIOR FILING DATE: 1998-07-02  
 ; PRIOR APPLICATION NUMBER: 60/091982  
 ; PRIOR FILING DATE: 1998-07-07

Query Match 99.9%; Score 1625.4; DB 14; Length 1647;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |     |                                                              |     |
|----|-----|--------------------------------------------------------------|-----|
| QY | 1   | GCTTCAGCTGAAAGAAAGAGAGGAATGAAGCGCTTCTGCTTCTGCTTGGTCTTTTATAA  | 60  |
| Db | 1   | GCTTCAGCTGAAAGAAAGAGAGGAATGAAGCGCTTCTGCTTCTGCTTGGTCTTTTATAA  | 60  |
| QY | 61  | GATTTTCTTCTGCATTTCCCTTAGTCGGATGACGGAAATGAAGAAATATGCAACTGG    | 120 |
| Db | 61  | CATTTTCTTCTGCATTTCCCTTAGTCGGATGACGGAAATGAAGAAATATGCAACTGG    | 120 |
| QY | 121 | CTCAGGCATATCTCAACAGTTCTACTCTCTTGAATAGAAGGAATCATCTTGTTCAAA    | 180 |
| Db | 121 | CTCAGGCATATCTCAACAGTTCTACTCTCTTGAATAGAAGGAATCATCTTGTTCAAA    | 180 |
| QY | 181 | GCAAGAAATAGGAGTCTCATAGATGACAAATTCGGGAAATGCAAGCATTTTGTGATTTGA | 240 |
| Db | 181 | GCAAGAAATAGGAGTCTCATAGATGACAAATTCGGGAAATGCAAGCATTTTGTGATTTGA | 240 |
| QY | 241 | CAGTGACTGGAAAACCTGGAATCAAAACCCCTTGAGATCATGAAGACACCCAGGTGGGG  | 300 |
| Db | 241 | CAGTGACTGGAAAACCTGGAATCAAAACCCCTTGAGATCATGAAGACACCCAGGTGGGG  | 300 |
| QY | 301 | TGCTGATGTGGGCGAGTATGCTACACCTCCCTGGGTGGAGAAATACAACTCACT       | 360 |
| Db | 301 | TGCTGATGTGGGCGAGTATGCTACACCTCCCTGGGTGGAGAAATACAACTCACT       | 360 |
| QY | 361 | ACAGAATAATAAATCTACTCCGGATATGGCAGGCTGCTGTGGATGAGGCTATCCCAAG   | 420 |
| Db | 361 | ACAGAATAATAAATCTACTCCGGATATGGCAGGCTGCTGTGGATGAGGCTATCCCAAG   | 420 |
| QY | 421 | AGGTTTGAAGTGTGGAGAAAGTCACTCCATCAAAATTCACCAAGATTTCAAAGGGGA    | 480 |
| Db | 421 | AGGTTTGAAGTGTGGAGAAAGTCACTCCATCAAAATTCACCAAGATTTCAAAGGGGA    | 480 |
| QY | 481 | TTGCAGACATCATGATGCTTTTAGGACTCGAGTCCATGGTGGTGGTCTGCTATTTTG    | 540 |
| Db | 481 | TTGCAGACATCATGATGCTTTTAGGACTCGAGTCCATGGTGGTGGTCTGCTATTTTG    | 540 |
| QY | 541 | ATGGTCCCTTGGGAGTGTCTGGCCATGCTTTCTCTGCTGGTCCGGGTCTGGGTGGTGA   | 600 |
| Db | 541 | ATGGTCCCTTGGGAGTGTCTGGCCATGCTTTCTCTGCTGGTCCGGGTCTGGGTGGTGA   | 600 |
| QY | 601 | CTCATTTTGTAGGATGAATACTGGACCAAGGATGGAGCAGGATTCAACTTTGTTCTTG   | 660 |
| Db | 601 | CTCATTTTGTAGGATGAATACTGGACCAAGGATGGAGCAGGATTCAACTTTGTTCTTG   | 660 |
| QY | 661 | TGGCTGCTCATGATTTGGTTCATGCTAGTGGGCTCTCTCACTCAATGATCAACAGCCT   | 720 |
| Db | 661 | TGGCTGCTCATGATTTGGTTCATGCTAGTGGGCTCTCTCACTCAATGATCAACAGCCT   | 720 |

RESULT 4  
 US-10-140-808-191  
 ; Sequence 191, Application US/10140808  
 ; Publication No. US20030017563A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeForge, Laura

|    |      |                                                               |      |
|----|------|---------------------------------------------------------------|------|
| QY | 721  | TGATGTTCCCAATTAATGCTCTCCCTGGATCCAGAAAAATACCCACTTTCTCAGATGATA  | 780  |
| Db | 721  | TGATGTTCCCAATTAATGCTCTCCCTGGATCCAGAAAAATACCCACTTTCTCAGATGATA  | 780  |
| QY | 781  | TCAATGGAATCCAGTCCATCTATGAGGTCTGCTAAGGTACCTGCTAGCCAAAGAAC      | 840  |
| Db | 781  | TCAATGGAATCCAGTCCATCTATGAGGTCTGCTAAGGTACCTGCTAGCCAAAGAAC      | 840  |
| QY | 841  | CCACTATACCCATGCTGTGACCCCTGACTTGACTTTTGCAGCTATCAACAATTTCCGCA   | 900  |
| Db | 841  | CCACTATACCCATGCTGTGACCCCTGACTTGACTTTTGCAGCTATCAACAATTTCCGCA   | 900  |
| QY | 901  | GAGAGTATGTTCTTTAAAGGAGGACCTATGAGGATCTATTATGATATCAGGATG        | 960  |
| Db | 901  | GAGAGTATGTTCTTTAAAGGAGGACCTATGAGGATCTATTATGATATCAGGATG        | 960  |
| QY | 961  | TTGAGTTTGAATTAATTTGCTTCTGCGCATCTCTGCGCATCTCTGCGCATCTCTGCGCAT  | 1020 |
| Db | 961  | TTGAGTTTGAATTAATTTGCTTCTGCGCATCTCTGCGCATCTCTGCGCATCTCTGCGCAT  | 1020 |
| QY | 1021 | ACGAGAACCCAGAGATTAAGATTCTGGTTTTTAAAGATGAAAACTTCTGGATGATCAGAG  | 1080 |
| Db | 1021 | ACGAGAACCCAGAGATTAAGATTCTGGTTTTTAAAGATGAAAACTTCTGGATGATCAGAG  | 1080 |
| QY | 1081 | GATATGCTGCTTGGCAGATTAATCCCAATCCATCCATCATATAGGTTTTCCAGGACGTG   | 1140 |
| Db | 1081 | GATATGCTGCTTGGCAGATTAATCCCAATCCATCCATCATATAGGTTTTCCAGGACGTG   | 1140 |
| QY | 1141 | TGAAGAAAATAGATGACGCGTCTGTGATAGACCAAGAAAAACCTTCTTTTGG          | 1200 |
| Db | 1141 | TGAAGAAAATAGATGACGCGTCTGTGATAGACCAAGAAAAACCTTCTTTTGG          | 1200 |
| QY | 1201 | GCATTTGGTGTGGAGGTTTGATGAAATGACCCAAACCATGGACAAAGGATTTCCGCGAGA  | 1260 |
| Db | 1201 | GCATTTGGTGTGGAGGTTTGATGAAATGACCCAAACCATGGACAAAGGATTTCCGCGAGA  | 1260 |
| QY | 1261 | GAGTGTAAAAACACTTTCTCGAATCAGTATCCGTTGGTGTGCTCTTTCCAGTACAAAG    | 1320 |
| Db | 1261 | GAGTGTAAAAACACTTTCTCGAATCAGTATCCGTTGGTGTGCTCTTTCCAGTACAAAG    | 1320 |
| QY | 1321 | GATTTCTTTTTCAGCGTGGATCAAGCAATTTGAATCAACATTAAGCAAAAGATA        | 1380 |
| Db | 1321 | GATTTCTTTTTCAGCGTGGATCAAGCAATTTGAATCAACATTAAGCAAAAGATA        | 1380 |
| QY | 1381 | TTACCCGAATCATGAGAACTAATATCTTGGTTTTCAATGCAAAAGAACCAAGAACTCTCAT | 1440 |
| Db | 1381 | TTACCCGAATCATGAGAACTAATATCTTGGTTTTCAATGCAAAAGAACCAAGAACTCTCAT | 1440 |
| QY | 1441 | TTGGTTTGTATATCAAGGAAAAAGCACATTCAGGAGGATTAAGATATTGTATCATATA    | 1500 |
| Db | 1441 | TTGGTTTGTATATCAAGGAAAAAGCACATTCAGGAGGATTAAGATATTGTATCATATA    | 1500 |
| QY | 1501 | AGAGTTTAAAGCTTGTATTATTTTGGTATTGTTTCTGTAATAAACAATTTCTATTATC    | 1560 |
| Db | 1501 | AGAGTTTAAAGCTTGTATTATTTTGGTATTGTTTCTGTAATAAACAATTTCTATTATC    | 1560 |
| QY | 1561 | AATAAATTCATAGACCTTAAATAAACCTCAACAGGTCTTTTAAATATAAATTCGCTCAA   | 1620 |
| Db | 1561 | AATAAATTCATAGACCTTAAATAAACCTCAACAGGTCTTTTAAATATAAATTCGCTCAA   | 1620 |
| QY | 1621 | AATAGAA 1627                                                  |      |
| Db | 1621 | AATAGAA 1627                                                  |      |



```

; Sequence 191, Application US/10121049
; Publication No. US20030022239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin J.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; Prior Application removed - See File Wrapper or PalM
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-121-049-191

Query Match      99.9%; Score 1625.4; DB 14; Length 1647;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTCAGCTGGAAGAGAGAGGAATGAAGCGCTCTCTGCTCTCTGTTGTTGTTCTTTATAA 60
Db 1 GCTTCAGCTGAAGAGAGAGGAATGAAGCGCTCTCTGCTCTCTGTTGTTGTTCTTTATAA 60

QY 61 CATTTTCTTCGATTTCCCTTAGTCGGATGACGGAAATGAAGAAATATGCAACTGG 120
Db 61 CATTTTCTTCGATTTCCCTTAGTCGGATGACGGAAATGAAGAAATATGCAACTGG 120

QY 121 CTCAGGCATATCTCAACAGATTCTACTCTCTTGAATAGAGGAATCATCTGTTCAAA 180
Db 121 CTCAGGCATATCTCAACAGATTCTACTCTCTTGAATAGAGGAATCATCTGTTCAAA 180

QY 181 GCAGAAATAGGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTGTGATTGA 240
Db 181 GCAGAAATAGGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTGTGATTGA 240

QY 241 CAGTGACTGGAAAACTGGACTCAAAACACCTTTGAGATCATGAAGACACCCAGGTGTGGG 300
Db 241 CAGTGACTGGAAAACTGGACTCAAAACACCTTTGAGATCATGAAGACACCCAGGTGTGGG 300

QY 301 TGCCTGATGTGGCCAGTATGCTACACCTCCCTGGGTGGGAAATACACCTCACCT 360
Db 301 TGCCTGATGTGGCCAGTATGCTACACCTCCCTGGGTGGGAAATACACCTCACCT 360

QY 361 ACAGAAATATAACTATATCTCCGATATGGACGAGCTGCTGTGATGAGGCTATCCCAAG 420
Db 361 ACAGAAATATAACTATATCTCCGATATGGACGAGCTGCTGTGATGAGGCTATCCCAAG 420

QY 421 AAGGTTTGAAGTGTGGAGCAAGTCACTCCACTAAAATTCACCAAGATTTCAAAGGGGA 480
Db 421 AAGGTTTGAAGTGTGGAGCAAGTCACTCCACTAAAATTCACCAAGATTTCAAAGGGGA 480

QY 481 TTGCAGACATCATGATTCCTTTAGGACTCGAGTCCATGGTGGTCTGCTCTATTTTG 540
Db 481 TTGCAGACATCATGATTCCTTTAGGACTCGAGTCCATGGTGGTCTGCTCTATTTTG 540

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QY 541 ATGGTCCCTTGGAGTGCTTGGCCATGCTTTCTCTCTGTCGGGTCTGGGTGGTGACA 600
Db 541 ATGGTCCCTTGGAGTGCTTGGCCATGCTTTCTCTCTGTCGGGTCTGGGTGGTGACA 600

QY 601 CTCATTTTGTATGAGGATGAAAACTGGACCAAGATGGAGCAGGATTCAACTGTTCTTG 660
Db 601 CTCATTTTGTATGAGGATGAAAACTGGACCAAGATGGAGCAGGATTCAACTGTTCTTG 660

QY 661 TGGCTGCTCATGAATTTGTGTCATGCACTGGGGCTCTCTCACTCAATGATCAACAGCCT 720
Db 661 TGGCTGCTCATGAATTTGTGTCATGCACTGGGGCTCTCTCACTCAATGATCAACAGCCT 720

QY 721 TGATGTTCCCAAAATATGCTCCCTGGATCCAGAAAAATACCCACTTTCTCAGGATGATA 780
Db 721 TGATGTTCCCAAAATATGCTCCCTGGATCCAGAAAAATACCCACTTTCTCAGGATGATA 780

QY 781 TCAATGGAATCCAGTCCATCTATGGAGGTCTGCCTAAGGTACTCTGCTAGGCCAAAGGAAC 840
Db 781 TCAATGGAATCCAGTCCATCTATGGAGGTCTGCCTAAGGTACTCTGCTAGGCCAAAGGAAC 840

QY 841 CCATATATCCCATGCTGTGACCCCTGACTTGATTTTGAAGTATCACAACTTTCCGCA 900
Db 841 CCATATATCCCATGCTGTGACCCCTGACTTGATTTTGAAGTATCACAACTTTCCGCA 900

QY 901 GAGAAATATGTTCTTTAAAGGCAGCACCCTATGGAGGATCTATTATGATATCAAGGATG 960
Db 901 GAGAAATATGTTCTTTAAAGGCAGCACCCTATGGAGGATCTATTATGATATCAAGGATG 960

QY 961 TTGAGTTTGAATTAATTTGCTTCAATCTGSCCATCTCTGCAGCTGATCTGCAAGCTGCAT 1020
Db 961 TTGAGTTTGAATTAATTTGCTTCAATCTGSCCATCTCTGCAGCTGATCTGCAAGCTGCAT 1020

QY 1021 ACAGAAACCCAGAGATTAAGATCTGGTTTTTAAAGATGAAAACTTTCTGGATGATCAGAG 1080
Db 1021 ACAGAAACCCAGAGATTAAGATCTGGTTTTTAAAGATGAAAACTTTCTGGATGATCAGAG 1080

QY 1081 GATATGCTGTCTTGGCAGATTATCCCAATCCATCCATACATTAGGTTTTCAGGACGTG 1140
Db 1081 GATATGCTGTCTTGGCAGATTATCCCAATCCATCCATACATTAGGTTTTCAGGACGTG 1140

QY 1141 TGAAGAAATAGATGCAGCCGTCTGTGATAGACCAAGAAAAACCTTACTTCTTTTGG 1200
Db 1141 TGAAGAAATAGATGCAGCCGTCTGTGATAGACCAAGAAAAACCTTACTTCTTTTGG 1200

QY 1201 GCATTTGTGCTGAGGTTTGATGAATGACCCAAACCATGGACAAAGATTTCCCGCAGA 1260
Db 1201 GCATTTGTGCTGAGGTTTGATGAATGACCCAAACCATGGACAAAGATTTCCCGCAGA 1260

QY 1261 GAGTGTAAAAACACTTTTCCCTGGAATCAGTATCCGTTGTGATGCTGCTTCCAGTACAAAG 1320
Db 1261 GAGTGTAAAAACACTTTTCCCTGGAATCAGTATCCGTTGTGATGCTGCTTCCAGTACAAAG 1320

QY 1321 GATTTCTTTTTCAGCCGTGGATCAAAAGCAATTTGAATCAACAATTAAGACAAAGATA 1380
Db 1321 GATTTCTTTTTCAGCCGTGGATCAAAAGCAATTTGAATCAACAATTAAGACAAAGATA 1380

QY 1381 TTACCCGAATCATGAGAACTAATACTTGGTTTCAATGCAAGAACCAAGAACTCTCAT 1440
Db 1381 TTACCCGAATCATGAGAACTAATACTTGGTTTCAATGCAAGAACCAAGAACTCTCAT 1440

QY 1441 TTGTTTTTGTATCAACAGGAAAAAGCACATTCAGGAGGCATTAAGATATTGTATCATATA 1500
Db 1441 TTGTTTTTGTATCAACAGGAAAAAGCACATTCAGGAGGCATTAAGATATTGTATCATATA 1500

QY 1501 AGAGTTTAAAGCTGTTTATTTTGGTATTGTTCAATTTGCTGAAAAACACTTCTATTATC 1560
Db 1501 AGAGTTTAAAGCTGTTTATTTTGGTATTGTTCAATTTGCTGAAAAACACTTCTATTATC 1560

QY 1561 AATAAATTCATAGACCTTAAATAAAACCTCAACAGGTCTTTTAAATATATAAATTCGCTTCAA 1620
Db 1561 AATAAATTCATAGACCTTAAATAAAACCTCAACAGGTCTTTTAAATATATAAATTCGCTTCAA 1620

QY 1621 AATAGAA 1627

```

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Db      1621 AATAGAA 1627
|||||||
RESULT 6
US-10-123-904-191
; Sequence 191, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-123-904-191

Query Match      99.9%; Score 1625.4; DB 14; Length 1647;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GCCTCAGCTCAAGAAAGAGAGGATGAAGCGCCTCTGCTTCTGTGTTTGTCTTTTATAA 60
Db      |||
Qy      1  GCCTCAGCTCAAGAAAGAGAGGATGAAGCGCCTCTGCTTCTGTGTTTGTCTTTATAA 60
Db      |||
Qy      61  CATTTCCTCTGCAATTTCCCTTAGTCCGGATGACGGAAATGAAGAAATATGCAACTGG 120
Db      |||
Qy      61  CATTTCCTCTGCAATTTCCCTTAGTCCGGATGACGGAAATGAAGAAATATGCAACTGG 120
Db      |||
Qy      121  CTCAGGATATCTCAACAGTTCTACTCTCTTGAATAGAGGAATCATCTTGTTCAAA 180
Db      |||
Qy      121  CTCAGGATATCTCAACAGTTCTACTCTCTTGAATAGAGGAATCATCTTGTTCAAA 180
Db      |||
Qy      181  GCAGATAGAGTCTCTATAGTACACAAATTCGGAAATGCAAGCATTTTTCGATTGA 240
Db      |||
Qy      181  GCAGATAGAGTCTCTATAGTACACAAATTCGGAAATGCAAGCATTTTTCGATTGA 240
Db      |||
Qy      241  CAGTGACTGGAAAACTGGAATCAAAACACCCCTTGAGATCATGAAGACACCCAGGTGGGG 300
Db      |||
Qy      241  CAGTGACTGGAAAACTGGAATCAAAACACCCCTTGAGATCATGAAGACACCCAGGTGGGG 300
Db      |||
Qy      301  TGCTGATGTGGGCCAGTATGGCTACACCCCTCCCTGGGTGGAGAAATACACCTCACCT 360
Db      |||
Qy      301  TGCTGATGTGGGCCAGTATGGCTACACCCCTCCCTGGGTGGAGAAATACACCTCACCT 360
Db      |||
Qy      361  ACAGATATATAATATCTACTCCGATATGGCAGCTGCTGTGATGAGGCTATCCAAAG 420
Db      |||
Qy      361  ACAGATATATAATATCTACTCCGATATGGCAGCTGCTGTGATGAGGCTATCCAAAG 420
Db      |||
Qy      421  AAGGTTTAAAGTGTGGAGCAAAAGTCACTCCATAAAATTCACCAAGATTTCAAAGGGA 480
Db      |||

421  AAGGTTTAAAGTGTGGAGCAAAAGTCACTCCATAAAATTCACCAAGATTTCAAAGGGA 480
481  TTGCGACATCATGATTTGCTTTAGGACTCGAGTCCATGCTCGGTCTCTCGCTATTTTG 540
481  TTGCGACATCATGATTTGCTTTAGGACTCGAGTCCATGCTCGGTCTCTCGCTATTTTG 540
541  ATGGTCCCTTGGGAGTGTGGCCATGCTTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
541  ATGGTCCCTTGGGAGTGTGGCCATGCTTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
601  CTCATTTTGAAGGATGAAGAACTGACCAAGATGAGGATGAGGATCAACTTGTCTTCTT 660
601  CTCATTTTGAAGGATGAAGAACTGACCAAGATGAGGATGAGGATCAACTTGTCTTCTT 660
661  TGGCTGCTCATGAATTTGGTTCATGCACTGGGCTCTCTCACTCAATGATCAAAAGCCT 720
661  TGGCTGCTCATGAATTTGGTTCATGCACTGGGCTCTCTCACTCAATGATCAAAAGCCT 720
721  TGAATGTTCCCAAAATATGCTCTCCCTGGATCCCAAGAAATAACCCACTTCTCAGATGATA 780
721  TGAATGTTCCCAAAATATGCTCTCCCTGGATCCCAAGAAATAACCCACTTCTCAGATGATA 780
781  TCAATGGAATCCAGTCCATCTATGAGGCTGCTGCTAAGGTACCTGCTAAGCAAGAAAC 840
781  TCAATGGAATCCAGTCCATCTATGAGGCTGCTGCTAAGGTACCTGCTAAGCAAGAAAC 840
841  CCATATACCCCATGCTGTGACCCCTGACTTGACTTTTGACGCTATCACAACTTTCCGCA 900
841  CCATATACCCCATGCTGTGACCCCTGACTTGACTTTTGACGCTATCACAACTTTCCGCA 900
901  GAGAAGTAAATGTTCTTTTAAAGGAGGACCATATGAGGATCTATTAATGATATCAAGATG 960
901  GAGAAGTAAATGTTCTTTTAAAGGAGGACCATATGAGGATCTATTAATGATATCAAGATG 960
961  TTGAGTTGAATTAATGTTCTTTTAAAGGAGGACCATATGAGGATCTATTAATGATATCAAGATG 1020
961  TTGAGTTGAATTAATGTTCTTTTAAAGGAGGACCATATGAGGATCTATTAATGATATCAAGATG 1020
1021  ACCAGAACCCGAGATGAAGATCTGTTTAAAGATGAAGAACTCTGATGATGATCAGAG 1080
1021  ACCAGAACCCGAGATGAAGATCTGTTTAAAGATGAAGAACTCTGATGATGATCAGAG 1080
1081  GATATGCTGTCTTCCAGATTTATCCCAATCCATCCATATAGTATGATGATGATGATGATGAT 1140
1081  GATATGCTGTCTTCCAGATTTATCCCAATCCATCCATATAGTATGATGATGATGATGATGATGAT 1140
1141  TGAAGAAATAGATGAGCGCTCTGATGAGGACCAAGAAATCCATCTCTTCTTCTTCTTCTTCT 1200
1141  TGAAGAAATAGATGAGCGCTCTGATGAGGACCAAGAAATCCATCTCTTCTTCTTCTTCTTCTT 1200
1201  GCATTTGCTGCTGGAGTTTGAATGAAATGACCCAAACCATGGAAGAAAGGATTCCTCGAGA 1260
1201  GCATTTGCTGCTGGAGTTTGAATGAAATGACCCAAACCATGGAAGAAAGGATTCCTCGAGA 1260
1261  GAGTGTGAAACACTTTCTTGGATCAGTATCGGTGTGATGCTGCTTTCAGTATCAAG 1320
1261  GAGTGTGAAACACTTTCTTGGATCAGTATCGGTGTGATGCTGCTTTCAGTATCAAG 1320
1321  GATTTCTTTTTCAGCGGTGATCAAGCAATTTGAATACACATTAAGCAAGAAAGATA 1380
1321  GATTTCTTTTTCAGCGGTGATCAAGCAATTTGAATACACATTAAGCAAGAAAGATA 1380
1381  TTACCCGAATCATGAGAACTAAATCTTTGTTTCAATGCAAGAAACCAAGAACTCTCAT 1440
1381  TTACCCGAATCATGAGAACTAAATCTTTGTTTCAATGCAAGAAACCAAGAACTCTCAT 1440
1441  TTGTTTGTGATATCAAGAAAGAAAGCAATTCAGGAGGATTAAGATATTTGATATCA 1500
1441  TTGTTTGTGATATCAAGAAAGAAAGCAATTCAGGAGGATTAAGATATTTGATATCA 1500
1501  AGAGTTTAAAGCTGTTTATTTTGGTATTTGTTCTATTTGCTGAAAGAACTCTTATTTATC 1560
1501  AGAGTTTAAAGCTGTTTATTTTGGTATTTGTTCTATTTGCTGAAAGAACTCTTATTTATC 1560
```





|    |      |                                                                 |      |
|----|------|-----------------------------------------------------------------|------|
| Db | 1441 | TTGGTTTGGTATCAACNAGGAAAGACATTCAGAGGCATAAAGATATTGTTATCATA        | 1500 |
| Qy | 1501 | AGAGTTTAAAGCTTGTTTATTTTTGGTATGTTTCATTTGCTGAAACACATTCATTATTATC   | 1560 |
| Db | 1501 | AGAGTTTAAAGCTTGTTTATTTTTGGTATGTTTCATTTGCTGAAACACATTCATTATTATC   | 1560 |
| Qy | 1561 | AATAAAATTCATAGACCTTAAATAAAGCTCAACAGGCTTTTTTAATATAAAATTCGTCTTCAA | 1620 |
| Db | 1561 | AATAAAATTCATAGACCTTAAATAAAGCTCAACAGGCTTTTTTAATATAAAATTCGTCTTCAA | 1620 |
| Qy | 1621 | AATAGAA                                                         | 1627 |
| Db | 1621 | AATAGAA                                                         | 1627 |

## RESULT 8

```

US-10-175-746-191
; Sequence 191, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Flvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-175-746-191

```

|      |    |                                                                |      |
|------|----|----------------------------------------------------------------|------|
| 241  | Db | CAGTCACTGGAAACTGGACTCAAAACACCCCTTGAGATCATGAAGACACACCCAGGTGTGGG | 300  |
| 301  | Qy | TGCCTGATGTGGGCCAGFATCGCTACACCCCTCCCTGGGTGGAGAAATACAACTCACCT    | 360  |
| 301  | Db | TGCCTGATGTGGGCCAGFATGCTACACCCCTCCCTGGGTGGAGAAATACAACTCACCT     | 360  |
| 361  | Qy | ACAGAAATAAATATATCTACCTCCGGATATGGCACAGCTGCTGCGATGAGGCTATCCAAG   | 420  |
| 361  | Db | ACAGAAATAAATATATCTACTCCGATATGGCACAGCTGCTTGTGATGAGGCTATCCAAG    | 420  |
| 421  | Qy | AAAGTTTAGAAGTGTGGAGCAAAAGTCACTCCACATAAAATTCACCAAGATTTCAAAGGGGA | 480  |
| 421  | Db | AAAGTTTAGAAGTGTGGAGCAAAAGTCACTCCACTAAAAATTCACCAAGATTTCAAAGGGGA | 480  |
| 481  | Qy | TTGCAGACATCATGATTCGCTTTAGGACTCGAGTCCATGGTCCGTGCTCGCTATTTTG     | 540  |
| 481  | Db | TTGCAGACATCATGATTCGCTTTAGGACTCGAGTCCATGGTCCGTGCTCGCTATTTTG     | 540  |
| 541  | Qy | ATGTCCTCTGGGAGTGTGTGGCCATGCTTTCTCTCTGGTCCGGGCTGGGTGGTGACA      | 600  |
| 541  | Db | ATGTCCTCTGGGAGTGTGTGGCCATGCTTTCTCTCTGGTCCGGTCTGGGTGGTGACA      | 600  |
| 601  | Qy | CTCATTTTGATGAGGATGAAACTCGGAACCAAGGATGGAGCAGGATTCAACTTGTTCTTTG  | 660  |
| 601  | Db | CTCATTTTGATGAGGATGAAACTCGGACCAAGGATGGAGCAGGATTCAACTTGTTCTTTG   | 660  |
| 661  | Qy | TGGCTGCTCATGAATTTGGTCAATGACATGGGCTCTCTCACTCCAAATGATCAAAACAGCCT | 720  |
| 661  | Db | TGGCTGCTCATGAATTTGGTCAATGACATGGGCTCTCTCACTCCAAATGATCAAAACAGCCT | 720  |
| 721  | Qy | TGATGTTTCCAAATTAATGTTCTCCCTGGATCCACAGAAATACCCACTTTCTCAGGATGATA | 780  |
| 721  | Db | TGATGTTTCCAAATTAATGTTCTCCCTGGATCCACAGAAATACCCACTTTCTCAGGATGATA | 780  |
| 781  | Qy | TCAATGGAAATCAGTCCATCTATGAGGCTCTGCTTAAGGATCCTGCTAAGCCCAAGGAAC   | 840  |
| 781  | Db | TCAATGGAAATCAGTCCATCTATGAGGCTCTGCTTAAGGATCCTGCTAAGCCCAAGGAAC   | 840  |
| 841  | Qy | CCACTATACCCCATGCTGTGACCCCTGACTTGACTTTTGACGCTATCAAACTTTCCGCA    | 900  |
| 841  | Db | CCACTATACCCCATGCTGTGACCCCTGACTTGACTTTTGACGCTATCAAACTTTCCGCA    | 900  |
| 901  | Qy | GAGAAGTAATGTTCTTTAAAGGAGGACCTATGGAGGATCTATTATGATATCAGGATG      | 960  |
| 901  | Db | GAGAAGTAATGTTCTTTAAAGGAGGAGCACTATGGAGGATCTATTATGATATCAGGATG    | 960  |
| 961  | Qy | TTGAGTTTGAATTAATTTGCTTCATTTCTGCCCATCTCTGCCAGCTGATCTGCAAGCTGCAT | 1020 |
| 961  | Db | TTGAGTTTGAATTAATTTGCTTCATTTCTGCCCATCTCTGCCAGCTGATCTGCAAGCTGCAT | 1020 |
| 1021 | Qy | ACCAGAAACCCAGAGATAAGATTCTGGTTTTTAAAGATGAAAACCTTCTGGATGATCAGAG  | 1080 |
| 1021 | Db | ACCAGAAACCCAGAGATAAGATTCTGGTTTTTAAAGATGAAAACCTTCTGGATGATCAGAG  | 1080 |
| 1081 | Qy | GATATGCTGTCTTGCCAGATTATCCCAATCCATCCATACATTAGTGTTCAGAGACGTG     | 1140 |
| 1081 | Db | GATATGCTGTCTTGCCAGATTATCCCAAAATCCATCCATACATTAGTGTTCAGAGACGTG   | 1140 |
| 1141 | Qy | TGAAGAAATATAGATCAGACCGCTGTGTGATAAGACCAACAGAAAAAACTACTCTTTGTGG  | 1200 |
| 1141 | Db | TGAAGAAATATAGATCAGACCGCTGTGTGATAAGACCAACAGAAAAAACTACTCTTTGTGG  | 1200 |
| 1201 | Qy | GCATTTGGTCTCGAGGTTTGATGAAATGACCCAAACCATGGCAAGGATTTCCCGCACA     | 1260 |
| 1201 | Db | GCATTTGGTCTCGAGGTTTGATGAAATGACCCAAACCATGGCAAGGATTTCCCGCACA     | 1260 |
| 1261 | Qy | GAGTGGTAAACACTTTCCTGGAAATCAGTATCCGTGTGTGATGCTGCTTTCCAGTACAAAG  | 1320 |
| 1261 | Db | GAGTGGTAAACACTTTCCTCGGAATCAGTATCCGTGTGTGATGCTGCTTTCCAGTACAAAG  | 1320 |
| 1321 | Qy | GATTCTCTTTTTCAGCCGTGGATCAAAGCAATTTGATCAACATTAAGACAAAGATA       | 1380 |
| 1321 | Db | GATTCTCTTTTTCAGCCGTGGATCAAAGCAATTTGATCAACATTAAGAAAGATA         | 1380 |

```
QY 1381 TTACCGGAATCATGAGAACTAATACTTGGTTTCAATGCAAGAACCAAGAACTCTCTCAT 1440
Db 1381 TTACCGGAATCATGAGAACTAATACTTGGTTTCAATGCAAGAACCAAGAACTCTCTCAT 1440
QY 1441 TTGGTTTGTGATATCAACAGAGAAAAGACACATTCAGAGGCATPAAGATATTGTATCAT 1500
Db 1441 TTGGTTTGTGATATCAACAGAGAAAAGACACATTCAGAGGCATPAAGATATTGTATCAT 1500
QY 1501 AGAGTTTAAGCTTGTATTTTGGTATTGTTTCAATTTGCTGAAAAACACTTCTATTATC 1560
Db 1501 AGAGTTTAAGCTTGTATTTTGGTATTGTTTCAATTTGCTGAAAAACACTTCTATTATC 1560
QY 1561 AATAAATTCATAGACCTAAAAATAAACTCAACAGAGTCTTTTAAATAAAATTCGCTTCAA 1620
Db 1561 AATAAATTCATAGACCTAAAAATAAACTCAACAGAGTCTTTTAAATAAAATTCGCTTCAA 1620
QY 1621 AATAGAA 1627
Db 1621 AATAGAA 1627
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## RESULT 9

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US-10-176-918-191
; Sequence 191, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bersini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC382
; CURRENT APPLICATION NUMBER: US/10/176,918
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 191
; LENGTH: 1647
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-918-191
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Query Match 99.9%; Score 1625.4; DB 14; Length 1647;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTCAGCTGAAGAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTGTTTGTCTTTATAA 60
Db 1 GCTTCAGCTGAAGAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTGTTTGTCTTTATAA 60
QY 61 CATTTTCTTCTGCAATTCCTTTAGTCCGGATGACGGAATAAAGAAAAATGAACAATGCAACTGG 120
Db 61 CATTTTCTTCTGCAATTCCTTTAGTCCGGATGACGGAATAAAGAAAAATGAACAATGCAACTGG 120
QY 121 CTCAGGCATATCTCAACAGTTCTACTCTCTTGAATGAAGGGAATCATCTTGTTCAAA 180
Db 121 CTCAGGCATATCTCAACAGTTCTACTCTCTTGAATGAAGGGAATCATCTTGTTCAAA 180
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QY 181 GCAAGTAATAGGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCAATTTTGGATTGA 240
Db 181 GCAAGTAATAGGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCAATTTTGGATTGA 240
QY 241 CAGTGACTGGAAAACTGGACTCAAAACACCTTCAGATCATGAAGACACCCAGGTGTGGGG 300
Db 241 CAGTGACTGGAAAACTGGACTCAAAACACCTTCAGATCATGAAGACACCCAGGTGTGGGG 300
QY 301 TGCCTGATGTGGGCCAGTATGCTACACCTCCCTGGGTGGAGAAAATAACAACCTCACCT 360
Db 301 TGCCTGATGTGGGCCAGTATGCTACACCTCCCTGGGTGGAGAAAATAACAACCTCACCT 360
QY 361 ACAGATAATAAATACTACTCCGGATATGCGACGAGCTGCTGTGGATGAGGCTATCCAAG 420
Db 361 ACAGATAATAAATACTACTCCGGATATGCGACGAGCTGCTGTGGATGAGGCTATCCAAG 420
QY 421 AAGGTTTAGAAGTGTGGAGCAAAAGTCACCTCCACTAAAAATTCACCAAGATTTCAAAGGGGA 480
Db 421 AAGGTTTAGAAGTGTGGAGCAAAAGTCACCTCCACTAAAAATTCACCAAGATTTCAAAGGGGA 480
QY 481 TTGCAGACATCATGATATGCTTTAGACTCGAGTCCATGGTCGGTCTCGCTATTTTG 540
Db 481 TTGCAGACATCATGATATGCTTTAGACTCGAGTCCATGGTCGGTCTCGCTATTTTG 540
QY 541 ATGCTCCCTTGGAGTGCTTGGCCATGCTTTCTCTCTGCTGGTCCGGGTCTGGGTGTGACA 600
Db 541 ATGCTCCCTTGGAGTGCTTGGCCATGCTTTCTCTCTGCTGGTCCGGGTCTGGGTGTGACA 600
QY 601 CTCATTTTATGATGAGGATGAAAACTGGACCAAGATGGAGCAGGATTCAACTTGTTCCTTG 660
Db 601 CTCATTTTATGATGAGGATGAAAACTGGACCAAGATGGAGCAGGATTCAACTTGTTCCTTG 660
QY 661 TGGCTGCTCATGAAATTTGGTCAATGCACTGGGCTCTCTCACTCCAATGATCAACAGCCT 720
Db 661 TGGCTGCTCATGAAATTTGGTCAATGCACTGGGCTCTCTCACTCCAATGATCAACAGCCT 720
QY 721 TGATGTTCCCAAAATATGCTCTCCCTGGATCCAGAAAATACCCACTTCTCAGGATGATA 780
Db 721 TGATGTTCCCAAAATATGCTCTCCCTGGATCCAGAAAATACCCACTTCTCAGGATGATA 780
QY 781 TCAATGGAATCCAGTCCCATCTATGGAGTCTGCTTAAGTACTCTGAAGCAAAAGGAC 840
Db 781 TCAATGGAATCCAGTCCCATCTATGGAGTCTGCTTAAGTACTCTGAAGCAAAAGGAC 840
QY 841 CCATATACCCCAATGCTCTGACCCCTGACTTTTGAACGCTATCAACACTTCCGCA 900
Db 841 CCATATACCCCAATGCTCTGACCCCTGACTTTTGAACGCTATCAACACTTCCGCA 900
QY 901 GAGAGTAATCTCTTTAAAGCAGGCACCTATGGAGATCTATATGATATCAGGATG 960
Db 901 GAGAGTAATCTCTTTAAAGCAGGCACCTATGGAGATCTATATGATATCAGGATG 960
QY 961 TTGAGTTTGAATTAATTTGCTTCAATTCGGCCATCTCTGCCAGCTGATCTGCAAGCTGAT 1020
Db 961 TTGAGTTTGAATTAATTTGCTTCAATTCGGCCATCTCTGCCAGCTGATCTGCAAGCTGAT 1020
QY 1021 ACAGAACCCCAAGATGAAGATTTCTGGTTTAAAGATGAAAACTTCTGGATGATCAGAG 1080
Db 1021 ACAGAACCCCAAGATGAAGATTTCTGGTTTAAAGATGAAAACTTCTGGATGATCAGAG 1080
QY 1081 GATATGCTCTTCCAGATTTATCCCAATCCATCAATAGGTTTTCAGGAGCTG 1140
Db 1081 GATATGCTCTTCCAGATTTATCCCAATCCATCAATAGGTTTTCAGGAGCTG 1140
QY 1141 TGAAGAAAAATAGATGACAGCGCTGTGTATGAAGACCAAGAAAAACCTACTTCTTTGG 1200
Db 1141 TGAAGAAAAATAGATGACAGCGCTGTGTATGAAGACCAAGAAAAACCTACTTCTTTGG 1200
QY 1201 GCATTTGGTGTGGAGTTTGTGAAATGACCCAAACCATGGAACAAAGGATTTCCCGAGA 1260
Db 1201 GCATTTGGTGTGGAGTTTGTGAAATGACCCAAACCATGGAACAAAGGATTTCCCGAGA 1260
QY 1261 GAGTGTAAACACACTTTCCTGGAAATCAGTATCCGTGTGATGCTGCTTCCAGTACAAAG 1320
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Db 1261 GAGTGGTAAACACATTTCTGGAAATCAGTATCCGTTGATGCTGCTTCCAGTACAAAG 1320  
Qy 1321 GATTTCTTTCTTTTCCAGCCGTGGATCAAGCAATTTGAATAACAATTAAGACAAAGATA 1380  
Db 1321 GATTTCTTTTTCAGCCGTGGATCAAGCAATTTGAATACAAATTAAGACAAAGATA 1380  
Qy 1381 TTACCCGAATCATGAGAACTAATACATTTGGTTTCAATGCAAGAACCAAGAACTCTCAT 1440  
Db 1381 TTACCCGAATCATGAGAACTAATACATTTGGTTTCAATGCAAGAACCAAGAACTCTCAT 1440  
Qy 1441 TTGGTTTGTATATCAACAGGAAAGACATTCAGAGGCATATAAGATATTCTATCAT 1500  
Db 1441 TTGGTTTGTATATCAACAGGAAAGACATTCAGAGGCATATAAGATATTCTATCAT 1500  
Qy 1501 AGAGTTTAAAGCTTGTATTTTGGTATTGTTTCAATTTGCTGAAACACATTCATTATC 1560  
Db 1501 AGAGTTTAAAGCTTGTATTTTGGTATTGTTTCAATTTGCTGAAACACATTCATTATC 1560  
Qy 1561 AATAAATTCATAGACCTAAATAAACCCTCAAGAGTCTTTTATATATAAATTCGCTCAA 1620  
Db 1561 AATAAATTCATAGACCTAAATAAACCCTCAAGAGTCTTTTATATATAAATTCGCTCAA 1620  
Qy 1621 AATAGAA 1627  
Db 1621 AATAGAA 1627

## RESULT 10

US-10-176-921-191  
; Sequence 191, Application US/10176921  
; Publication No. US20030027276A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: DeNoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zenin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C288  
; CURRENT APPLICATION NUMBER: US/10/176,921  
; CURRENT FILING DATE: 2002-06-20  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 191  
; LENGTH: 1647  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-176-921-191

Query Match 99.9%; Score 1625.4; DB 14; Length 1647;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 GCTTCAGCTGAGAAAGAGAGGAATGAAGCCCTCTGCTCTGTTGTTTCTTTATAA 60  
Db 1 GCTTCAGCTGAGAAAGAGAGGAATGAAGCCCTCTGCTCTGTTGTTTCTTTATAA 60  
Qy 61 CATTTTCTTCTGCAATTTCCCTTAGTCCGGATGACGGAAATGAAGAAATATGCAACTGG 120

Db 61 CATTTTCTTCTGCAATTTCCCTTAGTCCGGATGACGGAAATGAAGAAATATGCAACTGG 120  
Qy 121 CTCAGGCATATCTCAACAGATTTCTACTCTCTTGAAATAGAAGGGAATCATCTTTGTTCAA 180  
Db 121 CTCAGGCATATCTCAACAGATTTCTACTCTCTTGAAATAGAAGGGAATCATCTTTGTTCAA 180  
Qy 181 GCAAGAAATAGGAGTCTCATAGATGACAAATTCGGGAAATGCAAGCATTTTTGGATTGA 240  
Db 181 GCAAGAAATAGGAGTCTCATAGATGACAAATTCGGGAAATGCAAGCATTTTTGGATTGA 240  
Qy 241 CAGTGAATGAGAACTGGAATGCAACACCCCTTGAGATCATGAAGACACCAGGTGTTGGG 300  
Db 241 CAGTGAATGAGAACTGGAATGCAACACCCCTTGAGATCATGAAGACACCAGGTGTTGGG 300  
Qy 301 TGCTCATGTTGGCCAGTATGCTACACCTCTCGGTGGGAGAAATACAACTCACCT 360  
Db 301 TGCTCATGTTGGCCAGTATGCTACACCTCTCGGTGGGAGAAATACAACTCACCT 360  
Qy 361 ACAGAAATATAAATACTATCTCCGGATATGCGACAGCTGCTGTGGATGAGGCTATCCAAG 420  
Db 361 ACAGAAATATAAATACTATCTCCGGATATGCGACAGCTGCTGTGGATGAGGCTATCCAAG 420  
Qy 421 AAGGTTTAGAAGTGTGGAGCAAAAGTCACTCACTAAATTCACCAAGATTTCAAGAGGGA 480  
Db 421 AAGGTTTAGAAGTGTGGAGCAAAAGTCACTCACTAAATTCACCAAGATTTCAAGAGGGA 480  
Qy 481 TTGCAGACATCATGATTGGCTTTAGGACTCGAGTCCATGGTCCGTTCTCGCTATTTTG 540  
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Qy 541 ATGGTCCCTTTGGGAGTGTGGCCATGCTCTCTGGTCCGGGTCTGGGTGGTGACA 600  
Db 541 ATGGTCCCTTTGGGAGTGTGGCCATGCTCTCTGGTCCGGGTCTGGGTGGTGACA 600  
Qy 601 CTCATTTTGTAGAGGATGAAACTGACCAAGAGTGGAGCAGGATCAACTGTTTCTTG 660  
Db 601 CTCATTTTGTAGAGGATGAAACTGACCAAGAGTGGAGCAGGATCAACTGTTTCTTG 660  
Qy 661 TGCGTCTCATGAAATTTGGTCAATGCTCTCTCTGCTCCGGTCTGGGTGGTGACA 720  
Db 661 TGCGTCTCATGAAATTTGGTCAATGCTCTCTCTGCTCCGGTCTGGGTGGTGACA 720  
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Db 721 TGATGTTTCCCAAAATTAATGCTCTCCCTGGATCCCAAGAAATACCCACTTTCTCAGATGATA 780  
Qy 781 TCAATGGAATCCAGTCCATCTATGAGAGTCTGCTTAAGGTACCTGCTAAAGCAAGAAC 840  
Db 781 TCAATGGAATCCAGTCCATCTATGAGAGTCTGCTTAAGGTACCTGCTAAAGCAAGAAC 840  
Qy 841 CCATATACCCCATGCTCTGACCTGACCTTGACTTTTGACGCTATCACAACCTTTCCGCA 900  
Db 841 CCATATACCCCATGCTCTGACCTGACCTTGACTTTTGACGCTATCACAACCTTTCCGCA 900  
Qy 901 GAGAAGTAAATGTTCTTTAAAGGCGAGGACCTATGAGAGATCTATATGATATCAGGATG 960  
Db 901 GAGAAGTAAATGTTCTTTAAAGGCGAGGACCTATGAGAGATCTATATGATATCAGGATG 960  
Qy 961 TTGAGTTTGAATTAATTTGCTTCAATCTGGCCATCTCTGCGAGTGTGCAAGCTCAT 1020  
Db 961 TTGAGTTTGAATTAATTTGCTTCAATCTGGCCATCTCTGCGAGTGTGCAAGCTCAT 1020  
Qy 1021 ACAGAAACCCAGAGATAAGATTTCTGTTTAAAGATGAAGAACTTTCTGGATGATCAGAG 1080  
Db 1021 ACAGAAACCCAGAGATAAGATTTCTGTTTAAAGATGAAGAACTTTCTGGATGATCAGAG 1080  
Qy 1081 GATATGCTGTTTCCAGATTTATCCCAATCCATCCATACATTAAGTTTTCAGGACCTG 1140  
Db 1081 GATATGCTGTTTCCAGATTTATCCCAATCCATCCATACATTAAGTTTTCAGGACCTG 1140  
Qy 1141 TGAAGAAATAGATGCGCCCTCTGTGATAGACCAAGAAACCTTACTTCTTTTGG 1200  
Db 1141 TGAAGAAATAGATGCGCCCTCTGTGATAGACCAAGAAACCTTACTTCTTTTGG 1200



1081 GATATGCTGCTTGGCAGATTATCCCAATCCATCATATAGTTTCCAGAGCTG 1140  
1141 TGAAGAAAATAGATGAGCGCTGTGTATAGACCAAGAAAACCTACTTTGTGG 1200  
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1201 GCATTTGGTCTGGAGTTTGTAGAAATGACCCAAACCATGGACAAAGGATTCGGCAGA 1260  
1201 GCATTTGGTCTGGAGTTTGTAGAAATGACCCAAACCATGGACAAAGGATTCGGCAGA 1260  
1261 GAGTGTAAACACTTTCTCGGATCAGTATCCGTGTGTGCTTTCCAGTACAAAG 1320  
1261 GAGTGTAAACACTTTCTCGGATCAGTATCCGTGTGTGCTTTCCAGTACAAAG 1320  
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1441 TTGGTTTGTATCAACAGGAAAAGCAGTTCAGGAGGCATAAAGATATTGTATCAT 1500  
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RESULT 12  
US-10-140-474-191  
; Sequence 191, Application US/10140474  
; Publication No. US20030032156A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C162  
; CURRENT APPLICATION NUMBER: US/10/140,474  
; CURRENT FILING DATE: 2002-05-06  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 191  
; LENGTH: 1647  
; TYPE: DNA  
; ORGANISM: Homo Sapien

US-10-140-474-191

Query Match 99.9%; Score 1625.4; DB 14; Length 1647;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 GCTTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTGTGTCTTCTTCTTATAA 60  
Db 1 GCTTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTGTGTCTTCTTCTTATAA 60  
QY 61 CATTTTCTTCTGCAATTCCTTAGTCCGGATGCGGAAATGAAGAAATGAAGAAATATGCAACTGG 120  
Db 61 CATTTTCTTCTGCAATTCCTTAGTCCGGATGCGGAAATGAAGAAATGAAGAAATATGCAACTGG 120  
QY 121 CTGAGGCATATCTCAACCAAGTCTCTCTCTGAATAGAGGAATCACTCTTGTTCAAA 180  
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QY 181 GCAAGAAATAGAGTCTCATAGATGACAAAATTCGGGAAATTCGAAGCAATTTTGGATTGA 240  
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QY 241 CAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 300  
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QY 301 TGCCTGATGTCGCGGAGTATGCTTACACCTCTCTGCTGCGGAGTGAAGAAATCAACCTCACCT 360  
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QY 361 ACAGAAATATAAATACTATACCTCCGATATGCGAGTCTGCTGCGGAGTGAAGTGAAGTGAAG 420  
Db 361 ACAGAAATATAAATACTATACCTCCGATATGCGAGTCTGCTGCGGAGTGAAGTGAAGTGAAG 420  
QY 421 AAGTTTGAAGTGTGGAGCAAGTCACTCCATTAATAATTCACCAAGATTTCAAAGGGGA 480  
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Db 481 TTGCAGACATCATGATTCCTTTAGGACTCGAGTCCATGCTGCGGTGCTCTGCTTATTTTG 540  
QY 541 ATGGTCTCTTGGGAGTCTTGGCCATGCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
Db 541 ATGGTCTCTTGGGAGTCTTGGCCATGCTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600  
QY 601 CTCATTTTGTAGAGGATGAAGAACTGGACCAAGGATGGAGCAGGATTCACACTTTGTTCTTG 660  
Db 601 CTCATTTTGTAGAGGATGAAGAACTGGACCAAGGATGGAGCAGGATTCACACTTTGTTCTTG 660  
QY 661 TGGCTGCTCATGAATTTGGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
Db 661 TGGCTGCTCATGAATTTGGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
QY 721 TGATGTTTCCCAAAATTAATGCTCTCCCTGGATCCAGAAAATACCCACTTTCTCAGGATGATA 780  
Db 721 TGATGTTTCCCAAAATTAATGCTCTCCCTGGATCCAGAAAATACCCACTTTCTCAGGATGATA 780  
QY 781 TCAATGGAATCCAGTCCATCTATGAGAGTCTGCTTAAAGTACCTGCTTAAAGCAAGGAAAC 840  
Db 781 TCAATGGAATCCAGTCCATCTATGAGAGTCTGCTTAAAGTACCTGCTTAAAGCAAGGAAAC 840  
QY 841 CCACATATACCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
Db 841 CCACATATACCCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900  
QY 901 GAGAAGTAAATGTTCTTTAAAGGAGGACCTATGAGAGATCTATATGATATACGAGATG 960  
Db 901 GAGAAGTAAATGTTCTTTAAAGGAGGACCTATGAGAGATCTATATGATATACGAGATG 960  
QY 961 TTGAGTTTGAATTAATGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020  
Db 961 TTGAGTTTGAATTAATGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1020

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QY 1021 ACAGAACCCAGAGATAAGATTCTGGTTTAAAGATGAAACTTCTGGATGATCAGAG 1080
DB |||||||
QY 1021 ACAGAACCCAGAGATAAGATTCTGGTTTAAAGATGAAACTTCTGGATGATCAGAG 1080
DB |||||||
QY 1081 GATATGCTGCTTGCCAGATTATCCAAATCCATCCATCATCATAGGTTTCCAGGACGTG 1140
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QY 1201 GCATTTGGTGTGGAGTTTGATGAAATGACCAACCAACCAAGGATTTCCCGCAGA 1260
DB |||||||
QY 1261 GAGTGGTAAACACATTTCTCGAATCAGTATCCGTTGATGCTGCTTCCAGTACAAAG 1320
DB |||||||
QY 1321 GATTTCTTTTTCAGCGTGATCAAGCAATTTGAATACAAATTAAGACAAAGAATA 1380
DB |||||||
QY 1381 TTACCCGAATCATGAGAACTAATACTTGGTTTCAATGCAAGAAACCAAGAAACTCTCAT 1440
DB |||||||
QY 1441 TTGGTTTTGATATCAACAGGAAAGACATTCAGGAGGCATTAAGATATTGTATCAT 1500
DB |||||||
QY 1501 AGAGTTTAAGCTGTTTATTTTGGTATGTTTCATTTGCTGAAACACTTCTATTTATC 1560
DB |||||||
QY 1561 AATAAATTCATAGACCTAAATATAAACCCTCAACAGGTCTTTTAATAAATTCGTTCAA 1620
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QY 1621 AATAGAA 1627
DB |||||||
QY 1621 AATAGAA 1627
DB |||||||
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## RESULT 13

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US-10-142-431-191
; Sequence 191, Application US/10142431
; Publication No. US20030036179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C251
; CURRENT APPLICATION NUMBER: US/10/142,431
; CURRENT FILING DATE: 2002-05-10
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; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 191

; LENGTH: 1647

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-142-431-191

Query Match 99.9%; Score 1625.4; DB 14; Length 1647;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTCAGCTGGAAGAAGAGAGGAATCAAGCGCTTCTGCTCTCTGCTCTGCTCTTTATAA 60

DB 1 GCTTCAGCTGGAAGAAGAGAGGAATCAAGCGCTTCTGCTCTCTGCTCTGCTCTTTATAA 60

QY 61 CATTTTCTTCTCATTTTCCCTTAGTCCGGATGACGGAATAAGAAAAATATGCAACTGG 120

DB 61 CATTTTCTTCTCATTTTCCCTTAGTCCGGATGACGGAATAAGAAAAATATGCAACTGG 120

QY 121 CTCAGGCATATCTCAACCGATTCTACTCTCTTGAATAAGAGGAATCATCTTGTTCAAA 180

DB 121 CTCAGGCATATCTCAACCGATTCTACTCTCTTGAATAAGAGGAATCATCTTGTTCAAA 180

QY 181 GCAAGAAATAGGAGTCTCATAGATGACAAATTCGGGAAATGCAAGCATTTTGTGATGA 240

DB 181 GCAAGAAATAGGAGTCTCATAGATGACAAATTCGGGAAATGCAAGCATTTTGTGATGA 240

QY 241 CAGTGACTGGAAAACTGGACTCAAAACACCTTTGAGATCATGAAGACACCCAGGTGTGGG 300

DB 241 CAGTGACTGGAAAACTGGACTCAAAACACCTTTGAGATCATGAAGACACCCAGGTGTGGG 300

QY 301 TGCCTGATGTGGCCAGTATGGCTACACCTCCCTGGGTGGAGAAATAACAACCTCACT 360

DB 301 TGCCTGATGTGGCCAGTATGGCTACACCTCCCTGGGTGGAGAAATAACAACCTCACT 360

QY 361 ACAGAAATATAAATCTACTCCGGATATGGCAGAGCTGTGTGATGAGGCTATCCAG 420

DB 361 ACAGAAATATAAATCTACTCCGGATATGGCAGAGCTGTGTGATGAGGCTATCCAG 420

QY 421 AAGGTTTGAAGTGTGGAGCAAAAGTCACTCCACTAAAAATTCACCAAGATTTCAAAGGGA 480

DB 421 AAGGTTTGAAGTGTGGAGCAAAAGTCACTCCACTAAAAATTCACCAAGATTTCAAAGGGA 480

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QY 541 ATGGTCCCTTGGGAGTGTGGCCATGCTTTCTCTCTGCTCCGGTCTGGGTGGTGACA 600

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QY 661 TGGCTGCTCATGAATTTGGTCAATGCACTGGGGCTCTCTCACTCCAATGATCAACAGCCT 720

DB 661 TGGCTGCTCATGAATTTGGTCAATGCACTGGGGCTCTCTCACTCCAATGATCAACAGCCT 720

QY 721 TGATGTTCCCAAAATATGCTCTCCCTGGATCCAGAAATACCCACTTTCTCAGGATGATA 780

DB 721 TGATGTTCCCAAAATATGCTCTCCCTGGATCCAGAAATACCCACTTTCTCAGGATGATA 780

QY 781 TCAATGGAATCCAGTCCATCTATGAGGCTCTGCTTAAGTACCTGCTAAGCAAGGAAC 840

DB 781 TCAATGGAATCCAGTCCATCTATGAGGCTCTGCTTAAGTACCTGCTAAGCAAGGAAC 840

QY 841 CCATATACCCCATGCTGTGACCTGACTGATTTTGACGCTATCAAACTTTCCGCA 900

DB 841 CCATATACCCCATGCTGTGACCTGACTGATTTTGACGCTATCAAACTTTCCGCA 900

QY 901 GAGAAGTAATGTTCTTTAAAGGAGGACCTATGAGGATCTATATGATATCAGGATG 960



901 GAGAAGTAATGTTCTTTAAAGGAGGACCTATGGAGGATCTATTATGATATCAGGATG 960  
961 TTGAGTTTGAATTAATGCTTCAATCTGCGCAATCTCTGCCAGCTGATCTGCAAGCTGCAT 1020  
961 TTGAGTTTGAATTAATGCTTCAATCTGCGCAATCTCTGCCAGCTGATCTGCAAGCTGCAT 1020  
1021 ACAGAAACCCAGAGATAGATTTCTGTTTAAAGATGAAAATCTTGGATGATCAGAG 1080  
1021 ACAGAAACCCAGAGATAGATTTCTGTTTAAAGATGAAAATCTTGGATGATCAGAG 1080  
1081 GATATGCTGCTGTCGAGATTTATCCCAATCCATCATATAGGTTTCCAGGAGCTG 1140  
1081 GATATGCTGCTGTCGAGATTTATCCCAATCCATCATATAGGTTTCCAGGAGCTG 1140  
1141 TGAAGAAAATAGATGACGCGCTGTGATAGACCAAGAAAACCTACTTCTTTGTGG 1200  
1141 TGAAGAAAATAGATGACGCGCTGTGATAGACCAAGAAAACCTACTTCTTTGTGG 1200  
1201 GCATTTGGTCTGAGGTTTGATGAATGACCCCAACCATGGACAAAGGATTCGCCGAGA 1260  
1201 GCATTTGGTCTGAGGTTTGATGAATGACCCCAACCATGGACAAAGGATTCGCCGAGA 1260  
1261 GAGTGTAAACACTTTCTCGGAATCAGTATCCGTGTTGATGCTGCTTTCCAGTACAAAG 1320  
1261 GAGTGTAAACACTTTCTCGGAATCAGTATCCGTGTTGATGCTGCTTTCCAGTACAAAG 1320  
1321 GATTTCTTTTTCAGCGTGGATCAAAAGCAATTTGAATACCAATTAAGACAAAGAAATA 1380  
1321 GATTTCTTTTTCAGCGTGGATCAAAAGCAATTTGAATACCAATTAAGACAAAGAAATA 1380  
1381 TTACCCGAATCATGAGAACTAATACTTGGTTTGAATGCAAGAACCAAGAACTCCCTCAT 1440  
1381 TTACCCGAATCATGAGAACTAATACTTGGTTTGAATGCAAGAACCAAGAACTCCCTCAT 1440  
1441 TTGTTTGGTATATCAAGAGAAAAGCACATTCAGGAGGATATAAGATATTGTATCATATA 1500  
1441 TTGTTTGGTATATCAAGAGAAAAGCACATTCAGGAGGATATAAGATATTGTATCATATA 1500  
1501 AGAGTTTAAAGCTGTTTATTTTGGTATTGTTTCAATTTGCTGAAAAACACTTCTATTATC 1560  
1501 AGAGTTTAAAGCTGTTTATTTTGGTATTGTTTCAATTTGCTGAAAAACACTTCTATTATC 1560  
1561 AATAAATTCATAGACCTAAATTAACCTCAACAGCTCTTTTAAATATAAATTCGCTCAA 1620  
1561 AATAAATTCATAGACCTAAATTAACCTCAACAGCTCTTTTAAATATAAATTCGCTCAA 1620  
1621 AATAGAA 1627  
1621 AATAGAA 1627

RESULT 14  
US-10-143-114-191  
; Sequence 191, Application US/10143114  
; Publication No. US20030036180A1  
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: F3330RIC211  
; CURRENT APPLICATION NUMBER: US/10/143,114  
; CURRENT FILING DATE: 2002-05-09  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 191  
; LENGTH: 1647  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-143-114-191  
  
Query Match 99.9%; Score 1625.4; DB 14; Length 1647;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 GCTTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTTCTGTTCTTTATAA 60  
DB 1 GCTTTCAGCTGAAGAAAGAGAGGAATGAAGCGCCTTCTGCTTCTGTTCTGTTCTTTATAA 60  
  
QY 61 CATTTTCTTCTGATTTCCCTTAGTCCGATGAGGAAATGAAGAAAATATGCAACTGG 120  
DB 61 CATTTTCTTCTGATTTCCCTTAGTCCGATGAGGAAATGAAGAAAATATGCAACTGG 120  
  
QY 121 CTCAGGCATATCTCAACAGTCTCTCTCTTGAATAGAGGGAATCATCTGTTCAAA 180  
DB 121 CTCAGGCATATCTCAACAGTCTCTCTCTTGAATAGAGGGAATCATCTGTTCAAA 180  
  
QY 181 GCAAGAAATAGGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCAATTTTTGGATGA 240  
DB 181 GCAAGAAATAGGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCAATTTTTGGATGA 240  
  
QY 241 CAGTGACTGAAAACCTGGAATCAAAAACCTTGGATCATGAGACACCCAGGTGTGGG 300  
DB 241 CAGTGACTGAAAACCTGGAATCAAAAACCTTGGATCATGAGACACCCAGGTGTGGG 300  
  
QY 301 TGCTGATGTTGGGCGAGTATGGCTTACACCTCTCTGCTGGTGGAGAAAATACAACTCACCT 360  
DB 301 TGCTGATGTTGGGCGAGTATGGCTTACACCTCTCTGCTGGTGGAGAAAATACAACTCACCT 360  
  
QY 361 ACAGAAATATAAATACTATACTCCGGATATGGACAGCTGCTGTGGATGAGGCTATCAAG 420  
DB 361 ACAGAAATATAAATACTATACTCCGGATATGGACAGCTGCTGTGGATGAGGCTATCAAG 420  
  
QY 421 AAGTTTATAGAGTGTGGAGCAAGTCACTCACTAAAATTCACCAAGATTTCAAAGGGGA 480  
DB 421 AAGTTTATAGAGTGTGGAGCAAGTCACTCACTAAAATTCACCAAGATTTCAAAGGGGA 480  
  
QY 481 TTGCAGACATCATGATTGCTTTTAGGACTCGAGTCCATGGTCTGCTCGCTATTATTG 540  
DB 481 TTGCAGACATCATGATTGCTTTTAGGACTCGAGTCCATGGTCTGCTCGCTATTATTG 540  
  
QY 541 ATGCTCCCTTTGGGAGTCTTTGGCCATGCTTCTCTCTGCTGGTCTGGGTGGTGA 600  
DB 541 ATGCTCCCTTTGGGAGTCTTTGGCCATGCTTCTCTCTGCTGGTCTGGGTGGTGA 600  
  
QY 601 CTCATTTTATGAGGATGAAAATCTGGACCAAGGATGAGGAGGATTTCAACTTTGTTCTG 660  
DB 601 CTCATTTTATGAGGATGAAAATCTGGACCAAGGATGAGGAGGATTTCAACTTTGTTCTG 660  
  
QY 661 TGGCTGCTCATGAATTTGGTCTATGCACTGCGGCTCTCTCACTCCAATGATCAACAGCCT 720  
DB 661 TGGCTGCTCATGAATTTGGTCTATGCACTGCGGCTCTCTCACTCCAATGATCAACAGCCT 720  
  
QY 721 TGATGTTCCCAAAATATGTTCTTCCCTGGATCCAGAAAATACCCACTTTCTCAGGATGATA 780  
DB 721 TGATGTTCCCAAAATATGTTCTTCCCTGGATCCAGAAAATACCCACTTTCTCAGGATGATA 780  
  
QY 781 TCAATGGAATCCAGTCCATCTATGAGGTCTGCTTAAGTACCTGCTTAAGCCAAAGGAAC 840  
DB 781 TCAATGGAATCCAGTCCATCTATGAGGTCTGCTTAAGTACCTGCTTAAGCCAAAGGAAC 840



QY 841 CCACTATACCCCATGCTGTGACCCCTGACTTTTGACGCTATCAAACTTCCGGA 900  
DB 841 CCACTATACCCCATGCTGTGACCCCTGACTTTTGACGCTATCAAACTTCCGGA 900  
QY 901 GAGAAGTAAATGTTCTTTAAAGCAGGACCACTATGAGGATCTATTATGATATCAAGGATG 960  
DB 901 GAGAAGTAAATGTTCTTTAAAGCAGGACCACTATGAGGATCTATTATGATATCAAGGATG 960  
QY 961 TTGAGTTGAATTAATGTTCTTTAAAGCAGGACCACTATGAGGATCTATTATGATATCAAGGATG 1020  
DB 961 TTGAGTTGAATTAATGTTCTTTAAAGCAGGACCACTATGAGGATCTATTATGATATCAAGGATG 1020  
QY 1021 ACAGAGACCCAGAGATAGATTCTGTGTTTAAAGATGAAAACCTTCTGGATGATCAGAG 1080  
DB 1021 ACAGAGACCCAGAGATAGATTCTGTGTTTAAAGATGAAAACCTTCTGGATGATCAGAG 1080  
QY 1081 GATATGCTGCTTTCGACAGATATCCAAATCCATATCATTAGTGTTCAGGACGTTG 1140  
DB 1081 GATATGCTGCTTTCGACAGATATCCAAATCCATATCATTAGTGTTCAGGACGTTG 1140  
QY 1141 TGAAGAAATAGATGACGCGCTGTGTGATAAGACCAAGAAAACCTTACTTCTTTGGG 1200  
DB 1141 TGAAGAAATAGATGACGCGCTGTGTGATAAGACCAAGAAAACCTTACTTCTTTGGG 1200  
QY 1201 GCATTTGGTGGAGGTTTGTGATGAATGACCCCAACCATGACAAAGGATTCGCCGAGA 1260  
DB 1201 GCATTTGGTGGAGGTTTGTGATGAATGACCCCAACCATGACAAAGGATTCGCCGAGA 1260  
QY 1261 GAGTGGTAAAAACACTTTCCTGGAATCAGTATCCGTTGTGATGCTGCTTTCAGTACAAG 1320  
DB 1261 GAGTGGTAAAAACACTTTCCTGGAATCAGTATCCGTTGTGATGCTGCTTTCAGTACAAG 1320  
QY 1321 GATTCCTTTTTCAGCGCTGGATCAAGCAATTTGAATPAACAATTAAGA CAAGAATA 1380  
DB 1321 GATTCCTTTTTCAGCGCTGGATCAAGCAATTTGAATPAACAATTAAGA CAAGAATA 1380  
QY 1381 TTACCCGATCATGAGACTTAATCTGTTTCAATGCAAGAACCAAGAACTCTCAT 1440  
DB 1381 TTACCCGATCATGAGACTTAATCTGTTTCAATGCAAGAACCAAGAACTCTCAT 1440  
QY 1441 TTGGTTTGTATATCAAGGAAAAAGCACTTTCAGGAGGCATTAAGATATTGTATCAT 1500  
DB 1441 TTGGTTTGTATATCAAGGAAAAAGCACTTTCAGGAGGCATTAAGATATTGTATCAT 1500  
QY 1501 AGAGTTTAAGCTGTTTATTTTGGTATTTGTTCAATTTGCTGAAAAACA CTCTTATTC 1560  
DB 1501 AGAGTTTAAGCTGTTTATTTTGGTATTTGTTCAATTTGCTGAAAAACA CTCTTATTC 1560  
QY 1561 AATAAATTCATAGACCTAAATAAACCCTCAACAGGTCCTTTAATAAATTCGCTTCAA 1620  
DB 1561 AATAAATTCATAGACCTAAATAAACCCTCAACAGGTCCTTTAATAAATTCGCTTCAA 1620  
QY 1621 AATAGAA 1627  
DB 1621 AATAGAA 1627

## RESULT 15

US-10-140-002-191

; Sequence 191, Application US/10140002

; Publication No. US20030037623A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C59  
; CURRENT APPLICATION NUMBER: US/10/140,002  
; CURRENT FILING DATE: 2002-05-06  
; Prior Application removed - See Palm or File Wrapper  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 191  
; LENGTH: 1647  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-140-002-191

Query Match 99.9%; Score 1625.4; DB 14; Length 1647;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1626; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCTTCAGCTGAAGAAGAGAGGAATGAAGCGCTTCTGCTTCTGTGTTTGTCTTTATAA 60  
DB 1 GCTTCAGCTGAAGAAGAGAGGAATGAAGCGCTTCTGCTTCTGTGTTTGTCTTTATAA 60  
QY 61 CATTTTCTTCTGCAATTCCTTTAGTCCGGATGACGGAAAAATGAAGAAAATATGCAACTGG 120  
DB 61 CATTTTCTTCTGCAATTCCTTTAGTCCGGATGACGGAAAAATGAAGAAAATATGCAACTGG 120  
QY 121 CTCAGGCATATCTCAACAGTCTTACTCTCTTGAATAGAGGGAATCATCTTGTTCAAA 180  
DB 121 CTCAGGCATATCTCAACAGTCTTACTCTCTTGAATAGAGGGAATCATCTTGTTCAAA 180  
QY 181 GCAAGAAATAGGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTGTGATGA 240  
DB 181 GCAAGAAATAGGAGTCTCATAGATGACAAAATTCGGGAAATGCAAGCATTTTGTGATGA 240  
QY 241 CAGTCACTGGAAAACTGGACTCAAAACCCCTTGAGATCATGAAGACACCCAGGTGTGGGG 300  
DB 241 CAGTCACTGGAAAACTGGACTCAAAACCCCTTGAGATCATGAAGACACCCAGGTGTGGGG 300  
QY 301 TGCCCTGATGTGGCCAGTATGSCCTACACCCCTCCCTGGGTGGAGAAAATACACCTCACCT 360  
DB 301 TGCCCTGATGTGGCCAGTATGSCCTACACCCCTCCCTGGGTGGAGAAAATACACCTCACCT 360  
QY 361 ACAGAAATATAAATACTATCTCCGGATATGGACGAGCTGCTGTGATGAGGCTATCCAAAG 420  
DB 361 ACAGAAATATAAATACTATCTCCGGATATGGACGAGCTGCTGTGATGAGGCTATCCAAAG 420  
QY 421 AAGGTTTGAAGTGTGGAGCAAAAGTCACTCCACTAAAAATTCACCAAGATTTCAAAGGGA 480  
DB 421 AAGGTTTGAAGTGTGGAGCAAAAGTCACTCCACTAAAAATTCACCAAGATTTCAAAGGGA 480  
QY 481 TTGCAGACATCATGATTTGCTTTAGGACTCGAGTCCAGTCCAGTCCCTCTCTCTATTTTG 540  
DB 481 TTGCAGACATCATGATTTGCTTTAGGACTCGAGTCCAGTCCAGTCCCTCTCTCTATTTTG 540  
QY 541 ATGGTCCCTTTGGAGTGTCTTGGCCATGCTTTCCTCTGCTCCGGTCTGGGTGTGACGA 600  
DB 541 ATGGTCCCTTTGGAGTGTCTTGGCCATGCTTTCCTCTCTGCTCCGGTCTGGGTGTGACGA 600  
QY 601 CTCATTTTGAAGGATGAAAACTGGACCAAGGATGGAGGATTCAACTTGTTCCTTG 660  
DB 601 CTCATTTTGAAGGATGAAAACTGGACCAAGGATGGAGGATTCAACTTGTTCCTTG 660  
QY 661 TGGCTGCTCATGAATTTGGTCTATGCACTGGGCTCTCTCACTCCAATGATCAACAGCT 720  
DB 661 TGGCTGCTCATGAATTTGGTCTATGCACTGGGCTCTCTCACTCCAATGATCAACAGCT 720  
QY 721 TGATGTTCCCAATTTATGTCTCTCCCTGGATCCAGAAAAATACCCACTTTTCTCAGGATGATA 780



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 15, 2004, 20:58:11 ; Search time 94 seconds  
(without alignments)  
1930.949 Million cell updates/sec

Title: US-10-729-807-10

Perfect score: 2763

Sequence: 1 MKRLLLCUFIITFSSAFPL.....SLSLFIFGIVHLKNTSIYQ 513

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 segs, 353819137 residues

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/FCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
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13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
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16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US16\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Match | Length | DB ID | Description        |
|------------|-------|-------|--------|-------|--------------------|
| 1          | 2763  | 100.0 | 513    | 10    | US-09-862-631-4    |
| 2          | 2763  | 100.0 | 513    | 16    | US-10-729-807-10   |
| 3          | 2752  | 99.6  | 513    | 10    | US-09-759-1308-173 |
| 4          | 2752  | 99.6  | 513    | 14    | US-10-028-072-192  |
| 5          | 2752  | 99.6  | 513    | 14    | US-10-140-808-192  |
| 6          | 2752  | 99.6  | 513    | 14    | US-10-421-049-192  |
| 7          | 2752  | 99.6  | 513    | 14    | US-10-123-304-192  |
| 8          | 2752  | 99.6  | 513    | 14    | US-10-140-470-192  |
| 9          | 2752  | 99.6  | 513    | 14    | US-10-175-746-192  |
| 10         | 2752  | 99.6  | 513    | 14    | US-10-176-918-192  |
| 11         | 2752  | 99.6  | 513    | 14    | US-10-176-921-192  |
| 12         | 2752  | 99.6  | 513    | 14    | US-10-137-865-192  |
| 13         | 2752  | 99.6  | 513    | 14    | US-10-140-474-192  |

|    |      |      |     |    |                    |                   |
|----|------|------|-----|----|--------------------|-------------------|
| 14 | 2752 | 99.6 | 513 | 14 | US-10-142-431-192  | Sequence 192, App |
| 15 | 2752 | 99.6 | 513 | 14 | US-10-143-114-192  | Sequence 192, App |
| 16 | 2752 | 99.6 | 513 | 14 | US-10-140-002-192  | Sequence 192, App |
| 17 | 2752 | 99.6 | 513 | 14 | US-10-142-419-192  | Sequence 192, App |
| 18 | 2752 | 99.6 | 513 | 14 | US-10-123-262-192  | Sequence 192, App |
| 19 | 2752 | 99.6 | 513 | 14 | US-10-142-423-192  | Sequence 192, App |
| 20 | 2752 | 99.6 | 513 | 14 | US-10-121-050-192  | Sequence 192, App |
| 21 | 2752 | 99.6 | 513 | 14 | US-10-141-755-192  | Sequence 192, App |
| 22 | 2752 | 99.6 | 513 | 14 | US-10-143-032-192  | Sequence 192, App |
| 23 | 2752 | 99.6 | 513 | 14 | US-10-123-108-192  | Sequence 192, App |
| 24 | 2752 | 99.6 | 513 | 14 | US-10-123-236-192  | Sequence 192, App |
| 25 | 2752 | 99.6 | 513 | 14 | US-10-123-261-192  | Sequence 192, App |
| 26 | 2752 | 99.6 | 513 | 14 | US-10-140-921-192  | Sequence 192, App |
| 27 | 2752 | 99.6 | 513 | 14 | US-10-140-928-192  | Sequence 192, App |
| 28 | 2752 | 99.6 | 513 | 14 | US-10-121-045-192  | Sequence 192, App |
| 29 | 2752 | 99.6 | 513 | 14 | US-10-123-903-192  | Sequence 192, App |
| 30 | 2752 | 99.6 | 513 | 14 | US-10-124-819-192  | Sequence 192, App |
| 31 | 2752 | 99.6 | 513 | 14 | US-10-124-825A-192 | Sequence 192, App |
| 32 | 2752 | 99.6 | 513 | 14 | US-10-124-822-192  | Sequence 192, App |
| 33 | 2752 | 99.6 | 513 | 14 | US-10-160-498-192  | Sequence 192, App |
| 34 | 2752 | 99.6 | 513 | 14 | US-10-124-824-192  | Sequence 192, App |
| 35 | 2752 | 99.6 | 513 | 14 | US-10-127-825A-192 | Sequence 192, App |
| 36 | 2752 | 99.6 | 513 | 14 | US-10-127-835A-192 | Sequence 192, App |
| 37 | 2752 | 99.6 | 513 | 14 | US-10-127-839A-192 | Sequence 192, App |
| 38 | 2752 | 99.6 | 513 | 14 | US-10-127-901A-192 | Sequence 192, App |
| 39 | 2752 | 99.6 | 513 | 14 | US-10-128-693A-192 | Sequence 192, App |
| 40 | 2752 | 99.6 | 513 | 14 | US-10-131-813A-192 | Sequence 192, App |
| 41 | 2752 | 99.6 | 513 | 14 | US-10-131-818A-192 | Sequence 192, App |
| 42 | 2752 | 99.6 | 513 | 14 | US-10-131-824A-192 | Sequence 192, App |
| 43 | 2752 | 99.6 | 513 | 14 | US-10-131-824A-192 | Sequence 192, App |
| 44 | 2752 | 99.6 | 513 | 14 | US-10-131-824A-192 | Sequence 192, App |
| 45 | 2752 | 99.6 | 513 | 14 | US-10-131-824A-192 | Sequence 192, App |

#### ALIGNMENTS

RESULT 1  
US-09-862-631-4  
; Sequence 4, Application US/09862631  
; Publication No. US20030032164M1  
; GENERAL INFORMATION:  
; APPLICANT: Holmgren, Erik  
; APPLICANT: Kihlen, Mats  
; APPLICANT: Wood, Tim  
; APPLICANT: Ekblom, Jonas  
; TITLE OF INVENTION: Novel Matrix Metalloproteinases  
; FILE REFERENCE: 00014regus  
; CURRENT APPLICATION NUMBER: US/09/862,631  
; CURRENT FILING DATE: 2000-05-22  
; PRIOR APPLICATION NUMBER: 206119  
; PRIOR FILING DATE: 2000-05-22  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 513  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-862-631-4

|                       |                 |                                                            |           |             |
|-----------------------|-----------------|------------------------------------------------------------|-----------|-------------|
| Query Match           | 100.0%;         | Score 2763;                                                | DB 10;    | Length 513; |
| Best Local Similarity | 100.0%;         | Pred. No. 1.2e-257;                                        |           |             |
| Matches 513;          | Conservative 0; | Mismatches 0;                                              | Indels 0; | Gaps 0;     |
| QY                    | 1               | MKRLLLLCLFFITFSSAPFLVMTENENMQLAQAYLNQFYSLEIEGNHLVQSKNRSLID | 60        |             |
| Db                    | 1               | MKRLLLLCLFFITFSSAPFLVMTENENMQLAQAYLNQFYSLEIEGNHLVQSKNRSLID | 60        |             |
| QY                    | 61              | DKIREMOAFFGLTVTGKLDSTNLEIMKTRCGVDPVGVGYTLPGRWKYNLTVRIINWTP | 120       |             |
| Db                    | 61              | DKIREMOAFFGLTVTGKLDSTNLEIMKTRCGVDPVGVGYTLPGRWKYNLTVRIINWTP | 120       |             |
| QY                    | 121             | DMARAAVDEIAQEGLEVWSKVTLKFTKISKGIADIMIAFRTRVHGRCPRYFDGVLG   | 180       |             |

Db 121 DMARAAVDEAIOEGLEWMSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180  
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Db 181 HAPFPGGLGGDTHFDEENWTKGAGFNLFLVAAHEFGHALGLSHNDOTALMFPNYVS 240  
Qy 241 LDPKPYPLSQDDINGIQSIYGLPKVPAPKPKPTTIPHACDPLDTPDAITTFREVMFFKG 300  
Db 241 LDPKPYPLSQDDINGIQSIYGLPKVPAPKPKPTTIPHACDPLDTPDAITTFREVMFFKG 300  
Qy 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKLVKFDENFWMIRGYAVLPDY 360  
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKLVKFDENFWMIRGYAVLPDY 360  
Qy 361 PKSHTLGPGRVKKIDAAVCDKTRTKTYFFVGIWCRFDEMTQTDKGFQPVVXHPFG 420  
Db 361 PKSHTLGPGRVKKIDAAVCDKTRTKTYFFVGIWCRFDEMTQTDKGFQPVVXHPFG 420  
Qy 421 ISIRVDAAFQYKGFFFSRGSKOFEYNIKTNTIRMTNFWFQCKEPKNSFGFDINKE 480  
Db 421 ISIRVDAAFQYKGFFFSRGSKOFEYNIKTNTIRMTNFWFQCKEPKNSFGFDINKE 480  
Qy 481 KAHSGGKILYHKSLSLFIFGIHVHLKNTSIYQ 513  
Db 481 KAHSGGKILYHKSLSLFIFGIHVHLKNTSIYQ 513

RESULT 2  
US-10-729-807-10  
; Sequence 10, Application US/10729807  
; Publication No. US20040132158A1  
; GENERAL INFORMATION:  
; APPLICANT: BANDMAN, Olga; HILLMAN, Jennifer L.  
; APPLICANT: YUE, Henry; AZIMZAI, Yalda  
; APPLICANT: BAUGHN, Marian R.; LU, Dyoung Aina M.  
; TITLE OF INVENTION: HUMAN PEPTIDASES  
; FILE REFERENCE: PF-0651-1 DIV  
; CURRENT APPLICATION NUMBER: US/10729,807  
; CURRENT FILING DATE: 2003-12-05  
; PRIOR APPLICATION NUMBER: US 09/889,238  
; PRIOR FILING DATE: 2002-01-24  
; PRIOR APPLICATION NUMBER: PCT/US00/00641  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: US 60/172,247  
; PRIOR FILING DATE: 1999-01-11  
; PRIOR APPLICATION NUMBER: US 60/132,253  
; PRIOR FILING DATE: 1999-05-03  
; PRIOR APPLICATION NUMBER: US 60/136,653  
; PRIOR FILING DATE: 1999-05-27  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PERL Program  
; SEQ ID NO 10  
; LENGTH: 513  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: 3772696CD1  
US-10-729-807-10  
Query Match 100.0%; Score 2763; DB 16; Length 513;  
Best Local Similarity 100.0%; Pred. No. 1.2e-257;  
Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKRLLLCLFFTFSSAPFLVMTNEENWQAAVLNPFYSLEIEGHNHLSVQSKNSLID 60  
Db 1 MKRLLLCLFFTFSSAPFLVMTNEENWQAAVLNPFYSLEIEGHNHLSVQSKNSLID 60  
Qy 61 DKIREMQAFGLTVTKGLDSNTLEIMKTPRCGVPDVGQYGYTLPGWRKYNLYRIINYTP 120  
Db 61 DKIREMQAFGLTVTKGLDSNTLEIMKTPRCGVPDVGQYGYTLPGWRKYNLYRIINYTP 120

Qy 121 DMARAAVDEAIOEGLEWMSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180  
Db 121 DMARAAVDEAIOEGLEWMSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180  
Qy 181 HAPFPGGLGGDTHFDEENWTKGAGFNLFLVAAHEFGHALGLSHNDOTALMFPNYVS 240  
Db 181 HAPFPGGLGGDTHFDEENWTKGAGFNLFLVAAHEFGHALGLSHNDOTALMFPNYVS 240  
Qy 241 LDPKPYPLSQDDINGIQSIYGLPKVPAPKPKPTTIPHACDPLDTPDAITTFREVMFFKG 300  
Db 241 LDPKPYPLSQDDINGIQSIYGLPKVPAPKPKPTTIPHACDPLDTPDAITTFREVMFFKG 300  
Qy 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKLVKFDENFWMIRGYAVLPDY 360  
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKLVKFDENFWMIRGYAVLPDY 360  
Qy 361 PKSHTLGPGRVKKIDAAVCDKTRTKTYFFVGIWCRFDEMTQTDKGFQPVVXHPFG 420  
Db 361 PKSHTLGPGRVKKIDAAVCDKTRTKTYFFVGIWCRFDEMTQTDKGFQPVVXHPFG 420  
Qy 421 ISIRVDAAFQYKGFFFSRGSKOFEYNIKTNTIRMTNFWFQCKEPKNSFGFDINKE 480  
Db 421 ISIRVDAAFQYKGFFFSRGSKOFEYNIKTNTIRMTNFWFQCKEPKNSFGFDINKE 480  
Qy 481 KAHSGGKILYHKSLSLFIFGIHVHLKNTSIYQ 513  
Db 481 KAHSGGKILYHKSLSLFIFGIHVHLKNTSIYQ 513

RESULT 3  
US-09-759-130B-173  
; Sequence 173, Application US/09759130B  
; Publication No. US20030022279A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: McCarthy, Sean A  
; APPLICANT: Fraser, Christopher C  
; APPLICANT: Sharp, John D  
; APPLICANT: Barnes, Thomas S  
; APPLICANT: Kfirst, Susan J  
; APPLICANT: Mackay, Charles R  
; APPLICANT: Myers, Paul S  
; APPLICANT: Leiby, Kevin R  
; APPLICANT: Wrighton, Nicolas  
; APPLICANT: Goodearl, Andrew  
; APPLICANT: Holtzman, Douglas A  
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING  
; TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER  
; FILE REFERENCE: MPI00-5350MMIM  
; CURRENT APPLICATION NUMBER: US/09/759,130B  
; CURRENT FILING DATE: 2002-09-16  
; PRIOR APPLICATION NUMBER: US 09/479,249  
; PRIOR FILING DATE: 2000-01-07  
; PRIOR APPLICATION NUMBER: US 09/559,497  
; PRIOR FILING DATE: 2000-04-27  
; PRIOR APPLICATION NUMBER: US 09/578,063  
; PRIOR FILING DATE: 2000-05-24  
; PRIOR APPLICATION NUMBER: US 09/333,159  
; PRIOR FILING DATE: 1999-06-14  
; PRIOR APPLICATION NUMBER: US 09/596,194  
; PRIOR FILING DATE: 2000-07-14  
; PRIOR APPLICATION NUMBER: US 09/342,364  
; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: US 09/608,452  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/393,996  
; PRIOR FILING DATE: 1999-09-10  
; PRIOR APPLICATION NUMBER: US 09/602,871  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 09/420,707  
; PRIOR FILING DATE: 1999-10-19

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; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 173
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-173

Query Match      99.6%; Score 2752; DB 10; Length 513;
Best Local Similarity 99.8%; Pred. No. 1.4e-256;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLILCLPFITSSAFFPLVRMTENENMQLAQYLNQFYSLEIEGNHLVQSKNRLSD 60
Db 1 MKRLILCLPFITSSAFFPLVRMTENENMQLAQYLNQFYSLEIEGNHLVQSKNRLSD 60
QY 61 DKIREMAFFGLTVTGKLSNTLEIMKTGCGVDPDVGQYGTLPGRWKYNTLYRIINYTP 120
Db 61 DKIREMAFFGLTVTGKLSNTLEIMKTGCGVDPDVGQYGTLPGRWKYNTLYRIINYTP 120
QY 121 DMARAAVDEAIQSGLEWWSKVTPFKFTKISKGIADIMAFRTVRVHGRCPRYFDGPGLVLG 180
Db 121 DMARAAVDEAIQSGLEWWSKVTPFKFTKISKGIADIMAFRTVRVHGRCPRYFDGPGLVLG 180
QY 181 HAPPGPGGLGGDTHFDEDENTWTKDAGFNLFLVAHHEFGHALGSHSNDQTALMFPNYVS 240
Db 181 HAPPGPGGLGGDTHFDEDENTWTKDAGFNLFLVAHHEFGHALGSHSNDQTALMFPNYVS 240
QY 241 LDPKPYLSQDDINGLQSIYGGLPKVPKAPKEPTIPHACDPDLTFDAITTFREVMFFKG 300
Db 241 LDPKPYLSQDDINGLQSIYGGLPKVPKAPKEPTIPHACDPDLTFDAITTFREVMFFKG 300
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAVENPRDKILVFKDENFWMIIRGYAVLPDY 360
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAVENPRDKILVFKDENFWMIIRGYAVLPDY 360
QY 361 PKSIHTLGGPGVKKIDAAVCDKTRTKTYFFVGICWCRFDEMTQTMKGFQQRVVKHFFG 420
Db 361 PKSIHTLGGPGVKKIDAAVCDKTRTKTYFFVGICWCRFDEMTQTMKGFQQRVVKHFFG 420
QY 421 ISIRVDAAFQYKGFFFSFGSKQFENYIKNTKTRIMRTNTWFOCKEPKNSFGFDINKE 480
Db 421 ISIRVDAAFQYKGFFFSFGSKQFENYIKNTKTRIMRTNTWFOCKEPKNSFGFDINKE 480
QY 481 KAHSGGKILYHKLSLFTFGIVHLLKNTSIYQ 513
Db 481 KAHSGGKILYHKLSLFTFGIVHLLKNTSIYQ 513

RESULT 4
US-10-028-072-192
; Sequence 192, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028.072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059836
; PRIOR FILING DATE: 1997-09-24
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062285
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/062814
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/062816
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063045
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063082
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/063127
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063327
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063329
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063550
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063561
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063704
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063733
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063735
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063738
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063755
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064248
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/064809
; PRIOR FILING DATE: 1997-11-07
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065846
; PRIOR FILING DATE: 1997-11-17
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066453
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066511
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066770
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;; PRIOR APPLICATION NUMBER: 60/088730  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088741  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088810  
;; PRIOR FILING DATE: 1998-06-10  
;; PRIOR APPLICATION NUMBER: 60/088858  
;; PRIOR FILING DATE: 19/98-06-11  
;; PRIOR APPLICATION NUMBER: 60/089532  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089599  
;; PRIOR FILING DATE: 1998-06-17  
;; PRIOR APPLICATION NUMBER: 60/089907  
;; PRIOR FILING DATE: 1998-06-18  
;; PRIOR APPLICATION NUMBER: 60/089947  
;; PRIOR FILING DATE: 1998-06-19  
;; PRIOR APPLICATION NUMBER: 60/090349  
;; PRIOR FILING DATE: 1998-06-23  
;; PRIOR APPLICATION NUMBER: 60/090429  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090445  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090538  
;; PRIOR FILING DATE: 1998-06-24  
;; PRIOR APPLICATION NUMBER: 60/090863  
;; PRIOR FILING DATE: 1998-06-26  
;; PRIOR APPLICATION NUMBER: 60/091360  
;; PRIOR FILING DATE: 1998-07-01  
;; PRIOR APPLICATION NUMBER: 60/091519  
;; PRIOR FILING DATE: 1998-07-02  
;; PRIOR APPLICATION NUMBER: 60/091982  
;; PRIOR FILING DATE: 1998-07-07  
Query Match 99.6%; Score 2752; DB 14; Length 513;  
Best Local Similarity 99.8%; Pred. No. 1.4e-256;  
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MKRLLLLCLFFITPSSAPPLVRMTENEENMOLAQAYLNQFYSLEIEGHLVQSKNRSLLD 60  
Db 1 MKRLLLLFLFFITPSSAPPLVRMTENEENMOLAQAYLNQFYSLEIEGHLVQSKNRSLLD 60  
Qy 61 DKIREMQAFFGLTGTGKLDSTNLEIMKTGCGVDPVGGYGLTLCGRKYNLTIRLINTP 120  
Db 61 DKIREMQAFFGLTGTGKLDSTNLEIMKTGCGVDPVGGYGLTLCGRKYNLTIRLINTP 120  
Qy 121 DMARAANDDEALTOEGLEVWSKVTLKFTKISKGIAIMIAFRTVHGRCPRYFDGFLGVLG 180  
Db 121 DMARAANDDEALTOEGLEVWSKVTLKFTKISKGIAIMIAFRTVHGRCPRYFDGFLGVLG 180  
Qy 181 HAFPPGPGGLGGDTHEDEENMTKOGAGFNLFLVAAHEFGHALGLSHSNDQTALMFPNYS 240  
Db 181 HAFPPGPGGLGGDTHEDEENMTKOGAGFNLFLVAAHEFGHALGLSHSNDQTALMFPNYS 240  
Qy 241 LDPRKYPISQDDINGIQSIYGLPKVPAPKPEPTIPHACDPLTDALITTFREVMFFKG 300  
Db 241 LDPRKYPISQDDINGIQSIYGLPKVPAPKPEPTIPHACDPLTDALITTFREVMFFKG 300  
Qy 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360  
Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360  
Qy 361 PKSIIHTLGPFGGRVKXIDAAVCDKTKTKTYFFVGICWWRDEMTQTMKDGFPQVRVKKHFG 420  
Db 361 PKSIIHTLGPFGGRVKXIDAAVCDKTKTKTYFFVGICWWRDEMTQTMKDGFPQVRVKKHFG 420  
Qy 421 ISIRVDAAFOYKGFPPFFSRGSKQFENIKTKNITRIMRTNTWFOCKEPKNSSGFGDINKE 480  
Db 421 ISIRVDAAFOYKGFPPFFSRGSKQFENIKTKNITRIMRTNTWFOCKEPKNSSGFGDINKE 480  
Qy 481 KAHSGGKILYKHSLSLFFIGIVHLLKNTSIYQ 513  
Db 481 KAHSGGKILYKHSLSLFFIGIVHLLKNTSIYQ 513

;; PRIOR FILING DATE: 1997-11-24  
;; PRIOR APPLICATION NUMBER: 60/069212  
;; PRIOR FILING DATE: 1997-12-11  
;; PRIOR APPLICATION NUMBER: 60/069278  
;; PRIOR FILING DATE: 1997-12-11  
;; PRIOR APPLICATION NUMBER: 60/069334  
;; PRIOR FILING DATE: 1997-12-11  
;; PRIOR APPLICATION NUMBER: 60/069694  
;; PRIOR FILING DATE: 1997-12-16  
;; PRIOR APPLICATION NUMBER: 60/072320  
;; PRIOR FILING DATE: 1998-01-23  
;; PRIOR APPLICATION NUMBER: 60/073612  
;; PRIOR FILING DATE: 1998-02-04  
;; PRIOR APPLICATION NUMBER: 60/074086  
;; PRIOR FILING DATE: 1998-02-09  
;; PRIOR APPLICATION NUMBER: 60/074092  
;; PRIOR FILING DATE: 1998-02-09  
;; PRIOR APPLICATION NUMBER: 60/077791  
;; PRIOR FILING DATE: 1998-03-12  
;; PRIOR APPLICATION NUMBER: 60/078910  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/079294  
;; PRIOR FILING DATE: 1998-03-25  
;; PRIOR APPLICATION NUMBER: 60/079663  
;; PRIOR FILING DATE: 1998-02-27  
;; PRIOR APPLICATION NUMBER: 60/079728  
;; PRIOR FILING DATE: 1998-03-27  
;; PRIOR APPLICATION NUMBER: 60/080165  
;; PRIOR FILING DATE: 1998-03-31  
;; PRIOR APPLICATION NUMBER: 60/081203  
;; PRIOR FILING DATE: 1998-04-09  
;; PRIOR APPLICATION NUMBER: 60/081229  
;; PRIOR FILING DATE: 1998-04-09  
;; PRIOR APPLICATION NUMBER: 60/081695  
;; PRIOR FILING DATE: 1998-04-14  
;; PRIOR APPLICATION NUMBER: 60/081817  
;; PRIOR FILING DATE: 1998-04-15  
;; PRIOR APPLICATION NUMBER: 60/081818  
;; PRIOR FILING DATE: 1998-04-15  
;; PRIOR APPLICATION NUMBER: 60/082999  
;; PRIOR FILING DATE: 1998-04-24  
;; PRIOR APPLICATION NUMBER: 60/083322  
;; PRIOR FILING DATE: 1998-04-28  
;; PRIOR APPLICATION NUMBER: 60/083545  
;; PRIOR FILING DATE: 1998-04-29  
;; PRIOR APPLICATION NUMBER: 60/084600  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084627  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/084637  
;; PRIOR FILING DATE: 1998-05-07  
;; PRIOR APPLICATION NUMBER: 60/085149  
;; PRIOR FILING DATE: 1998-05-12  
;; PRIOR APPLICATION NUMBER: 60/085323  
;; PRIOR FILING DATE: 1998-05-13  
;; PRIOR APPLICATION NUMBER: 60/085338  
;; PRIOR FILING DATE: 1998-05-13  
;; PRIOR APPLICATION NUMBER: 60/085339  
;; PRIOR FILING DATE: 1998-05-13  
;; PRIOR APPLICATION NUMBER: 60/085579  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/086414  
;; PRIOR FILING DATE: 1998-05-22  
;; PRIOR APPLICATION NUMBER: 60/086430  
;; PRIOR FILING DATE: 1998-05-22  
;; PRIOR APPLICATION NUMBER: 60/087106  
;; PRIOR FILING DATE: 1998-05-28  
;; PRIOR APPLICATION NUMBER: 60/088026  
;; PRIOR FILING DATE: 1998-06-04

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RESULT 5
US-10-140-808-192
; Sequence 192, Application US/10140808
; Publication No. US20030017563A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/140,808
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-808-192

Query Match
Best Local Similarity 99.8%; Score 2752; DB 14; Length 513;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLLCLFFITFSAPFLVMTENEENMQLAQAYLNQFYSLEIEGHNHLVQSKNRLSD 60
DB 1 MKRLLLLCLFFITFSAPFLVMTENEENMQLAQAYLNQFYSLEIEGHNHLVQSKNRLSD 60
QY 61 DKIREMQAFFGLTVTGKLDNSTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINYP 120
DB 61 DKIREMQAFFGLTVTGKLDNSTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINYP 120
QY 121 DMARAANDVAIOEGLEVMSKVTPKFTKISGIADIMIAFRTRVHGRCPRYFDGPIGLVG 180
DB 121 DMARAANDVAIOEGLEVMSKVTPKFTKISGIADIMIAFRTRVHGRCPRYFDGPIGLVG 180
QY 181 HAPPPGGLGGDTHDEENWTKDGENNLFVAHAHEFGHALGLSHSNDQTALMFPNYS 240
DB 181 HAPPPGGLGGDTHDEENWTKDGENNLFVAHAHEFGHALGLSHSNDQTALMFPNYS 240
QY 241 LDPRKYPISQDDINGIQSIYGLPKVPKPKPTIIPACDPDLTDAITTTFRREVMFPKG 300
DB 241 LDPRKYPISQDDINGIQSIYGLPKVPKPKPTIIPACDPDLTDAITTTFRREVMFPKG 300
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFDENFWMIRGYAVLPDY 360
DB 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFDENFWMIRGYAVLPDY 360
QY 361 PKSIHTLGFGRVKKIDAAVCDKTRTKTYFFVGIWCFWRFDEMTQMDKGFQVRVVKHFP 420
DB 361 PKSIHTLGFGRVKKIDAAVCDKTRTKTYFFVGIWCFWRFDEMTQMDKGFQVRVVKHFP 420
QY 421 ISIRVDAAFQYKGFPPFSRGSQFQYNIKTNIITRIMTNTWFOCKEPKNSFFGFINKE 480
DB 421 ISIRVDAAFQYKGFPPFSRGSQFQYNIKTNIITRIMTNTWFOCKEPKNSFFGFINKE 480
QY 481 KAHSGGIKILYHKSLSLFIIGIVHLKNTSIYQ 513

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DB 481 KAHSGGIKILYHKSLSLFIIGIVHLKNTSIYQ 513

RESULT 6
US-10-121-049-192
; Sequence 192, Application US/10121049
; Publication No. US20030022239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-121-049-192

```

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Query Match
Best Local Similarity 99.6%; Score 2752; DB 14; Length 513;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLLCLFFITFSAPFLVMTENEENMQLAQAYLNQFYSLEIEGHNHLVQSKNRLSD 60
DB 1 MKRLLLLCLFFITFSAPFLVMTENEENMQLAQAYLNQFYSLEIEGHNHLVQSKNRLSD 60
QY 61 DKIREMQAFFGLTVTGKLDNSTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINYP 120
DB 61 DKIREMQAFFGLTVTGKLDNSTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINYP 120
QY 121 DMARAANDVAIOEGLEVMSKVTPKFTKISGIADIMIAFRTRVHGRCPRYFDGPIGLVG 180
DB 121 DMARAANDVAIOEGLEVMSKVTPKFTKISGIADIMIAFRTRVHGRCPRYFDGPIGLVG 180
QY 181 HAPPPGGLGGDTHDEENWTKDGENNLFVAHAHEFGHALGLSHSNDQTALMFPNYS 240
DB 181 HAPPPGGLGGDTHDEENWTKDGENNLFVAHAHEFGHALGLSHSNDQTALMFPNYS 240
QY 241 LDPRKYPISQDDINGIQSIYGLPKVPKPKPTIIPACDPDLTDAITTTFRREVMFPKG 300
DB 241 LDPRKYPISQDDINGIQSIYGLPKVPKPKPTIIPACDPDLTDAITTTFRREVMFPKG 300
QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFDENFWMIRGYAVLPDY 360
DB 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFDENFWMIRGYAVLPDY 360
QY 361 PKSIHTLGFGRVKKIDAAVCDKTRTKTYFFVGIWCFWRFDEMTQMDKGFQVRVVKHFP 420
DB 361 PKSIHTLGFGRVKKIDAAVCDKTRTKTYFFVGIWCFWRFDEMTQMDKGFQVRVVKHFP 420
QY 421 ISIRVDAAFQYKGFPPFSRGSQFQYNIKTNIITRIMTNTWFOCKEPKNSFFGFINKE 480

```



Db 421 ISIRVDAAPQYKGFPPFSRSGSKQFEYNIKNTIRMTNTWFOCKEPKNSFGPDINKE 480  
 QY 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513  
 Db 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513

RESULT 7

US-10-123-904-192  
 ; Sequence 192, Application US/10123904  
 ; Publication No. US20030022328A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: Deforge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Goddard, Paul J.  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3330R1C54  
 ; CURRENT APPLICATION NUMBER: US/10/123,904  
 ; CURRENT FILING DATE: 2002-04-16  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 192  
 ; LENGTH: 513  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-123-904-192

Query Match 99.6%; Score 2752; DB 14; Length 513;  
 Best Local Similarity 99.8%; Pred. No. 1.4e-256;  
 Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLCLFFITFSSAPFLVRMTENEENMQLAQAYLNQFYSLEIEGHNHLSVQSKNRSLLID 60  
 Db 1 MKRLLLCLFFITFSSAPFLVRMTENEENMQLAQAYLNQFYSLEIEGHNHLSVQSKNRSLLID 60  
 QY 61 DKIREMQAFGLTVTGKLSNTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINYP 120  
 Db 61 DKIREMQAFGLTVTGKLSNTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINYP 120  
 QY 121 DMARAADVAIIOEGLEVMSKVTPKFTKISKGIADIMIAFRTRVHRCRCRYFDGPGVLG 180  
 Db 121 DMARAADVAIIOEGLEVMSKVTPKFTKISKGIADIMIAFRTRVHRCRCRYFDGPGVLG 180  
 QY 181 HAPPPGPGGGDTHFDEENWTKDAGFNLFLVAAHEFGHALGSHNSNDQTALMFNPNYS 240  
 Db 181 HAPPPGPGGGDTHFDEENWTKDAGFNLFLVAAHEFGHALGSHNSNDQTALMFNPNYS 240  
 QY 241 LDPKPYLSQDDINGIQSIYGGIIPKVPAPKPKPTIPHACDPLTDFDAITTFREVMFFKG 300  
 Db 241 LDPKPYLSQDDINGIQSIYGGIIPKVPAPKPKPTIPHACDPLTDFDAITTFREVMFFKG 300  
 QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360  
 Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360  
 QY 361 PKSIHTLGFGRVKKIDAAVCDDKTRTKTYFVGIWCRFDEMTQTDKGPQVRVXHFPG 420  
 Db 361 PKSIHTLGFGRVKKIDAAVCDDKTRTKTYFVGIWCRFDEMTQTDKGPQVRVXHFPG 420

QY 421 ISIRVDAAPQYKGFPPFSRSGSKQFEYNIKNTIRMTNTWFOCKEPKNSFGPDINKE 480  
 Db 421 ISIRVDAAPQYKGFPPFSRSGSKQFEYNIKNTIRMTNTWFOCKEPKNSFGPDINKE 480  
 QY 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513  
 Db 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513

RESULT 8

US-10-140-470-192  
 ; Sequence 192, Application US/10140470  
 ; Publication No. US20030022331A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: Deforge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3330R1C160  
 ; CURRENT APPLICATION NUMBER: US/10/140,470  
 ; CURRENT FILING DATE: 2002-05-06  
 ; Prior Application removed - See Palm or File Wrapper  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 192  
 ; LENGTH: 513  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 US-10-140-470-192

Query Match 99.6%; Score 2752; DB 14; Length 513;  
 Best Local Similarity 99.8%; Pred. No. 1.4e-256;  
 Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLCLFFITFSSAPFLVRMTENEENMQLAQAYLNQFYSLEIEGHNHLSVQSKNRSLLID 60  
 Db 1 MKRLLLCLFFITFSSAPFLVRMTENEENMQLAQAYLNQFYSLEIEGHNHLSVQSKNRSLLID 60  
 QY 61 DKIREMQAFGLTVTGKLSNTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINYP 120  
 Db 61 DKIREMQAFGLTVTGKLSNTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINYP 120  
 QY 121 DMARAADVAIIOEGLEVMSKVTPKFTKISKGIADIMIAFRTRVHRCRCRYFDGPGVLG 180  
 Db 121 DMARAADVAIIOEGLEVMSKVTPKFTKISKGIADIMIAFRTRVHRCRCRYFDGPGVLG 180  
 QY 181 HAPPPGPGGGDTHFDEENWTKDAGFNLFLVAAHEFGHALGSHNSNDQTALMFNPNYS 240  
 Db 181 HAPPPGPGGGDTHFDEENWTKDAGFNLFLVAAHEFGHALGSHNSNDQTALMFNPNYS 240  
 QY 241 LDPKPYLSQDDINGIQSIYGGIIPKVPAPKPKPTIPHACDPLTDFDAITTFREVMFFKG 300  
 Db 241 LDPKPYLSQDDINGIQSIYGGIIPKVPAPKPKPTIPHACDPLTDFDAITTFREVMFFKG 300  
 QY 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360  
 Db 301 RHLWRIYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360

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QY 361 PKSIHTLGFGRVKKIDAAVCDKTRTKTYFFVGIWCRFDEMTQTMKGFPQRRVVKHFP 420
Db 361 PKSIHTLGFGRVKKIDAAVCDKTRTKTYFFVGIWCRFDEMTQTMKGFPQRRVVKHFP 420
QY 421 ISIRVDAAFQYKGFPPFSRSGSKQFEYNIKNTNTRIMRTNTWFOCKEPPKNSFGFDINKE 480
Db 421 ISIRVDAAFQYKGFPPFSRSGSKQFEYNIKNTNTRIMRTNTWFOCKEPPKNSFGFDINKE 480
QY 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513
Db 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513

RESULT 9
US-10-175-746-192
; Sequence 192, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-192

Query Match 99.6%; Score 2752; DB 14; Length 513;
Best Local Similarity 99.8%; Pred. No. 1.4e-256;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLLCFFITFSAPPLVMTNEENMQLAQAYLNQFYSLEIEGHNHLSVQSKNSRLID 60
Db 1 MKRLLLLCFFITFSAPPLVMTNEENMQLAQAYLNQFYSLEIEGHNHLSVQSKNSRLID 60
QY 61 DKIREMQAFFGLTVTGKLDNTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINYP 120
Db 61 DKIREMQAFFGLTVTGKLDNTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINYP 120
QY 121 DMARAANDBAIQEGLEVMSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180
Db 121 DMARAANDBAIQEGLEVMSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180
QY 181 HAPPPGGLGGTHFDEDEENWKDGAGFNLFLVAHFHGHALGSLHNSNDQTALMPFNYS 240
Db 181 HAPPPGGLGGTHFDEDEENWKDGAGFNLFLVAHFHGHALGSLHNSNDQTALMPFNYS 240
QY 241 LDPRKYPISQDDINGIQSIYGLGLPKVPKPKPTPIPHACDPLTDAITTFRRVWVFPKG 300
Db 241 LDPRKYPISQDDINGIQSIYGLGLPKVPKPKPTPIPHACDPLTDAITTFRRVWVFPKG 300
QY 301 RHLWRIYYDITDVEFELIASFWPSLPADLQAAYENPRDKILVFKDENFWMIRGVAVLDPY 360

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Db 301 RHLWRIYYDITDVEFELIASFWPSLPADLQAAYENPRDKILVFKDENFWMIRGVAVLDPY 360
QY 361 PKSIHTLGFGRVKKIDAAVCDKTRTKTYFFVGIWCRFDEMTQTMKGFPQRRVVKHFP 420
Db 361 PKSIHTLGFGRVKKIDAAVCDKTRTKTYFFVGIWCRFDEMTQTMKGFPQRRVVKHFP 420
QY 421 ISIRVDAAFQYKGFPPFSRSGSKQFEYNIKNTNTRIMRTNTWFOCKEPPKNSFGFDINKE 480
Db 421 ISIRVDAAFQYKGFPPFSRSGSKQFEYNIKNTNTRIMRTNTWFOCKEPPKNSFGFDINKE 480
QY 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513
Db 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513

```

```

RESULT 10
US-10-176-918-192
; Sequence 192, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-918-192

```

```

Query Match 99.6%; Score 2752; DB 14; Length 513;
Best Local Similarity 99.8%; Pred. No. 1.4e-256;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLLLLCFFITFSAPPLVMTNEENMQLAQAYLNQFYSLEIEGHNHLSVQSKNSRLID 60
Db 1 MKRLLLLCFFITFSAPPLVMTNEENMQLAQAYLNQFYSLEIEGHNHLSVQSKNSRLID 60
QY 61 DKIREMQAFFGLTVTGKLDNTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINYP 120
Db 61 DKIREMQAFFGLTVTGKLDNTLEIMKTPRCGVPDVGQGYTLPGWRKYNLTIRIINYP 120
QY 121 DMARAANDBAIQEGLEVMSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180
Db 121 DMARAANDBAIQEGLEVMSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPGVLG 180
QY 181 HAPPPGGLGGTHFDEDEENWKDGAGFNLFLVAHFHGHALGSLHNSNDQTALMPFNYS 240
Db 181 HAPPPGGLGGTHFDEDEENWKDGAGFNLFLVAHFHGHALGSLHNSNDQTALMPFNYS 240
QY 241 LDPRKYPISQDDINGIQSIYGLGLPKVPKPKPTPIPHACDPLTDAITTFRRVWVFPKG 300

```

Db241LDRPKYPLSODDINGIQSIYGGPLPKVPAPKEPTIPHACDPDLTDFDAITTRREVMPFKG300

QY301RHLWRIYYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVPKDFNFWMIRGYAVLPDY360

Db301RHLWRIYYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVPKDFNFWMIRGYAVLPDY360

QY361PKSIHTLGFGRVKKIDAAVCDKTRKTYFFVGIWCVWFDEMOTQMDKGFPPQVVKHFFPG420

Db361PKSIHTLGFGRVKKIDAAVCDKTRKTYFFVGIWCVWFDEMOTQMDKGFPPQVVKHFFPG420

QY421ISRVDAAFOYKGGFFFSRSGSKOPEYNIKTNITRIMRTNTWFOCKEPKNSFFGFDINKE480

Db421ISRVDAAFOYKGGFFFSRSGSKOPEYNIKTNITRIMRTNTWFOCKEPKNSFFGFDINKE480

QY481KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ513

Db481KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ513

RESULT 12

US-10-137-865-192

; Sequence 192, Application US/10137865

; Publication No. US20030032155A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330RLC154

; CURRENT APPLICATION NUMBER: US/10/137,865

; CURRENT FILING DATE: 2002-05-03

; Prior Application removed - See Palm or File Wrapper

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 192

; LENGTH: 513

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-137-865-192

Query Match99.6%; Score 2752; DB 14; Length 513;

Best Local Similarity99.8%; Pred. No. 1.4e-256;

Matches 512; Conservative0; Mismatches1; Indels0; Gaps0;

QY1MKRLLLLCIFFITFSAPFLVMTENEENMQLAQAYLNQFYSLEIEGHNHLSVQSKRSLID60

Db1MKRLLLLCIFFITFSAPFLVMTENEENMQLAQAYLNQFYSLEIEGHNHLSVQSKRSLID60

QY61DKIREMAQAFGLTVTKGLDSNTLEIMTKTPRCGVPDVGQGYTLPGWRKKNLYRIINYP120

Db61DKIREMAQAFGLTVTKGLDSNTLEIMTKTPRCGVPDVGQGYTLPGWRKKNLYRIINYP120

QY121DMARAADVAIOEGLEWVSKVTPFKTKISKGIADIMIAFRTRVHGRCPCRYFDGPGVLG180

Db121DMARAADVAIOEGLEWVSKVTPFKTKISKGIADIMIAFRTRVHGRCPCRYFDGPGVLG180

Db241LDRPKYPLSODDINGIQSIYGGPLPKVPAPKEPTIPHACDPDLTDFDAITTRREVMPFKG300

QY301RHLWRIYYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVPKDFNFWMIRGYAVLPDY360

Db301RHLWRIYYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVPKDFNFWMIRGYAVLPDY360

QY361PKSIHTLGFGRVKKIDAAVCDKTRKTYFFVGIWCVWFDEMOTQMDKGFPPQVVKHFFPG420

Db361PKSIHTLGFGRVKKIDAAVCDKTRKTYFFVGIWCVWFDEMOTQMDKGFPPQVVKHFFPG420

QY421ISRVDAAFOYKGGFFFSRSGSKOPEYNIKTNITRIMRTNTWFOCKEPKNSFFGFDINKE480

Db421ISRVDAAFOYKGGFFFSRSGSKOPEYNIKTNITRIMRTNTWFOCKEPKNSFFGFDINKE480

QY481KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ513

Db481KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ513

RESULT 11

US-10-176-921-192

; Sequence 192, Application US/10176921

; Publication No. US20030027276A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Sherwood, Steven

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K

; APPLICANT: Wood, William

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3330RLC288

; CURRENT APPLICATION NUMBER: US/10/176,921

; CURRENT FILING DATE: 2002-06-20

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 550

; SEQ ID NO 192

; LENGTH: 513

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-176-921-192

Query Match99.6%; Score 2752; DB 14; Length 513;

Best Local Similarity99.8%; Pred. No. 1.4e-256;

Matches 512; Conservative0; Mismatches1; Indels0; Gaps0;

QY1MKRLLLLCIFFITFSAPFLVMTENEENMQLAQAYLNQFYSLEIEGHNHLSVQSKRSLID60

Db1MKRLLLLCIFFITFSAPFLVMTENEENMQLAQAYLNQFYSLEIEGHNHLSVQSKRSLID60

QY61DKIREMAQAFGLTVTKGLDSNTLEIMTKTPRCGVPDVGQGYTLPGWRKKNLYRIINYP120

Db61DKIREMAQAFGLTVTKGLDSNTLEIMTKTPRCGVPDVGQGYTLPGWRKKNLYRIINYP120

QY121DMARAADVAIOEGLEWVSKVTPFKTKISKGIADIMIAFRTRVHGRCPCRYFDGPGVLG180

Db121DMARAADVAIOEGLEWVSKVTPFKTKISKGIADIMIAFRTRVHGRCPCRYFDGPGVLG180

QY181HAFFPPGPGGGDTHFDEDENTWKDAGFNLFLVAAHEFGHALGSLHSDQTALMFPNYS240

Db181HAFFPPGPGGGDTHFDEDENTWKDAGFNLFLVAAHEFGHALGSLHSDQTALMFPNYS240



```

Db 61 DKIREMOAFTGLVTGKLDNTLEIMKTPRCGVDVGQYGYTLFGWRKYNLTYYRIINYP 120
QY 121 DMARAAVDEAIQEGLEWVSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPLVIG 180
Db 121 DMARAAVDEAIQEGLEWVSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPLVIG 180
QY 181 HAFPPGGLGDDTHFDEENWTKDAGFNLFLVAAHEFGHALGLSHSNDQTALMFPNYS 240
Db 181 HAFPPGGLGDDTHFDEENWTKDAGFNLFLVAAHEFGHALGLSHSNDQTALMFPNYS 240
QY 241 LDPKPYLSODDINGIOSIYGGIPLKVPKAPKEPTIPHACDPDLTDFDAITTFREVMFPKG 300
Db 241 LDPKPYLSODDINGIOSIYGGIPLKVPKAPKEPTIPHACDPDLTDFDAITTFREVMFPKG 300
QY 301 RHLWRIYYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360
Db 301 RHLWRIYYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360
QY 361 PKSIIHTLGFPPGRVKKIDAAVCDKTRTKTYFFVGIWCMRFDGMTQMDKGFPPQVVKHFP 420
Db 361 PKSIIHTLGFPPGRVKKIDAAVCDKTRTKTYFFVGIWCMRFDGMTQMDKGFPPQVVKHFP 420
QY 421 ISIRVDAAFQYKGFPPFSRGSQOFENIKTKNITRIMRTNTWFOCKEPKNSSGFDINKE 480
Db 421 ISIRVDAAFQYKGFPPFSRGSQOFENIKTKNITRIMRTNTWFOCKEPKNSSGFDINKE 480
QY 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513
Db 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513

```

## RESULT 15

```

US-10-143-114-192
; Sequence 192, Application US/10143114
; Publication No. US20030036180A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C211
; CURRENT APPLICATION NUMBER: US/10/143,114
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 192
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-143-114-192

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Query Match 99.6%; Score 2752; DB 14; Length 513;
Best Local Similarity 99.8%; Fred. No. 1.4e-256;
Matches 512; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKRLLLCLEFFITSSAPPLVRMTENENMQLAQAYLNQFYSLIEGHNHLVQSKNRLID 60
Db 1 MKRLLLCLEFFITSSAPPLVRMTENENMQLAQAYLNQFYSLIEGHNHLVQSKNRLID 60

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QY 61 DKIREMOAFTGLVTGKLDNTLEIMKTPRCGVDVGQYGYTLFGWRKYNLTYYRIINYP 120
Db 61 DKIREMOAFTGLVTGKLDNTLEIMKTPRCGVDVGQYGYTLFGWRKYNLTYYRIINYP 120
QY 121 DMARAAVDEAIQEGLEWVSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPLVIG 180
Db 121 DMARAAVDEAIQEGLEWVSKVTPKFTKISKGIADIMIAFRTRVHGRCPRYFDGPLVIG 180
QY 181 HAFPPGGLGDDTHFDEENWTKDAGFNLFLVAAHEFGHALGLSHSNDQTALMFPNYS 240
Db 181 HAFPPGGLGDDTHFDEENWTKDAGFNLFLVAAHEFGHALGLSHSNDQTALMFPNYS 240
QY 241 LDPKPYLSODDINGIOSIYGGIPLKVPKAPKEPTIPHACDPDLTDFDAITTFREVMFPKG 300
Db 241 LDPKPYLSODDINGIOSIYGGIPLKVPKAPKEPTIPHACDPDLTDFDAITTFREVMFPKG 300
QY 301 RHLWRIYYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360
Db 301 RHLWRIYYDITDVEFELIASFWPSLPADLQAAAYENPRDKILVFKDENFWMIRGYAVLPDY 360
QY 361 PKSIIHTLGFPPGRVKKIDAAVCDKTRTKTYFFVGIWCMRFDGMTQMDKGFPPQVVKHFP 420
Db 361 PKSIIHTLGFPPGRVKKIDAAVCDKTRTKTYFFVGIWCMRFDGMTQMDKGFPPQVVKHFP 420
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Db 421 ISIRVDAAFQYKGFPPFSRGSQOFENIKTKNITRIMRTNTWFOCKEPKNSSGFDINKE 480
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Db 481 KAHSGGKILYHKSLSLFIFGIVHLLKNTSIYQ 513

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Search completed: November 15, 2004, 21:04:04  
Job time : 95 secs